

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:37:10 ; Search time 217.64 Seconds  
(without alignments)  
19.136 Million cell updates/sec

Title: US-09-713-136-1

Perfect score: 22

Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2.6/ptodata/1/lna/5A-COMB.seq.\*  
2: /cgn2.6/ptodata/1/lna/5B-COMB.seq.\*  
3: /cgn2.6/ptodata/1/lna/5A-COMB.seq.\*  
4: /cgn2.6/ptodata/1/lna/6B-COMB.seq.\*  
5: /cgn2.6/ptodata/1/lna/PCTUS-COMB.seq.\*  
6: /cgn2.6/ptodata/1/lna/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	92.7	22	4	US-09-092-314-2
2	18.8	85.5	22	4	US-09-092-314-1
3	18.8	85.5	22	4	US-09-092-314-3
4	18.8	85.5	22	4	US-09-092-314-10
5	17.2	78.2	22	4	US-09-092-314-4
6	15.6	70.9	22	4	US-09-092-314-5
7	15.6	70.9	22	4	US-09-092-314-7
8	15.6	70.9	22	4	US-09-092-314-8
9	15.6	70.9	1418	1	US-08-391-615-7
10	15.6	70.9	1830	4	US-09-019-931-2
11	15.6	70.9	2505	1	US-08-391-615-1
12	15.6	70.9	6909	2	US-08-804-196-1
13	15.6	70.9	6909	3	US-08-658-340-1
14	15.6	70.9	6909	2	US-08-746-111-26
15	15.2	69.1	1892	2	US-08-933-750C-66
16	15.2	69.1	1892	3	US-09-234-613-66
17	15.2	69.1	6638	2	US-08-070-301-2
18	14.8	67.3	882	1	US-08-622-354-4
19	14.6	66.4	404	4	US-09-060-756-303
20	14.6	66.4	913	2	US-08-975-316-61
21	14.6	66.4	1532	3	US-09-118-324-1
22	14.6	66.4	1614	4	US-09-046-894-29
23	14.6	66.4	2694	3	US-08-975-703-5
24	14.6	66.4	2694	4	US-09-515-884-5
25	14.6	66.4	5408	1	US-08-471-058-20
26	14.6	66.4	5408	1	US-08-471-057-20
27	14.2	64.5	864	4	US-08-998-416-297

Sequence 7, Appl1  
Sequence 17, Appl1  
Sequence 58, Appl1  
Sequence 258, Appl1  
Sequence 22, Appl1  
Sequence 22, Appl1  
Sequence 22, Appl1  
Sequence 22, Appl1  
Sequence 22, Appl1  
Sequence 10, Appl1  
Sequence 10, Appl1  
Sequence 22, Appl1  
Sequence 2, Appl1  
Sequence 2, Appl1  
Sequence 1, Appl1  
Sequence 1, Appl1  
Sequence 5, Appl1

28 14.2 64.5 1166 1 US-08-121-063-7  
29 14.2 64.5 176373 3 US-09-128-155-17  
30 14 63.6 77 1 US-08-399-412A-58  
31 14 63.6 95 5 PCT-US96-09455A-258  
32 14 63.6 657 2 US-08-479-733A-22  
33 14 63.6 657 3 US-08-487-427-22  
34 14 63.6 657 3 US-08-479-727A-22  
35 14 63.6 657 3 US-08-482-369A-22  
36 14 63.6 657 3 US-09-009-217-10  
37 14 63.6 657 3 US-09-009-656-10  
38 14 63.6 657 5 PCT-US95-07439-22  
39 14 63.6 672 1 US-07-816-679A-2  
40 14 63.6 672 5 PCT-US92-11270-2  
41 14 63.6 795 1 US-07-882-202A-1  
42 14 63.6 795 1 US-07-683-682B-3  
43 14 63.6 795 1 US-08-021-615A-1  
44 14 63.6 795 1 US-08-321-777-1  
45 14 63.6 795 1 US-08-463-931-5

#### ALIGNMENTS

RESULT 1  
US-09-092-314-2  
; Sequence 2, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eval  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-2

Query Match 92.7%; Score 20.4; DB 4; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.044; 1; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 1

QY 1 tgactgtgaacgttcgagatga 22  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2  
US-09-092-314-1  
; Sequence 1, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eval  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-1

Query Match 85.5%; Score 18.8; DB 4; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.29;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||| |||||  
Db 1 tgactgtgaagtttagatga 22

RESULT 3  
US-09-092-314-3  
; Sequence 3, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-3

Query Match 85.5%; Score 18.8; DB 4; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.29;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||| |||||  
Db 1 tgactgtgaaccttagatga 22

RESULT 4  
US-09-092-314-10  
; Sequence 10, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 10

; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-10

Query Match 85.5%; Score 18.8; DB 4; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.29;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||| |||||  
Db 1 tgactgtgaatgttagatga 22

RESULT 5  
US-09-092-314-4  
; Sequence 4, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-4

Query Match 78.2%; Score 17.2; DB 4; Length 22;  
Best Local Similarity 86.4%; Pred. No. 1.9;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||| |||||  
Db 1 tgactgtgaagcttagatga 22

RESULT 6  
US-09-092-314-5  
; Sequence 5, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
US-09-092-314-5

;  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-5

Query Match 70.9%; Score 15.6; DB 4; Length 22;  
Best Local Similarity 81.8%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22  
||||||| | |||||  
DB 1 tgactgtgttccttagagatga 22  
||||||| | |||||

## RESULT 7

US-09-092-314-7  
; Sequence 7, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-7

Query Match 70.9%; Score 15.6; DB 4; Length 22;  
Best Local Similarity 81.8%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22  
||||||| | |||||  
DB 1 tgactgtgagggtcagagatga 22  
||||||| | |||||

## RESULT 8

US-09-092-314-8  
; Sequence 8, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-8

Query Match 70.9%; Score 15.6; DB 4; Length 22;  
Best Local Similarity 81.8%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22  
||||||| | |||||  
DB 1 tgactgtgagggtcagagatga 22  
||||||| | |||||

## RESULT 9

US-08-391-615-7  
; Sequence 7, Application US/08391615  
; Patent No. 5550054  
; GENERAL INFORMATION:  
; APPLICANT: Witte, Owen  
; APPLICANT: Tsukada, Satoshi  
; APPLICANT: Saffran, Douglas  
; APPLICANT: Rawlings, David  
; TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,615  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/006,449  
; FILING DATE: 21-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20,015  
; REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299 FHT UR  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1418 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-391-615-7

Query Match 70.9%; Score 15.6; DB 1; Length 1418;  
Best Local Similarity 81.8%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22  
||||||| | |||||  
DB 218 TGACTTTGACGTCGGAGAGA 239  
||||||| | |||||

## RESULT 10

US-09-019-931-2  
; Sequence 2, Application US/09019931  
; Patent No. 6194148

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/391.615
  FILING DATE:
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/006,449
    FILING DATE: 21-JAN-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Rowland, Bertram I
    REGISTRATION NUMBER: 20,015
  REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 398-3249
    TELEFAX: (415) 398-3249
    TELEX: 910 277299 FHT UR
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 2505 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
    MOLECULE TYPE: cdna
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 137..2116
US-08-391-615-1

Query Match          70.9%   Score 15.6;   DB 1:   Length 2505;
Best Local Similarity 81.8%   Pred. No. 25;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps

QY      1  tgactgtgaacgttcgagatga 22
        ||||| ||||| ||||| |||||
Db      262  TGACCTTGAACGTGGGAGAAGA 283

RESULT 12
US-08-804-196-1/c
; Sequence 1, Application US/08804196
; Patent No. 5874256
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter
; TITLE OF INVENTION: A method for diagnosing an increased
; TITLE OF INVENTION: risk for thrombosis or a genetic defect causing
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5874256el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/454,353
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:

```



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: : TELEPHONE: (301) 948-7400
: : TELEFAX: (301) 948-9751
: : INFORMATION FOR SEQ ID NO: 1:
: : SEQUENCE CHARACTERISTICS:
: : LENGTH: 6909 base pairs
: : TYPE: nucleic acid
: : STRANDEDNESS: both
: : TOPOLOGY: unknown
: : MOLECULE TYPE: cDNA
US-08-804-196-1

Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative 0;

QY 1 tgactgtgaacgttcgaatga 22
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Db 793 TGACTGTGTACATTAGGATGA 772
|||||

RESULT 13
US-08-658-340-1/c
: Sequence 1: Application US/0865834-1
: Patent No. 5910576
: Patent No. 5910576
: GENERAL INFORMATION:
: APPLICANT: Bertina, Rogier
: APPLICANT: Reltsma, Pieter
: TITLE OF INVENTION: A method for
: TITLE OF INVENTION: risk for th
: TITLE OF INVENTION: thrombosis
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Akzo No. 5910576
: STREET: 1300 Piccard Drive,
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-
: SOFTWARE: PatentIn Release #
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/65
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/45
: FILING DATE: 06-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Gortmley, Mary E.
: REGISTRATION NUMBER: 34,409
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 948-7400
: TELEFAX: (301) 948-9751
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6909 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
US-08-658-340-1

Query Match 70.9%;
Best Local Similarity 81.8%;
Matches 18; Conservative 0;

QY 1 tgactgtgaacgttcgaatga 22
|||||

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; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933.750C
; FILING DATE: September 23, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127
; US-08-933-750C-66

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Query Match      69.1%; Score 15.2; DB 2; Length 1892;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttcgagat 20
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Db 1278 TGAATGTGAAGGTTCCGAGCT 1259

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Search completed: October 9, 2001, 15:41:58
Job time: 288 sec

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Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	AAV32079	Nucleotide sequence
2	22	100.0	22	AA336624	ISS-ODN DY1018 nuc
3	22	100.0	20	AAV80097	Immunomodulatory o
4	22	100.0	20	AAV80102	Immunomodulatory o
5	22	100.0	22	AAV80103	Immunomodulatory o
6	22	100.0	22	AAC64031	Immunostimulatory
7	22	100.0	22	AAA96253	Sequence of a stab
8	22	100.0	22	AAA90458	CpG adjuvant oligo
9	22	100.0	22	AAA14457	Immunostimulatory
10	22	100.0	22	AAA38085	Immunostimulatory
11	22	100.0	22	AAA38071	Immunostimulatory

PT New immunomodulatory compositions - comprising an antigen conjugated  
 PT to a polynucleotide that contains an immunostimulatory sequence  
 XX  
 PS Example 1; Page 36; 69pp; English.  
 XX  
 CC This is the nucleotide sequence of DY1018, which is conjugated to  
 CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule  
 CC (IMM), which comprises an antigen conjugated to a polynucleotide  
 CC (PN), that contains at least one immunostimulatory nucleotide sequence  
 CC (ISS). The conjugate synergistically boost the magnitude of the host  
 CC immune response against an antigen to a level greater than the host  
 CC immune response to either the IMM, antigen or ISS-PN alone. These  
 CC responses to ISS-PN/IMM conjugates are particularly acute during  
 CC the important early phase of the host immune response to an antigen.  
 CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular  
 CC (Th1 type) immune responses of the host. Thus, use of the method to  
 CC boost the immune responsiveness of a host to subsequent challenge by a  
 CC sensitising antigen without immunisation avoids the risk of  
 CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IGE  
 CC production in response to the antigen challenge. The conjugates can  
 CC also be used to combat pathogenic infection and to stimulate  
 CC therapeutic angiogenesis to treat conditions in which localised blood  
 CC flow plays a significant etiological role, e.g. retinopathies.  
 XX  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 19; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.025;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttcgagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 2  
 AAX36624  
 ID AAX36624 standard; DNA; 22 BP.  
 XX  
 AC AAX36624;  
 XX  
 DT 09-JUL-1999 (first entry)  
 XX  
 DE ISS-ODN DY1018 nucleotide sequence.

XX Antigen-stimulated inflammation; immunostimulatory oligonucleotide;  
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;  
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;  
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;  
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;  
 KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.  
 XX WO9911275-A2.  
 XX 11-MAR-1999.  
 PD  
 XX  
 PF 04-SEP-1998; 98WO-US18382.  
 XX  
 PR 05-SEP-1997; 97US-0927120.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.

XX Ray E;  
 XX WPI; 1999-312404/26.  
 XX Reducing antigen-stimulated granulocyte-mediated inflammation  
 XX  
 PS Example 2; Page 30; 69pp; English.  
 XX

CC This is the ISS-ODN DY1018 nucleotide sequence.  
 CC The invention relates to a method for preventing or reducing  
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:  
 CC (a) reduction in, or the absence of, a Th2 type immune response is  
 CC measured; or (b) there is a reduction or absence of other clinical signs  
 CC of inflammation in the host after antigen challenge. The method is used  
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
 CC and to modulate the host's immune responsiveness to an antigen.  
 CC particularly where the subject suffers from asthma, nasal polyposis,  
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
 CC antigen immunisation, the method is an antigen-independent method,  
 CC and avoids host production of both interleukin-4 (IL-4), which carries  
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
 CC adhesion to endothelia.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.025;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttcgagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 3  
 AAV80097  
 ID AAV80097 standard; DNA; 22 BP.  
 XX  
 AC AAV80097;  
 XX  
 DT 12-MAR-1999 (first entry)  
 XX  
 DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.  
 XX Synthetic.

XX WO9855495-A2.  
 XX 10-DEC-1998.  
 PD  
 XX 05-JUN-1998; 98WO-US11578.  
 XX  
 PR 06-JUN-1997; 97US-0048793.  
 XX  
 XX (DYNA-) DYNAX TECHNOLOGIES CORP.  
 XX  
 XX Dina D, Roman M, Schwartz D;  
 XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases  
 XX  
 PS Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.  
 CC  
 CC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.025;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 4  
 AAV80102  
 ID AAV80102 standard; DNA; 22 BP.  
 AC AAV80102;  
 XX  
 XX  
 XX 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 11  
 FT /\*tag= a  
 FT /note= "5-bromocytosine"  
 FT

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 23; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.025;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 5  
 AAV80103  
 ID AAV80103 standard; DNA; 22 BP.  
 XX  
 AC AAV80103;  
 XX  
 XX 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 11  
 FT /\*tag= a  
 FT /note= "5-bromocytosine"  
 FT

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

```

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
Query Match 100.0%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
AAC64051
ID AAC64051 standard; DNA; 22 BP.
XX AC
XX AAC64051;
XX DT
XX 15-FEB-2001 (first entry)
XX DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
XX KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
XX KW enhanced antigen presentation; antigen-presenting cell; APC;
XX KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
XX KW vaccine; ss.
XX OS Synthetic.
XX PN WO200062787-A1.
XX PD 26-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09664.
XX PR 15-APR-1999; 99US-0292278.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Raz E, Martin-Orozco E;
XX WPI; 2000-679548/66.
XX PT Enhancing antigen-presentation capabilities of T-cells for cancer
XX PT immunotherapy, by contacting cells with an immunostimulatory
XX PT oligonucleotide.
XX PS Example 1; Page 18; 42pp; English.
XX CC The invention relates to a method of inducing activation of T-cells
XX CC to respond to an antigen, comprising contacting antigen-presenting cells
XX CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
XX CC thus treated have enhanced antigen presenting capabilities compared to
XX CC antigen-activated APCs. APCs with enhanced antigen-presentation
XX CC capabilities then present the antigen to T-cells. The method is useful
XX CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
XX CC antigen presenting capacity of tumour cells, thereby inducing T-cell
XX CC activation, and is therefore useful for treating tumours. Additionally,
XX CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
XX CC ISS-ODN treated APCs are induced to take up antigen through upregulation
XX CC of Fe-receptor expression, to present antigen through upregulation of
XX CC major histocompatibility complex (MHC) Class I and II expression and
XX CC CD8 expression, to produce co-stimulatory factors (B7 and CD40), to
XX CC provide cell-to-cell adhesion through upregulation of intercellular
XX CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
XX CC cytokine production, all at levels greater than that achieved through
XX CC contact of APC with antigen alone. The present sequence represents
XX CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the
XX CC invention.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 7
AAA96253
ID AAA96253 standard; DNA; 22 BP.
XX AC
XX AAA96253;
XX DT 08-FEB-2001 (first entry)
XX DE Sequence of a stabilised oligonucleotide with antitumour activity.
XX KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
XX KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.
XX OS Synthetic.
XX PN WO200056342-A2.
XX PD 28-SEP-2000.
XX PF 17-MAR-2000; 2000WO-FR00676.
XX PR 19-MAR-1999; 99FR-0003433.
XX PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX PI Carpentier A;
XX WPI; 2000-602192/57.
XX PT Use of stabilized oligonucleotides as antitumor agents, particularly
XX PT against nervous system tumors, have optimal activity and are not toxic
XX PT .
XX PS Example 2; Page 16; 57pp; French.
XX CC The present sequence represents a stabilised oligonucleotide which has
XX CC antitumour activity. The oligonucleotide comprises an octamer motif
XX CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
XX CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
XX CC immunostimulatory, and are not toxic. They may be adapted for use in
XX CC animals or humans. The stabilised oligonucleotides are used for
XX CC treating tumours, of any type and any degree of anaplasia, particularly
XX CC human tumours in the peripheral or central nervous systems, specifically
XX CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 8
AAA90458
ID AAA90458 standard; DNA; 22 BP.
XX AC
XX AAA90458;

```

XX 10-JAN-2001 (first entry)  
XX CpG adjuvant oligonucleotide, SEQ ID NO:19.  
XX  
XX CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;  
KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;  
KW viral infection; bacterial infection; parasitic infection; HCV; HBV;  
KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;  
KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;  
KW rabies virus; cholera; diphtheria; tetanus; pertussis;  
KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.  
XX  
XX Synthetic.  
XX  
XX WO200050006-A2.  
XX  
XX 31-AUG-2000.  
XX  
XX 09-FEB-2000; 2000WO-US03331.  
XX  
XX 26-FEB-1999; 99US-0121858.  
XX  
XX 29-JUL-1999; 99US-0146391.  
XX  
XX 28-OCT-1999; 99US-0161997.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
XX O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Ugozzoli M, Singh M;  
PI Barackman J;  
XX  
XX WPI; 2000-587123/55.  
XX  
XX Microemulsion having an adsorbent surface comprising a microdroplet  
PT emulsion consisting of a metabolizable oil and an emulsifying agent  
PT which is a detergent, useful as a vaccine to treat bacterial, viral,  
PT and parasitic infection  
XX  
XX Claim 17; Page 40; 95pp; English.  
XX  
XX The invention relates to a microdroplet emulsion (microemulsion) with an  
CC adsorbent surface, and which comprises a metabolizable oil and an  
CC emulsifying agent (a detergent). It also relates to a composition  
CC comprising the microemulsion and a microparticle with an adsorbent  
CC surface, where the microparticle comprises a polymer selected from a  
CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a  
CC polycaprolactone, a polyorthoester, a polyhydride, and a  
CC polycyanoacrylate, and a second detergent. The surface of the  
CC microparticles efficiently adsorb biologically active macromolecules such  
CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,  
CC mediators of transcription or translation, metabolic intermediates and  
CC adjuvants. Additionally, a second biologically active molecule may be  
CC encapsulated within the microparticle. The microemulsion can be used in  
CC methods of immunising a host animal, particularly a human, against a  
CC viral, bacterial or parasitic infection, and in methods of increasing a  
CC Th1 immune response. The microemulsions (having the appropriate antigens  
CC adsorbed) may be particularly used as vaccines for hepatitis C virus  
CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human  
CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and  
CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and  
CC pertussis; Helicobacter pylori and Haemophilus influenzae; and  
CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1  
CC lymphocyte stimulating oligonucleotides containing at least one CpG motif  
CC which are claimed for use as adjuvants in the compositions of the  
XX invention.  
XX  
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22  
RESULT 9  
AA14467  
ID AAA14467 standard; DNA; 22 BP.  
XX  
XX AAA14467;  
XX  
XX 21-AUG-2000 (first entry)  
XX  
XX Immunostimulatory oligonucleotide (ISS-ODN) DY1018.  
XX  
XX Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;  
KW secretory immunoglobulin A production; sIgA; Th1 phenotype; ds.  
XX  
XX Synthetic.  
XX  
XX WO200020039-A1.  
XX  
XX 13-APR-2000.  
XX  
XX 15-SEP-1999; 99WO-US21203.  
XX  
XX 05-OCT-1998; 98US-0167039.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Raz E, Horner AA, Carson DA;  
PI  
XX  
XX WPI; 2000-303647/26.  
XX  
XX Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to  
PT an antigen in a mammalian host through production of secretory  
PT immunoglobulin A  
XX  
XX Claim 8; Page 21; 64pp; English.  
XX  
XX The invention relates to a method of inducing mucosal immunity to an  
CC antigen in a mammalian host, including the production of secretory  
CC immunoglobulin A (sIgA). Immune protection in the mucosa (the principal  
CC site of entry of most foreign antigens) is mediated by mucosa-associated  
CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory  
CC cell sub-populations. The primary immune response which characterises  
CC the induction of mucosal immunity to an antigen is sIgA production by  
CC activated B-cells. The method comprises introducing an immunostimulatory  
CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the  
CC ISS-ODN includes a core nucleotide sequence. The core nucleotide  
CC sequence is 5'-purine-purine-C-G-pyrimidine-pyrimidine-3', specific  
CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A  
CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used  
CC as an adjuvant with an antigen for stimulating mucosal immunity. The  
CC level of sIgA production induced in the host is at least 3 times the  
CC magnitude of sIgA production achievable in response to introduction of  
CC antigen alone into the mucosal tissue and is equivalent or greater than  
CC the magnitude of sIgA production achievable in response to introduction  
CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The  
CC host immune response is stimulated to antigen specific IgA production,  
CC biased towards the Th1 phenotype while antigen-induced IgE production is  
CC avoided. The adjuvant has little or no known toxicity in mammals and its  
CC efficacy is comparable to that of cholera toxin which is used as a  
CC mucosal adjuvant. The present sequence represents the immunostimulatory  
CC oligonucleotide DY1018.  
XX  
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.025;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22

```

Db      1 tgactgtgaacgttcgagatga 22
      |||
RESULT 10
AAA38065
ID      AAA38065 standard; DNA; 22 BP.
XX
XX
AC      AAA38065;
XX
DT      24-AUG-2000 (first entry)
XX
DE      Immunostimulatory sequence (ISS) #1.
XX
KW      Immunostimulatory sequence; ISS: immunomodulator; glycoprotein 120;
KW      gp120; human immunodeficiency virus; HIV; immune response; infection;
KW      development; ss.
XX
OS      Synthetic.
XX
PN      WO200021556-A1.
XX
PD      20-APR-2000.
XX
PF      08-OCT-1999; 99WO-US23677.
XX
PR      09-OCT-1998; 98US-0103733.
PR      07-OCT-1999; 99US-0415186.
XX
PA      (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI      Tighe H, Raz E, Schwartz D, Takabayashi K;
XX
DR      WPI: 2000-317846/27.
XX
PT      Anti-HIV composition comprises immunostimulatory polynucleotides and
PT      HIV glycoprotein gp120 useful for modulating, stimulating an immune
PT      response against HIV in an HIV infected individual.
XX
PS      Claim 3; Page 16; 65pp; English.
XX
CC      The present invention relates to an immunostimulatory composition
CC      comprising a human immunodeficiency virus (HIV) antigen, and an
CC      immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC      (ISS). This sequence represents an ISS that can be used in the
CC      composition. An immunostimulatory composition which comprises a gp120
CC      conjugated to an immunomodulatory polynucleotide, or is proximately
CC      associated to it and not conjugated, is used for modulating or
CC      stimulating a specific immune response against gp120 in an individual by
CC      producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC      is also used for suppressing or delaying development of HIV infection in
CC      an individual infected with HIV or an individual at risk of infection
CC      with HIV, respectively. It is also used for treating an individual
CC      infected with HIV in need of immune modulation.
XX
SQ      Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match      100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 tgactgtgaacgttcgagatga 22
      |||
Db      1 tgactgtgaacgttcgagatga 22
      |||
RESULT 11
AAA38071
ID      AAA38071 standard; DNA; 22 BP.
XX
XX
AC      AAA38071;
XX

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DT      24-AUG-2000 (first entry)
XX
DE      Immunostimulatory sequence (ISS) #7.
XX
KW      Immunostimulatory sequence; ISS: immunomodulator; glycoprotein 120;
KW      gp120; human immunodeficiency virus; HIV; immune response; infection;
KW      development; ss.
XX
OS      Synthetic.
XX
PH      Key      Location/Qualifiers
FT      modified_base 11
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "5-Bromocytosine"
XX
PN      WO200021556-A1.
XX
PD      20-APR-2000.
XX
PF      08-OCT-1999; 99WO-US23677.
XX
PR      09-OCT-1998; 98US-0103733.
PR      07-OCT-1999; 99US-0415186.
XX
PA      (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI      Tighe H, Raz E, Schwartz D, Takabayashi K;
XX
DR      WPI: 2000-317846/27.
XX
PT      Anti-HIV composition comprises immunostimulatory polynucleotides and
PT      HIV glycoprotein gp120 useful for modulating, stimulating an immune
PT      response against HIV in an HIV infected individual.
XX
PS      Disclosure; Page 17; 65pp; English.
XX
CC      The present invention relates to an immunostimulatory composition
CC      comprising a human immunodeficiency virus (HIV) antigen, and an
CC      immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC      (ISS). This sequence represents an ISS that can be used in the
CC      composition. An immunostimulatory composition which comprises a gp120
CC      conjugated to an immunomodulatory polynucleotide, or is proximately
CC      associated to it and not conjugated, is used for modulating or
CC      stimulating a specific immune response against gp120 in an individual by
CC      producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC      is also used for suppressing or delaying development of HIV infection in
CC      an individual infected with HIV or an individual at risk of infection
CC      with HIV, respectively. It is also used for treating an individual
CC      infected with HIV in need of immune modulation.
XX
SQ      Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match      100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 tgactgtgaacgttcgagatga 22
      |||
Db      1 tgactgtgaacgttcgagatga 22
      |||
RESULT 12
AAA38072
ID      AAA38072 standard; DNA; 22 BP.
XX
XX
AC      AAA38072;
XX
DT      24-AUG-2000 (first entry)
XX
DE      Immunostimulatory sequence (ISS) #7.
XX

```



KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
 KW development; ss.  
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 XX Synthetic.  
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 FT modified\_base /\*tag= b  
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 XX WO200021556-A1.  
 XX  
 XX 20-APR-2000.  
 XX  
 XX 08-OCT-1999; 99WO-US23677.  
 XX  
 XX 09-OCT-1998; 98US-0103733.  
 PR  
 PR 07-OCT-1999; 99US-0415186.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX Tighe H, Raz E, Schwartz D, Takabayashi K;  
 XX WPI; 2000-317846/27.  
 XX  
 XX Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual  
 PT  
 XX Disclosure; Page 17; 65pp; English.  
 XX  
 XX The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunostimulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory composition which comprises a gp120  
 CC conjugated to an immunostimulatory polynucleotide, or is proximately  
 CC associated to it and not conjugated, is used for modulating or  
 CC stimulating a specific immune response against gp120 in an individual by  
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
 CC is also used for suppressing or delaying development of HIV infection in  
 CC an individual infected with HIV or an individual at risk of infection  
 CC with HIV, respectively. It is also used for treating an individual  
 CC infected with HIV in need of immune modulation.  
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 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 Query Match 100.0%; Score 22; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.025;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 tgactgtgaacggttcgagatga 22  
 Db 1 tgactgtgaacggttcgagatga 22  
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 ID AAZ55876 standard; DNA; 22 BP.  
 XX  
 AC AAZ55876;  
 XX  
 XX 10-APR-2000 (first entry)  
 DT  
 XX Immunomodulatory oligonucleotide SEQ ID NO: 1.  
 DE  
 XX

KW Immunomodulation; immunostimulatory sequence; adjuvant;  
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
 KW asthma; immunosuppression; ss.  
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 XX Mus musculus.  
 OS Synthetic.  
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 XX WO9962923-A2.  
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 XX 09-DEC-1999.  
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 XX 04-JUN-1999; 99WO-US12538.  
 PF  
 XX 05-JUN-1998; 98US-0088310.  
 PR  
 PR 01-JUN-1999; 99US-0324191.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX Schwartz D;  
 PI  
 XX WPI; 2000-105687/09.  
 DR  
 XX Novel immunomodulatory oligonucleotide used to induce a Th1-type immune  
 PT response, e.g. to tumor antigens  
 PT  
 XX Example 1; Page 35; 54pp; English.  
 PS  
 XX Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory  
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,  
 CC AACGTC, AACGTC, AACGTC, AACGTC, AACGTC, AACGTC, AACGTC, AACGTC,  
 CC AACGTC and GACGTC). The invention relates to oligonucleotides  
 CC comprising one or more ISSs, where the ISS comprises at least  
 CC one modified cytosine with an electron-withdrawing moiety at  
 CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886  
 CC contain ISSs comprising at least one bromocytosine, whereas sequence  
 CC AAZ55876 contains an unmodified ISS. The immunomodulatory  
 CC oligonucleotides have an adjuvant-like effect; when formulated with an  
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,  
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),  
 CC while simultaneously downregulating the Th2-type response. The Th1  
 CC response is particularly effective for control of viruses and  
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
 CC particularly when formulated with an antigen or a facilitator, for  
 CC modulating immune responses. Such compositions may be used in tumour  
 CC therapy, in treatment of allergy (including asthma), for inducing a  
 CC vigorous cellular response (against a virus, bacterium, fungus or  
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
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 Best Local Similarity 100.0%; Pred. No. 0.025;  
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 ID AAF77040 standard; DNA; 22 BP.  
 XX  
 AC AAF77040;

XX 15-MAY-2001 (first entry)  
DT Immunomodulatory DNA.  
DE Modulate; immune; antigen; immunostimulatory; ds.  
KW Synthetic.  
XX WO200112223-A2.  
XX 22-FEB-2001.  
XX 18-AUG-2000; 2000WO-US22835.  
XX 19-AUG-1999; 99US-0149768.  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX Van Nest G;  
XX WPI; 2001-211136/21.  
XX Modulating immune response to a second antigen in humans involves  
PT administering an immunostimulatory polynucleotide comprising an  
PT immunostimulatory sequence and a first antigen  
XX Claim 31; Page 15; 63pp; English.  
XX The present invention relates to modulating an immune response to  
CC a second antigen in an individual, involving  
CC administering to the individual an immunomodulatory polynucleotide  
CC comprising an immunostimulatory sequence (ISS) and a first antigen.  
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
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AAF29800  
ID AAF29800 standard; DNA; 22 BP.  
XX  
AC AAF29800;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Cholera toxin immunostimulatory nucleotide sequence.  
XX  
KW Immunostimulatory nucleotide sequence; immune response; cancer;  
KW antibody production; IFNgamma release; CTL activity; Th1 response;  
KW infection; allergy; ds.  
XX  
OS Unidentified.  
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PN WO200102007-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 30-JUN-2000; 2000WO-US18229.  
XX  
PR 02-JUL-1999; 99US-0347343.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Raz E, Kobayashi H;

XX WPI; 2001-138066/14.  
DR  
XX Enhancing immune response against pathogen or antigen associated with  
PT infectious diseases, an allergen or cancer, involves administering  
PT immunostimulatory nucleotide sequence prior to antigen exposure -  
XX  
XX Example 1; Page 14; 47pp; English.  
XX The present invention describes a method for enhancing an immune response  
CC to a substance, comprising administering an immunostimulatory nucleotide  
CC sequence to a subject prior to exposure to the substance. This can be  
CC used to enhance antibody production, IFNgamma release, CTL activity and  
CC Th1 related effects. The method can be used in the prevention and  
CC treatment of allergies, cancer and infections.  
XX  
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
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Job time: 2977 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:37:10 ; Search time 2150.93 Seconds  
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Searched: 1344157 seqs, 7733874588 residues 2688314  
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Listing first 45 summaries

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98: em\_ba3:

Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	100.0	22	9 AX046993	AX046993 Sequence
3	22	100.0	22	10 AX083675	AX083675 Sequence
4	21	95.5	22	10 AX083681	AX083681 Sequence
5	20.4	92.7	22	9 AX036946	AX036946 Sequence
6	20.4	92.7	22	10 AX083676	AX083676 Sequence
7	20.4	92.7	22	10 AX083678	AX083678 Sequence
8	20	90.9	22	10 AX083682	AX083682 Sequence

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9 19.4 88.2 22 10 AX083680 Sequence
10 18.8 85.5 22 9 AX036944 Sequence
11 18.8 85.5 22 9 AX036952 Sequence
12 17.8 80.9 145939 79 AL158143 Homo sapi
13 17.8 80.9 165337 70 AC027442 Homo sapi
14 17.8 80.9 167237 86 AC007938 Homo sapi
15 17.8 80.9 201214 75 AC074012 Homo sapi
16 17.8 80.9 209777 69 AC024934 Homo sapi
17 17.2 78.2 127 5 AGXH8
18 17.2 78.2 552 14 RICSINEO4
19 17.2 78.2 12545 6 CEP42G10
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21 17.2 78.2 128216 93 HSDJ319M7
22 17.2 78.2 149912 76 AC079336 Homo sapi
23 17.2 78.2 169277 75 AC078940 Homo sapi
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## ALIGNMENTS

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DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS
SOURCE synthetic construct.
ORGANISM Carpentier,A.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL ASSIST PUBL HOPITAUX DE PARIS (FR)
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DEFINITION Sequence 2 from Patent WO0067787.
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS
SOURCE synthetic construct.
ORGANISM Mos,R.B.
REFERENCE 1 (bases 1 to 22)
AUTHORS Mos,R.B.
JOURNAL Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
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DEFINITION Sequence 1 from Patent WO0112223.
ACCESSION AX083675
VERSION AX083675.1 GI:13185407
KEYWORDS
SOURCE synthetic construct.
ORGANISM van Nest,G.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Methods of modulating an immune response using immunostimulatory s
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Patent: WO 0112223-A 1 22-FEB-2001;
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DEFINITION Sequence 7 from Patent WO0112223.
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ACCESSION AX083681
VERSION AX083681.1 GI:13185413
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SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 7 22-FEB-2001;
Dynamax Technologies Corporation (US)
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DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION AX036946
VERSION AX036946.1 GI:11226374
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
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ACCESSION AX083676
VERSION AX083676.1 GI:13185408
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 2 22-FEB-2001;
Dynamax Technologies Corporation (US)
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LOCUS AX083678 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 4 from Patent WO0112223.
ACCESSION AX083678
VERSION AX083678.1 GI:13185410
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 4 22-FEB-2001;
Dynamax Technologies Corporation (US)
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DEFINITION Sequence 8 from Patent WO0112223.
ACCESSION AX083682
VERSION AX083682.1 GI:13185414
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 2 22-FEB-2001;
Dynamax Technologies Corporation (US)
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----- Genome Center  
Center: Sanger Centre

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Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: dj107418
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 7% of reads Chemistry:
Dye-terminator Big Dye; 9% of reads
Consensus quality: 137464 bases at least Q40
Consensus quality: 141229 bases at least Q30
Consensus quality: 143037 bases at least Q20
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Quality size: 111741; 30.4% error; agarose-fp
Quality coverage: 6.03x in Q20 bases; sum-of-contigs Quality
coverage: 9.27x in Q20 bases; agarose-fp
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* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 3125 10834: contig of 7710 bp in length
* 10835 10934: gap of 100 bp
* 10935 13593: contig of 2661 bp in length
* 13596 13693: gap of 100 bp
* 13696 16092: contig of 2397 bp in length
* 16093 16192: gap of 100 bp
* 16193 22530: contig of 6338 bp in length
* 22531 22630: gap of 100 bp
* 22631 27253: contig of 4623 bp in length
* 27254 27353: gap of 100 bp
* 27354 30261: contig of 2908 bp in length
* 30262 30361: gap of 100 bp
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* 62931 63030: gap of 100 bp
* 63031 67419: contig of 4389 bp in length
* 67420 67519: gap of 100 bp
* 67520 145939: contig of 78420 bp in length.
*
* Location/Qualifiers
* 1..145939
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="X"
* /clone="RP5-107418"
* /clone_lib="RC1-5"
*
misc_feature
1..3024
/note="assembly_fragment:00567"
clone_end:SP6
vector_side:left
3125..10834
/note="assembly_fragment:00921"
fragment_chain:1

```

```

misc_feature 10935..13595
/note="assembly_fragment:01789"
fragment_chain:1
misc_feature 13696..16092
/note="assembly_fragment:01424"
fragment_chain:2
16193..22530
/note="assembly_fragment:01022"
fragment_chain:2
22631..27253
/note="assembly_fragment:00011"
27354..30261
/note="assembly_fragment:00127"
30362..33611
/note="assembly_fragment:00247"
33712..38262
/note="assembly_fragment:00335"
38363..40615
/note="assembly_fragment:00495"
40716..44299
/note="assembly_fragment:00561"
44400..47229
/note="assembly_fragment:00700"
47330..52776
/note="assembly_fragment:00832"
52877..60226
/note="assembly_fragment:00912"
60327..62930
/note="assembly_fragment:01119"
63031..67419
/note="assembly_fragment:01935"
67520..145939
/note="assembly_fragment:02239"
BASE COUNT 45121 a 27951 c 28095 g 43161 t 1611 others
ORIGIN

Query Match      80.9%; Score 17.8; DB 79; Length,145939;
Best Local Similarity 90.5%; Pred. No.73;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgacgttcgagatga 22
||||| ||||| ||||| |||||
Db 37628 GACTGTGAATGTTCCAGATGA 37648

RESULT 13
AC027442 165337 bp DNA HTG 27-APR-2000
LOCUS Homo sapiens clone RP11-439K16, WORKING DRAFT SEQUENCE, 31
DEFINITION Homo sapiens clone RP11-439K16, WORKING DRAFT SEQUENCE, 31
unordered pieces.
ACCESSION AC027442
VERSION AC027442.2 GI:7651981
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 165337)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
TITLE Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
JOURNAL Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
REFERENCE Campopiano,A., Castle,P., Dearellano,K., Dewar,K., Diaz,J.S.,
2 (bases 1 to 165337) Dodges,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
AUTHORS Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
TITLE Grand-Pierre,N., Grant,G., Heaford,A., Horton,L.,
JOURNAL Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
REFERENCE Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczeky,J.,

```

Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Melgrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivari, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 27, 2000 this sequence version replaced gi:7342171.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information  
Center project name: L8145  
Center clone name: 439\_K\_16

----- Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 149010 bases at least Q40  
Consensus quality: 157303 bases at least Q30  
Consensus quality: 160628 bases at least Q20  
Insert size: 170000; agarose-fp  
Insert size: 162337; sum-of-ctngs  
Quality coverage: 3.6 in Q20 bases; agarose-fp  
Quality coverage: 3.8 in Q20 bases; sum-of-ctngs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 31 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 1105: contig of 1105 bp in length  
\* 1106 1205: gap of 100 bp  
\* 1206 2479: contig of 1274 bp in length  
\* 2480 2579: gap of 100 bp  
\* 2580 4211: contig of 1632 bp in length  
\* 4212 4311: gap of 100 bp  
\* 4312 5781: contig of 1470 bp in length  
\* 5782 5881: gap of 100 bp  
\* 5882 7830: contig of 1949 bp in length  
\* 7831 7930: gap of 100 bp  
\* 7931 9913: contig of 1983 bp in length  
\* 9914 10013: gap of 100 bp  
\* 10014 12486: contig of 2473 bp in length  
\* 12487 12586: gap of 100 bp  
\* 12587 15592: contig of 3006 bp in length  
\* 15593 15692: gap of 100 bp  
\* 15693 19721: contig of 4029 bp in length  
\* 19722 19821: gap of 100 bp  
\* 19822 23269: contig of 3448 bp in length  
\* 23270 23369: gap of 100 bp  
\* 23370 26785: contig of 3416 bp in length  
\* 26786 26885: gap of 100 bp  
\* 26886 30363: contig of 3478 bp in length  
\* 30364 30463: gap of 100 bp  
\* 30464 33964: contig of 3501 bp in length  
\* 33965 34064: gap of 100 bp  
\* 34065 37794: contig of 3730 bp in length

\* 37795 37894: gap of 100 bp  
\* 37895 43354: contig of 5460 bp in length  
\* 43355 43454: gap of 100 bp  
\* 43455 47839: contig of 4385 bp in length  
\* 47840 47939: gap of 100 bp  
\* 47940 53326: contig of 5387 bp in length  
\* 53327 53426: gap of 100 bp  
\* 53427 58576: contig of 5150 bp in length  
\* 58577 58676: gap of 100 bp  
\* 58677 64554: contig of 5878 bp in length  
\* 64555 64654: gap of 100 bp  
\* 64655 68538: contig of 3884 bp in length  
\* 68539 68638: gap of 100 bp  
\* 68639 74650: contig of 6012 bp in length  
\* 74651 74750: gap of 100 bp  
\* 74751 80037: contig of 5287 bp in length  
\* 80038 80137: gap of 100 bp  
\* 80138 85646: contig of 5509 bp in length  
\* 85647 85746: gap of 100 bp  
\* 85747 92718: contig of 6972 bp in length  
\* 92719 92818: gap of 100 bp  
\* 92819 101098: contig of 8280 bp in length  
\* 101099 101198: gap of 100 bp  
\* 101199 108560: contig of 7362 bp in length  
\* 108561 108660: gap of 100 bp  
\* 108661 118118: contig of 9458 bp in length  
\* 118119 118218: gap of 100 bp  
\* 118219 128612: contig of 10394 bp in length  
\* 128613 128712: gap of 100 bp  
\* 128713 139860: contig of 11148 bp in length  
\* 139861 139960: gap of 100 bp  
\* 139961 151029: contig of 11069 bp in length  
\* 151030 151129: gap of 100 bp  
\* 151130 165337: contig of 14208 bp in length.

FEATURES  
Location/Qualifiers  
source  
1. 165337  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="RPC1-11 Human Male BAC"  
1. 11105  
/note="assembly\_fragment"  
1206. 2479  
/note="assembly\_fragment"  
2580. 4211  
/note="assembly\_fragment"  
4312. 5781  
/note="assembly\_fragment"  
5882. 7830  
/note="assembly\_fragment"  
7931. 9913  
/note="assembly\_fragment"  
10014. 12486  
/note="assembly\_fragment"  
12587. 15592  
/note="assembly\_fragment"  
15693. 19721  
/note="assembly\_fragment"  
19822. 23269  
/note="assembly\_fragment"  
23370. 26785  
/note="assembly\_fragment"  
26886. 30363  
/note="assembly\_fragment"  
30464. 33964  
/note="assembly\_fragment"  
34065. 37794  
/note="assembly\_fragment"  
37895. 43354  
/note="assembly\_fragment"  
43455. 47839  
/note="assembly\_fragment"  
47940. 53326



```

/misc_feature /note="assembly_fragment"
53427..58576
/misc_feature /note="assembly_fragment"
58677..64554
/misc_feature /note="assembly_fragment"
64655..68538
/misc_feature /note="assembly_fragment"
clone_end:r7
vector_side:right"
68639..74650
/misc_feature /note="assembly_fragment"
74751..80037
/misc_feature /note="assembly_fragment"
80138..85646
/misc_feature /note="assembly_fragment"
85747..92718
/misc_feature /note="assembly_fragment"
92819..101098
/misc_feature /note="assembly_fragment"
101199..108560
/misc_feature /note="assembly_fragment"
clone_end:SP6
vector_side:right"
108661..118118
/misc_feature /note="assembly_fragment"
118219..128612
/misc_feature /note="assembly_fragment"
128713..139860
/misc_feature /note="assembly_fragment"

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Query Match 80.9%; Score 17.8; DB 70; Length 165337;  
 Best Local Similarity 90.5%; Pred. No. 74;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaacgttcgagatga 22  
 ||||| ||||| ||||| |||||  
 Db 34792 GACTGTGAAGTTGAGATGA 34812

RESULT 14  
 AC007938  
 LOCUS AC007938 167237 bp DNA PRI 01-JUL-1999  
 DEFINITION Homo sapiens clone Rp11-2E11 from 7q31, complete sequence.  
 ACCESSION AC007938  
 VERSION AC007938.1 GI:5306288  
 KEYWORDS HTG.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 167237)  
 Iadonato,S.P., Yu,J., Wong,G.K.-S., Magness,C.L., Green,E.D.,  
 Green,P. and Olson,M.V.  
 Large-scale MCD Mapping and Sequencing of Human Chromosome 7  
 Unpublished  
 2 (bases 1 to 167237)  
 Bubb,K.L., Desmarais,C.L. and Ramsey,S.A.  
 Direct Submission  
 Submitted (01-JUL-1999) Human Genome Center, University of  
 Washington, Box 352145, Seattle, WA 98195, USA  
 Overlapping Sequences:  
 5': UMGC:mapping in progress  
 3': UMGC:mapping in progress  
 -----  
 Sequence Quality Assessment:  
 This entry has been annotated with sequence quality  
 estimates computed by the Phrap assembly program.  
 All manually edited bases have been reduced to quality zero.  
 Quality levels above 40 are expected to have less than  
 1 error in 10,000 bp.  
 Base-by-base quality values are not generally visible from the  
 GenBank flat file format but are available as part  
 of this entry's ASN.1 file.

Double stranded (DS) coverage: 92.1%  
 DS or two chemistry coverage: 98.8%  
 Single stranded regions: 7

# Sequence Validation:

This sequence has been validated by Multiple Complete Digest  
 fingerprinting. Comparison of the experimentally derived digest  
 fragments with sequence-predicted fragments is given below.  
 Small fragments below a variable cutoff (approximately 400-600)  
 are not resolved in the fingerprint and hence do not appear  
 in the table. There are no significant remaining discrepancies  
 between the experimental and predicted values. Uniquely ordered  
 fragment groups are separated by dashed lines.

FP	BgIII	Seq	FP	Seq	FP	Seq
3077.00	3085.00	927.00	886.00	11068.00	10994.00	
2272.00	2243.00	5763.00	5591.00	5800.00	5733.00	
3718.00	3675.00	5500.00	5306.00	5142.00	5034.00	
919.00	910.00	3401.00	3299.00	6594.00	6498.00	
4305.00	4299.00	1883.00	1827.00	18441.00	18235.00	
6535.00	6434.00	812.00	778.00	4853.00	4804.00	
3240.00	3314.00	13412.00	13046.00	6840.00	6860.00	
1830.00	1798.00	1034.00	991.00	621.00	620.00	
627.00	612.00	1250.00	1217.00	3494.00	3493.00	
4604.00	4477.00	1706.00	1678.00	5983.00	5978.00	
4042.00	3922.00	6884.00	6555.00	1287.00	1305.00	
8575.00	8564.00	2330.00	2244.00	739.00	734.00	
2272.00	2213.00	927.00	886.00	5320.00	5337.00	
3240.00	3225.00	1357.00	1327.00	4539.00	4524.00	
5550.00	5592.00	4521.00	4434.00	536.00	524.00	
2272.00	2276.00	5500.00	5369.00	1772.00	1747.00	
3403.00	3390.00	7689.00	7601.00	13147.00	13306.00	
5366.00	5371.00	2455.00	2409.00	2888.00	2874.00	
1680.00	1686.00	1357.00	1346.00	7752.00	7780.00	
2486.00	2488.00	6114.00	6085.00	5320.00	5365.00	
5915.00	5956.00	13412.00	13557.00	536.00	547.00	
7022.00	7028.00	5763.00	5618.00	1603.00	1611.00	
1198.00	1222.00	745.00	705.00	11298.00	11545.00	
3240.00	3211.00	1357.00	1315.00	3738.00	3726.00	
1198.00	1205.00	3007.00	2894.00	824.00	803.00	
5684.00	5673.00	1706.00	1729.00	18441.00	18868.00	
3156.00	3117.00	557.00	531.00	2133.00	2188.00	
3799.00	3803.00	4596.00	4528.00	6255.00	6266.00	
				18441.00		

```

2391.00 2382.00 1357.00 1347.00 -----
-----
652.00 656.00 14474.00 14507.00
-----
7746.00 7822.00 1021.00 986.00
-----
824.00 820.00 1357.00 1338.00
-----
919.00 898.00 3235.00 3209.00
-----
2000.00 2020.00 4073.00 3995.00
-----
2742.00 2779.00 4844.00 4741.00
-----
1137.00 1127.00 667.00 637.00
-----
7746.00 7672.00 9942.00 9815.00
-----
4401.00 4351.00 9942.00 9798.00
-----
1497.00 1483.00 1122.00 1094.00
-----
1137.00 1141.00 583.00 559.00
-----
3240.00 3204.00 4293.00 4217.00
-----
10233.00 10265.00 1883.00 1853.00
-----
2082.00 2106.00 3007.00 2890.00
-----
5366.00 5430.00 1642.00 1630.00
-----
3156.00 3149.00 -----
3403.00 -----
2082.00 -----
10785.00 -----

```

Unmatched fragments are due to vector-containing sequences. We expect 3, 1 and 1-2 such fragments in the BglII, EcoRI, and NsiI enzyme domains, respectively. The sum of these fragments can be calculated from the sequence of the BAC clone and, in this clone, should be 15 909, 8 992, and 17 890 for the three enzyme domains.

## FEATURES

## source

```

1. 167237
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /chromosome="7"
  /map="7q31"
  /clone="RP11-2E11"
  /cell_line="Male Blood"
  /clone_lib="RPC1-11 Human Male BAC library"
19. 57
  /rpt_family="MER33"
  complement(19..202)
  /rpt_family="MER3"
  complement(4274..4486)
  /rpt_family="MER44C"
  4579..4853
  /rpt_family="Alu"
  complement(5201..5265)
  /rpt_family="MER44C"
  complement(9355..9635)
  /rpt_family="Alu"
  complement(9820..10295)
  /rpt_family="Alu"
  complement(10848..11105)
  /rpt_family="Alu"
  12817..13056
  /rpt_family="Alu"
  complement(13484..13707)
  /rpt_family="Alu"
  complement(14659..14767)
  /rpt_family="MIR"

```

```

repeat_region 17458..17523
  /rpt_family="MER5"
repeat_region complement(19439..20044)
  /rpt_family="Alu"
repeat_region complement(26649..26806)
  /rpt_family="MIR"
repeat_region complement(26993..27274)
  /rpt_family="Alu"
repeat_region 30702..31044
  /rpt_family="Alu"
repeat_region complement(31117..31171)
  /rpt_family="MIR"
STS 31696..31875
  /standard_name="SWSS3351"
  /note="Genbank Accession: G13133"
repeat_region 31900..32236
  /rpt_family="THE1"
repeat_region complement(33690..33730)
  /rpt_family="Alu"
repeat_region 33899..34177
  /rpt_family="Alu"
repeat_region complement(37893..38494)

```

Query Match 80.9%; Score 17.8; DB 86; Length 167237;

Best Local Similarity 90.5%; Pred. No. 74; HTG 16-JUL-2000  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcagatg 21  
|||||

Db 21036 TGACTGTGAACGTCAGAGATG 21056

RESULT 15

AC074012/c

LOCUS AC074012 201214 bp DNA HTG 16-JUL-2000  
DEFINITION Homo sapiens chromosome 7 clone RP11-781M21, WORKING DRAFT  
SEQUENCE, 29 unordered pieces.

ACCESSION AC074012

VERSION AC074012.2 GI:9230873

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 201214)

AUTHORS Waterston,R.H.

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 201214)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (09-JUL-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

COMMENT On Jul 16, 2000 this sequence version replaced gi:8980982.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H\_NH0781M21

----- Summary Statistics -----

Sequencing vector: M13; 100%

Chemistry: Dye-primer ET; 100% of reads

Chemistry: Dye-terminator Big Dye; 0% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 185830 bases at least Q40

Consensus quality: 191039 bases at least Q30

Consensus quality: 193172 bases at least Q20

Insert size: 230000; agarose-gel

Insert size: 198414; sum-of-contigs

Quality coverage: 3.51 in Q20 bases; agarose-fp  
Quality coverage: 4.13 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 29 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1243: contig of 1243 bp in length  
\* 1244: gap of unknown length  
\* 1344: contig of 1470 bp in length  
\* 2814: gap of unknown length  
\* 2913: contig of 1291 bp in length  
\* 4205: gap of unknown length  
\* 4204: gap of unknown length  
\* 4305: contig of 2110 bp in length  
\* 6414: gap of unknown length  
\* 6514: gap of unknown length  
\* 8307: contig of 1793 bp in length  
\* 8407: gap of unknown length  
\* 8408: contig of 2960 bp in length  
\* 11367: gap of unknown length  
\* 11467: contig of 3049 bp in length  
\* 14516: gap of unknown length  
\* 14616: gap of unknown length  
\* 14617: contig of 3582 bp in length  
\* 18199: gap of unknown length  
\* 18299: contig of 2862 bp in length  
\* 21160: gap of unknown length  
\* 21261: gap of unknown length  
\* 24666: contig of 3406 bp in length  
\* 24667: gap of unknown length  
\* 24767: contig of 5516 bp in length  
\* 30382: gap of unknown length  
\* 30383: contig of 5221 bp in length  
\* 35603: gap of unknown length  
\* 35604: contig of 5907 bp in length  
\* 41611: gap of unknown length  
\* 41611: contig of 5846 bp in length  
\* 47556: gap of unknown length  
\* 47557: contig of 5357 bp in length  
\* 53013: gap of unknown length  
\* 53113: contig of 5713 bp in length  
\* 58826: gap of unknown length  
\* 58827: contig of 4201 bp in length  
\* 58927: gap of unknown length  
\* 63128: contig of 5140 bp in length  
\* 63228: gap of unknown length  
\* 68367: gap of unknown length  
\* 68468: contig of 8856 bp in length  
\* 77323: gap of unknown length  
\* 77324: contig of 10166 bp in length  
\* 77424: gap of unknown length  
\* 77424: contig of 10166 bp in length  
\* 87589: gap of unknown length  
\* 87590: contig of 6063 bp in length  
\* 93752: gap of unknown length  
\* 93753: contig of 10189 bp in length  
\* 93853: gap of unknown length  
\* 104042: contig of 9462 bp in length  
\* 104142: gap of unknown length  
\* 113603: gap of unknown length  
\* 113704: contig of 9747 bp in length  
\* 123451: gap of unknown length  
\* 123551: gap of unknown length  
\* 134211: contig of 10660 bp in length  
\* 134211: gap of unknown length  
\* 134310: contig of 11059 bp in length  
\* 145369: gap of unknown length  
\* 145370: contig of 14182 bp in length  
\* 145470: gap of unknown length  
\* 159651: contig of 17154 bp in length  
\* 159652: gap of unknown length  
\* 176905: contig of 17154 bp in length  
\* 176906: gap of unknown length  
\* 201214: contig of 24209 bp in length.

Location/Qualifiers  
1. 201214  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="7"

FEATURES  
source

misc\_feature 1. 1243 /clone="Rp11-781M21"  
misc\_feature 1344. 2813 /note="assembly\_name:Contig9"  
misc\_feature 2914. 4204 /note="assembly\_name:Contig10"  
misc\_feature 4305. 6414 /note="assembly\_name:Contig12"  
misc\_feature /note="assembly\_name:Contig13"  
6515. 8307 /note="assembly\_name:Contig14"  
clone\_end:SP6  
vector\_side:right  
8408. 11367 /note="assembly\_name:Contig15"  
misc\_feature 11468. 14516 /note="assembly\_name:Contig16"  
misc\_feature 14617. 18198 /note="assembly\_name:Contig17"  
misc\_feature 18299. 21160 /note="assembly\_name:Contig18"  
misc\_feature 21261. 24666 /note="assembly\_name:Contig19"  
misc\_feature 24767. 30282 /note="assembly\_name:Contig20"  
misc\_feature 30383. 35603 /note="assembly\_name:Contig21"  
misc\_feature 35704. 41610 /note="assembly\_name:Contig22"  
misc\_feature 41711. 47556 /note="assembly\_name:Contig23"  
misc\_feature 47657. 53013 /note="assembly\_name:Contig24"  
misc\_feature 53114. 58826 /note="assembly\_name:Contig25"  
misc\_feature 58927. 63127 /note="assembly\_name:Contig26"  
misc\_feature 63228. 68367 /note="assembly\_name:Contig27"  
misc\_feature 68468. 77323 /note="assembly\_name:Contig28"  
misc\_feature 77424. 87589 /note="assembly\_name:Contig29"  
misc\_feature 87690. 93752 /note="assembly\_name:Contig30"  
misc\_feature 93853. 104041 /note="assembly\_name:Contig31"  
misc\_feature 104142. 113603 /note="assembly\_name:Contig32"  
misc\_feature 113704. 123450 /note="assembly\_name:Contig33"  
misc\_feature 123551. 134210 /note="assembly\_name:Contig34"  
misc\_feature 134311. 145369 /note="assembly\_name:Contig35"  
misc\_feature 145470. 159651 /note="assembly\_name:Contig36"  
misc\_feature 159752. 176905 /note="assembly\_name:Contig37"  
misc\_feature 177006. 201214 /note="assembly\_name:Contig38"  
BASE COUNT 54381 a 43817 c 43277 g 56933 t 2806 others  
ORIGIN

Query Match 80.9%; Score 17.8; DB 75; Length 201214;  
Best Local Similarity 90.5%; Pred No. 75;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatg 21  
|||||  
Db 124437 TCACGTGTGACGTCAGAGATG 124417

Search completed: October 9, 2001, 16:18:18  
Job time: 2468 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:37:10 ; Search time 6788.49 Seconds  
(without alignments)  
30.635 Million cell updates/sec

Title: US-09-713-136-1  
Perfect score: 22  
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1:	gb_est1:
2:	gb_est2:
3:	gb_est3:
4:	gb_est4:
5:	gb_est5:
6:	gb_est6:
7:	gb_est7:
8:	gb_est8:
9:	gb_est9:
10:	gb_est10:
11:	gb_est11:
12:	gb_est12:
13:	gb_est13:
14:	gb_est14:
15:	gb_est15:
16:	gb_est16:
17:	gb_est17:
18:	gb_est18:
19:	gb_est19:
20:	gb_est20:
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23:	gb_est23:
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28:	gb_est36:
29:	gb_est37:
30:	gb_est38:
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32:	gb_est40:
33:	em_estba:
34:	em_estfun:
35:	em_esthum1:
36:	em_esthum2:
37:	em_esthum3:
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75:	em_estpl4:
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79:	em_estpl8:
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83:	em_estro2:
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102:	gb_est25:
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115:	gb_est46:
116:	gb_est47:

117: gb\_est48:\*  
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253: gb\_est184:\*  
254: gb\_est185:\*  
255: gb\_est186:\*  
256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JOURNAL COMMENT

Unpublished (2000)  
Contact: Friedman TB  
Laboratory of Molecular Genetics  
National Institute on Deafness and Other Communication Disorders,  
National Institutes of Health  
5 Research Court, Room 2A-15, Rockville, MD 20850, USA  
Tel: 301 402 7580  
Fax: 301 496 7882  
Email: friedman@nidcd.nih.gov  
Plate: 02 row: g column: 09  
Seq primer: -21M13 forward primer (ABI)  
Class: random plasmid subclone.  
Location/Qualifiers  
1. .561

FEATURES source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="ev02g09"  
/clone\_lib="PAX3 CASTing Library 'ev'"  
/sex="Male"  
/lab\_host="DH108"  
/note="vector: pGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAX3dO+ protein using a whole genome PCR-based strategy. DNA fragments containing putative PAX3dO+ binding sites were amplified by PCR and cloned into pGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."  
BASE COUNT 126 a 149 c 152 g 134 t  
ORIGIN

Query Match 80.9%; Score 17.8; DB 249; Length 561;  
Best Local Similarity 90.5%; Pred. No. 76;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatg 21  
|||||  
Db 461 TGACTGTGACGTCAGAGATG 441

RESULT 2

BF971856 961 bp mRNA EST 22-JAN-2001  
LOCUS 60224044AF1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4328890 5',  
DEFINITION mRNA sequence.  
ACCESSION BF971856  
VERSION BF971856.1 GI:12339071  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 961)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LUCM189 row: h column: 11  
High quality sequence stop: 555.  
Location/Qualifiers  
1. .961

FEATURES source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4328890"

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	17.8	80.9	561	249	AZ755668	ev02g09.x
C 2	17.8	80.9	961	172	BF971856	60224044
C 3	17.4	79.1	489	231	AZ060178	RPCI-23-4
C 4	17.4	79.1	530	251	AZ886419	RPCI-23-1
C 5	17.2	78.2	374	226	AQ245026	HS_2056.B
C 6	17.2	78.2	408	245	AZ536502	110300.96
C 7	17.2	78.2	424	139	BE723539	193384.MA
C 8	17.2	78.2	463	107	AU083559	AU083559
C 9	17.2	78.2	479	107	AU089685	AU089685
C 10	17.2	78.2	972	222	CNS05PD9	AL347814 Tetraodon
C 11	16.8	76.4	105	2	AA094019	cl1619.se
C 12	16.8	76.4	523	244	AZ483488	1M0309M12
C 13	16.8	76.4	526	245	AZ501799	1M0340J17
C 14	16.8	76.4	681	32	AV732648	AV732648
C 15	16.8	76.4	705	122	AW916461	EST347765
C 16	16.4	74.5	400	115	AW398307	EST298154
C 17	16.4	74.5	496	110	AW034934	EST279163
C 18	16.4	74.5	546	237	AZ058706	RPCI-23-4
C 19	16.4	74.5	554	241	AZ280611	RPCI-23-1
C 20	16.4	74.5	599	237	AZ068022	RPCI-23-4
C 21	16.4	74.5	633	155	BG570577	BG570577
C 22	16.4	74.5	747	174	BG127461	EST473107
C 23	16.4	74.5	934	220	CNS027SC	AL185061 Tetraodon
C 24	16.2	73.6	202	4	AA236074	zs05a04.r
C 25	16.2	73.6	236	127	BB183285	BB183285
C 26	16.2	73.6	236	171	BF932252	IL2-NT019
C 27	16.2	73.6	251	161	BB565758	BB565758
C 28	16.2	73.6	286	16	AI099019	AI099019 uc02h08.r
C 29	16.2	73.6	297	7	AA445764	vc63b04.s
C 30	16.2	73.6	300	156	C11370	C11370 Yuj1
C 31	16.2	73.6	304	230	AQ581066	RPCI-11-4
C 32	16.2	73.6	317	163	BE119339	UI-R-CAO-
C 33	16.2	73.6	360	26	AV189436	AV189436
C 34	16.2	73.6	398	167	BE428418	MTD006.G1
C 35	16.2	73.6	401	165	BE275964	601120704
C 36	16.2	73.6	416	231	AQ646593	RPCI193-DP
C 37	16.2	73.6	424	170	BF851024	IL5-EN008
C 38	16.2	73.6	441	22	AI597068	v344609.x
C 39	16.2	73.6	448	115	AW390277	CM2-ST018
C 40	16.2	73.6	457	166	BE367478	P11.8-F04
C 41	16.2	73.6	472	235	AQ904593	GSSTC0381
C 42	16.2	73.6	473	188	R83554	yq12d03.r1
C 43	16.2	73.6	474	167	BE419241	WNR021.G5
C 44	16.2	73.6	477	149	BF475131	WHE2111.B
C 45	16.2	73.6	479	142	BE946012	UI-M-BH3-

ALIGNMENTS

RESULT 1  
AZ755668/c 561 bp DNA GSS 01-MAR-2001  
LOCUS ev02g09.x1 PAX3 CASTing Library 'ev' Homo sapiens genomic clone  
DEFINITION ev02g09 random, cDNA sequence.  
ACCESSION AZ755668  
VERSION AZ755668.1 GI:13175090  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 561)  
AUTHORS Barber, T.D., Barber, M.C., Tomescu, O., Barr, F., Ruben, S. and Friedman, T.B.  
TITLE Cyclic amplification and selection of target genes regulated by pax3 and PAX3/FKHR in embryogenesis and alveolar rhabdomyosarcoma

```

/clone_lib="NIH_MGC_46"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOR87; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT      205 a      225 c      240 g      291 t
ORIGIN

```

```

Query Match      80.9%; Score 17.8; DB 172; Length 961;
Best Local Similarity 90.5%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 gactgtgaacgcttcgagatga 22
      ||||| ||||| |||||
Db  650 GACTGTGAACGCTTCGAGATGA 670

```

```

RESULT 3
AZ060178/c
LOCUS      489 bp      DNA      GSS      30-MAR-2000
DEFINITION RPCI-23-405E23.TJ RPCI-23 Mus musculus genomic clone RPCI-23-405E23
, DNA sequence.
ACCESSION  AZ060178
VERSION     AZ060178.1 GI:7351427
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-405E23.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 405 row: E column: 23
Seq primer: SP6
Class: BAC ends.

```

```

FEATURES
source
Location/Qualifiers
1..489
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-405E23"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

```

```

selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      162 a      61 c      67 g      198 t
ORIGIN

```

```

Query Match      79.1%; Score 17.4; DB 237; Length 489;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 tgactgtgaacgcttcgaga 19
      ||||| ||||| |||||
Db  170 TGACTGTGAACATTCGAGA 152

```

```

RESULT 4
AZ886419/c
LOCUS      530 bp      DNA      GSS      05-MAR-2001
DEFINITION RPCI-23-182I6.TJ RPCI-23 Mus musculus genomic clone RPCI-23-182I6,
DNA sequence.
ACCESSION  AZ886419
VERSION     AZ886419.1 GI:13205364
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-182I6.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 182 row: I column: 6
Seq primer: SP6
Class: BAC ends.

```

```

FEATURES
source
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-182I6"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      174 a      65 c      73 g      218 t
ORIGIN

```

```

Query Match      79.1%; Score 17.4; DB 251; Length 530;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```



Qy 1 tgactgtgaacgttcgaga 19  
 |||||  
 Db 189 TGACTGTGAACATTCGAGA 171

## RESULT 5

AQ245026 374 bp DNA GSS 03-OCT-1998  
 LOCUS HS\_2056\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo  
 DEFINITION septans genomic clone plate-2056 Col-5 Row-J, DNA sequence.  
 ACCESSION AQ245026  
 VERSION AQ245026.1 GI:3691600  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 374)  
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.  
 TITLE Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 2056 row: J column: 5  
 Class: BAC ends  
 High quality sequence stop: 374.

FEATURES  
source

1. 374  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="plate-2056 Col-5 Row-J"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /sex="male"  
 /note="Organ: sperm; Vector: pBelOAC11; BAC Clones in  
 E-Coli DH10B."  
 BASE COUNT 91 a 73 c 92 g 117 t 1 others  
 ORIGIN

Query Match 78.2%; Score 17.2; DB 226; Length 374;  
 Best Local Similarity 86.4%; Pred. No. 1.5e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
 |||||  
 Db 207 TGACTGTGAACGATTGAGATCA 228

## RESULT 6

AZ536502 408 bp DNA GSS 03-NOV-2000  
 LOCUS 110300\_96 Planococcus lillacinus DNA Planococcus lillacinus genomic,  
 DEFINITION DNA sequence.  
 ACCESSION AZ536502  
 VERSION AZ536502.1 GI:11093449  
 KEYWORDS GSS.  
 SOURCE liliac mealybug.  
 ORGANISM Planococcus lillacinus  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;  
 Aphidiformes; Coccoidea; Pseudococcidae; Planococcus.  
 REFERENCE 1 (bases 1 to 408)

AUTHORS Mohan,K.N. and Chandra,H.S.  
 TITLE Mealybug shotgun sequencing  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Mohan KN  
 Microbiology and Cell Biology  
 Indian Institute of Science  
 Sir C.V. Raman Avenue, Bangalore, Karnataka 560012, India  
 Email: mohan@mcbl.iisc.ernet.in

FEATURES  
source

1. 408  
 /organism="Planococcus lillacinus"  
 /db\_xref="taxon:40930"  
 /clone\_lib="Planococcus lillacinus DNA"  
 BASE COUNT 134 a 83 c 80 g 111 t  
 ORIGIN

Query Match 78.2%; Score 17.2; DB 245; Length 408;  
 Best Local Similarity 86.4%; Pred. No. 1.5e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
 |||||  
 Db 251 TGACTGTGAACGACGATATGA 272

## RESULT 7

BE723539 424 bp mRNA EST 14-SEP-2000  
 LOCUS 193384 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.  
 DEFINITION  
 ACCESSION BE723539  
 VERSION BE723539.1 GI:10124826  
 KEYWORDS EST.  
 SOURCE cow.  
 ORGANISM Bos taurus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 424)  
 AUTHORS Smith,T.P.L., Cases,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,  
 Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid  
 W.W. and Keele,J.W.  
 TITLE Design and use of four pooled tissue normalized cDNA libraries for  
 EST discovery in cattle  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390

Email: smith@mail.marc.usda.gov  
 Single pass sequencing. Bases called and alt\_trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 18  
 and -minmatch 12 options.

PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCACGACG  
 Plate: 92 row: E column: 14  
 Seq primer: ATTTAGGTGACACTATAG.  
 Location/Qualifiers  
 1. 424  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="MARC 4BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;  
 Library made from pooled tissue from day 20 and day 40  
 embryos."

BASE COUNT 107 a 107 c 87 g 123 t  
 ORIGIN

```

Query Match      78.2%; Score 17.2; DB 139; Length 424;
Best Local Similarity 86.4%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||||| |||||
Db 268 TGACTGTGAACGTTAGAGATGA 289

RESULT 8
LOCUS AU083559 463 bp mRNA EST 21-MAR-2000
DEFINITION AU083559 Rice green shoot Oryza sativa cDNA clone S14862, mRNA
sequence.
ACCESSION AU083559
VERSION AU083559.1 GI:7274015
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 463)
AUTHORS Sasaki,T. and Yamamoto,K.
TITLE Rice cDNA from green shoot (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai,Tsukuba
Ibaraki,
Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT = 'RGP'.
S14862_62.

FEATURES             Location/Qualifiers
     source           1..463
                     /organism="Oryza sativa"
                     /strain="Nipponbare"
                     /db_xref="taxon:4530"
                     /clone="S14862"
                     /clone_lib="Rice green shoot"
                     /notes="Green shoot (8 days old)"
BASE COUNT 151 a 74 c 109 g 127 t 2 others
ORIGIN

Query Match      78.2%; Score 17.2; DB 107; Length 463;
Best Local Similarity 86.4%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||||| |||||
Db 151 TGACTGTGAATGTTAGAGATGA 172

RESULT 9
LOCUS AU089685 479 bp mRNA EST 27-APR-2000
DEFINITION AU089685 Rice callus Oryza sativa subsp. japonica cDNA clone C40060
, mRNA sequence.
ACCESSION AU089685
VERSION AU089685.1 GI:7652165
KEYWORDS EST.
SOURCE Oryza sativa subsp. japonica.
ORGANISM Oryza sativa subsp. japonica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 479)

```

```

AUTHORS Sasaki,T. and Yamamoto,K.
TITLE Rice cDNA from callus (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai,Tsukuba
Ibaraki,
Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT = 'RGP'.
C40060_32.

FEATURES             Location/Qualifiers
     source           1..479
                     /organism="Oryza sativa subsp. japonica"
                     /strain="cultivar Nipponbare, sub_species Japonica"
                     /db_xref="taxon:39947"
                     /clone="C40060"
                     /clone_lib="Rice callus"
                     /note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
                     NotI; cDNA prepared from rice callus mRNAs by using
                     oligo(dT) as a primer and ligating to the SalI-NotI site
                     of pBluescript II SK+ phagemid."
BASE COUNT 149 a 96 c 104 g 130 t
ORIGIN

Query Match      78.2%; Score 17.2; DB 107; Length 479;
Best Local Similarity 86.4%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||||| |||||
Db 299 TGAGTGTGAATGTTAGAGATGA 320

RESULT 10
LOCUS CNS05PD9/c 972 bp DNA GSS 26-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
005F08 of library A from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL347814
VERSION AL347814.1 GI:8241584
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 972)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 972)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 972)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis

```

genome. For more information, please take a look at  
http://www.genoscope.cns.fr/tetraodon.

# FEATURES

source

1. .972

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="005F08"

/clone\_lib="A"

/note="Genoscope sequence ID : COAA005DC04C1-end : T7"  
BASE COUNT 195 a 268 c 199 g 297 t 13 others

# ORIGIN

Query Match 78.2%; Score 17.2; DB 222; Length 972;  
Best Local Similarity 86.4%; Pred. No. 1.7e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22

||||| ||||| ||||| ||||| |||||

Db 46 TGGCTGTGAAGGTCGAGATGA 25

# RESULT 11

AA094019

LOCUS

DEFINITION AA094019 105 bp mRNA EST 25-OCT-1996  
CDNA 5', mRNA sequence.

ACCESSION AA094019

VERSION AA094019.1 GI:1639612

KEYWORDS EST

SOURCE human.

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Liew.C.C.

TITLE CDNAs from fetal heart (1996)

UNPUBLISHED (1996)

CONTACT: Liew CC

DEPARTMENT OF Laboratory Medicine and Pathobiology

UNIVERSITY OF Toronto

Banting Institute, 100 College St., Toronto, Ontario, M5G1L5

Tel: 4165788758

Fax: 4165785650

Email: liewc@utcc.utoronto.ca

PCR Primers

FORWARD: 5' GCCAGCTCGAAATTAACCTCTACTAAAGG 3'

BACKWARD: 5' CCAGTGAATGTAAATACGACTCTACTAGGCG 3'

Seq primer: 5' GAATTAACCTCTACTAAAGG 3'

Location/Qualifiers

1. .105

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="Human fetal heart, Lambda ZAP Express"

/lab\_host="E. coli XL1-Blue"

/note="Vector: Lambda ZAP Express; Site1: EcoRI; Site2:

XhoI; mRNA was purified from human fetal hearts (8-10

weeks). cDNA was synthesized using a XhoI-Oligo dt

adaptor-primer. EcoRI adaptors were ligated, followed by

digestion with XhoI for directional cloning into

predigested lambda ZAP Express."

BASE COUNT 31 a 21 c 16 g 37 t

ORIGIN

Query Match 76.4%; Score 16.8; DB 2; Length 105;  
Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagat 20

||||| ||||| ||||| ||||| |||||

Db 43 TCAGTGTGAACCTTCAGAT 62

# RESULT 12

AZ483488

LOCUS

DEFINITION

1M0309M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0309M12 F, DNA sequence.

ACCESSION AZ483488

VERSION AZ483488.1 GI:10647510

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 523)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A.  
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

UNPUBLISHED (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF Utah Genome Center

UNIVERSITY OF Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0309 row: M column: 12

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 523.

Location/Qualifiers

1. .523

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0309M12"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gil4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 162 a 127 c 103 g 131 t

ORIGIN

Query Match 76.4%; Score 16.8; DB 244; Length 523;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 actgtgaacgttcgagatga 22

||||| ||||| ||||| ||||| |||||

Db 376 ACTGTGTACTTTCGAGATGA 395

```

RESULT 13
LOCUS      AZ501799      526 bp      DNA      GSS      05-OCT-2000
DEFINITION 1M0340J17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
ACCESSION  AZ501799
VERSION     AZ501799.1  GI:10683115
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 526)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL   plasmid inserts
COMMENT   Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0340 row: J column: 17
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 526.
FEATURES   source
            1..526
            /location/Qualifiers
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone_lib="UUGCLM0340J17"
            /clone_lib="UUGCLM0340J17"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /note="Vector: pMD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD42 (g1147321141gb1AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT 121 a 126 c 139 g 140 t
ORIGIN
            1 tgcactgtgaacgttcgagat 20
            ||||| ||||| ||||| |||||
Query Match 76.4%; Score 16.8; DB 245; Length 526;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 tgcactgtgaacgttcgagat 20

```

```

Db 60 TGACAGTGAACGTTCTAGAT 79
RESULT 14
LOCUS      AV732648/c      681 bp      mRNA      EST      17-OCT-2000
DEFINITION AV732648 HTF Homo sapiens cDNA clone HTFBLB03 5', mRNA sequence.
ACCESSION  AV732648
VERSION     AV732648.1  GI:10850193
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 681)
AUTHORS   Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
            Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
            S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
            Chen,J., Chen,Z. and Han,Z.
TITLE     Homo sapiens cDNA HTF clones
JOURNAL   Unpublished (2000)
COMMENT   Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES   source
            1..681
            /location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="HTFBLB03"
            /clone_lib="HTF"
            /tissue_type="Hypothalamus"
            /dev_stage="Adult"
            /lab_host="SOLR"
            /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
            XhoI"
BASE COUNT 202 a 137 c 156 g 184 t 2 others
ORIGIN
            1 tgcactgtgaacgttcgagatga 22
            ||||| ||||| ||||| |||||
Query Match 76.4%; Score 16.8; DB 32; Length 681;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 actgtgaacgttcgagatga 22
            ||||| ||||| ||||| |||||
Db 382 ACTGTGACATTGTGAGATCA 363
RESULT 15
LOCUS      AW916461      705 bp      mRNA      EST      25-MAY-2000
DEFINITION ES347765 Rat gene index, normalized rat, norvegicus, Bento Soares
            Rattus norvegicus cDNA clone RGID049 5' end, mRNA sequence.
ACCESSION  AW916461
VERSION     AW916461.1  GI:8082187
KEYWORDS   EST.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 705)
AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
TITLE     Rat Genome Project: Generation of a Rat EST (EST) Catalog & Rat
            Gene Index
JOURNAL   Unpublished (1998)
COMMENT   Contact: Lee, NH

```

The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org

This clone is available through the ATCC, contact the ATCC  
tel#703-365-2700 for further information

Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1..705

/organism="Rattus norvegicus"

/db\_xref="taxon:10116"

/clone="RGIDQ49"

/clone\_lib="Rat gene index, normalized rat, norvegicus,

Bento Soares"

/tissue\_type="mix - brain, ovary, placenta, kidney, lung,

liver, embryo, heart, muscle, spleen"

/lab\_host="SOLR"

/note="Vector: pBlueScript SK(-); Site\_1: EcoRI; Site\_2:

XhoI; Estimated insert size approx.1 kb"

177 a 201 c 169 g 157 t 1 others

BASE COUNT  
ORIGIN

Query Match 76.4%; Score 16.8; DB 122; Length 705;  
Best Local Similarity 90.0%; Pred. NO. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 actgtgaacgttcgagatga 22

||||| |||||

Db 150 ACTGTGACCTTCGAGATGA 169

Search completed: October 9, 2001, 18:20:11  
Job time: 9781 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:38:15 ; Search time 10334.3 Seconds  
(without alignments)  
31.457 Million cell updates/sec

Title: US-09-713-136-1

Perfect score: 22

Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq.\*

2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*

3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*

4: /cgn2\_6/ptodata/1/pna/US08\_COMB.seq.\*

5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*

7: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq.\*

8: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq.\*

9: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq.\*

10: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq.\*

11: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq.\*

12: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq.\*

13: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq.\*

14: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq.\*

15: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq.\*

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18: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq.\*

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21: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*

22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*

23: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*

24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*

25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*

26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*

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30: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq.\*

31: /cgn2\_6/ptodata/1/pna/US098\_COMB.seq.\*

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35: /cgn2\_6/ptodata/1/pna/US098D\_COMB.seq.\*

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37: /cgn2\_6/ptodata/1/pna/US098F\_COMB.seq.\*

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41: /cgn2\_6/ptodata/1/pna/US098J\_COMB.seq.\*

42: /cgn2\_6/ptodata/1/pna/US098K\_COMB.seq.\*

43: /cgn2\_6/ptodata/1/pna/US098L\_COMB.seq.\*

44: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq.\*

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54: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*

55: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq.\*

56: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq.\*

57: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*

58: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq.\*

59: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq.\*

60: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22	100.0	22	1	PCT-US00-18229-32	Sequence 32, Appl
2	22	100.0	22	1	PCT-US00-35064-1	Sequence 1, Appl
3	22	100.0	22	1	PCT-US01-03029-1	Sequence 1, Appl
4	22	100.0	22	1	PCT-US01-06034-1	Sequence 1, Appl
5	22	100.0	22	1	PCT-US01-10118-1	Sequence 1, Appl
6	22	100.0	22	1	PCT-US01-10118-3	Sequence 3, Appl
7	22	100.0	22	1	PCT-US01-11290-1	Sequence 1, Appl
8	22	100.0	22	1	PCT-US01-14508-1	Sequence 1, Appl
9	22	100.0	22	1	PCT-US99-21203-19	Sequence 19, Appl
10	22	100.0	22	13	US-08-927-120-19	Sequence 19, Appl
11	22	100.0	22	15	US-09-167-039-19	Sequence 19, Appl
12	22	100.0	22	16	US-09-235-742-19	Sequence 2, Appl
13	22	100.0	22	16	US-09-296-477-2	Sequence 1, Appl
14	22	100.0	22	17	US-09-308-036A-1	Sequence 1, Appl
15	22	100.0	22	17	US-09-324-191A-1	Sequence 1, Appl
16	22	100.0	22	17	US-09-347-343-32	Sequence 32, Appl
17	22	100.0	22	17	US-09-397-198-1	Sequence 1, Appl
18	22	100.0	22	18	US-09-415-186-1	Sequence 1, Appl
19	22	100.0	22	18	US-09-470-382-69	Sequence 69, Appl
20	22	100.0	22	22	US-09-565-906-2	Sequence 2, Appl
21	22	100.0	22	22	US-09-570-325-19	Sequence 19, Appl
22	22	100.0	22	25	US-09-642-492-1	Sequence 1, Appl
23	22	100.0	22	28	US-09-700-354-1	Sequence 1, Appl
24	22	100.0	22	28	US-09-713-136-1	Sequence 1, Appl
25	22	100.0	22	29	US-09-746-130-1	Sequence 1, Appl
26	22	100.0	22	30	US-09-774-403-1	Sequence 1, Appl
27	22	100.0	22	31	US-09-791-500-1	Sequence 1, Appl
28	22	100.0	22	31	US-09-820-484-1	Sequence 3, Appl
29	22	100.0	22	31	US-09-820-484-3	Sequence 1, Appl
30	22	100.0	22	31	US-09-828-505-1	Sequence 1, Appl
31	21.2	96.4	22	18	US-09-415-186-7	Sequence 7, Appl
32	21	95.5	22	16	US-09-296-477-15	Sequence 15, Appl
33	21	95.5	22	17	US-09-324-191A-5	Sequence 5, Appl
34	21	95.5	22	25	US-09-642-492-7	Sequence 7, Appl
35	21	95.5	22	28	US-09-713-136-7	Sequence 2, Appl
36	20.4	92.7	22	1	PCT-US00-35064-2	Sequence 2, Appl
37	20.4	92.7	22	1	PCT-US01-03029-2	Sequence 4, Appl
38	20.4	92.7	22	1	PCT-US01-06034-4	Sequence 5, Appl
39	20.4	92.7	22	1	PCT-US01-06034-5	Sequence 6, Appl
40	20.4	92.7	22	1	PCT-US01-10118-2	Sequence 2, Appl
41	20.4	92.7	22	1	PCT-US01-10118-6	Sequence 6, Appl
42	20.4	92.7	22	1	PCT-US01-11290-2	Sequence 2, Appl
43	20.4	92.7	22	1	PCT-US01-14508-10	Sequence 10, Appl
44	20.4	92.7	22	31	US-09-828-505-2	Sequence 2, Appl
45	20.4	92.7	22	31	US-09-828-505-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
PCT-US00-18229-32  
; Sequence 32, Application PC/TUS0018229  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Kobayashi, Hiroko  
; TITLE OF INVENTION: Method for Enhancing an Immune Response  
; FILE REFERENCE: 6510-189W01  
; CURRENT APPLICATION NUMBER: PCT/US00/18229  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
PCT-US00-18229-32

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
|||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2  
PCT-US00-35064-1  
; Sequence 1, Application PC/TUS0035064  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Method for Preventing an Anaphylactic  
; FILE REFERENCE: 06510/201W01  
; CURRENT APPLICATION NUMBER: PCT/US00/35064  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/171,830  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule  
PCT-US00-35064-1

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
|||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3  
PCT-US01-03029-1  
; Sequence 1, Application PC/TUS0103029  
; GENERAL INFORMATION:

; APPLICANT: Eyal Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi  
; APPLICANT: Dennis A. Carson  
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in  
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen  
; FILE REFERENCE: 06510/166W01  
; CURRENT APPLICATION NUMBER: PCT/US01/03029  
; CURRENT FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/179,353  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory sequence  
PCT-US01-03029-1

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
|||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 4  
PCT-US01-06034-1  
; Sequence 1, Application PC/TUS0106034  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Rachmilewitz, Daniel  
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.  
; FILE REFERENCE: 6510-202W0  
; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
; OTHER INFORMATION: oligonucleotide primer  
; OTHER INFORMATION: oligonucleotide primer  
PCT-US01-06034-1

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
|||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5  
PCT-US01-10118-1  
; Sequence 1, Application PC/TUS0110118  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Cho, Hearn Jay  
; APPLICANT: Richman, Douglas  
; APPLICANT: Horner, Anthony A.

RESULT 7  
PCT-US01-11290-1  
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T  
; FILE REFERENCE: 06510-188WO1  
; CURRENT APPLICATION NUMBER: PCT/US01/10118  
; CURRENT FILING DATE: 2001-03-17  
; PRIOR APPLICATION NUMBER: US 60/192,537  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/203,567  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/215,895  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: disulfide thymine  
PCT-US01-10118-1

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6  
PCT-US01-10118-3  
; Sequence 3, Application PC/TUS0110118  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Cho, Hearn Jay  
; APPLICANT: Richman, Douglas  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T  
; FILE REFERENCE: 06510-188WO1  
; CURRENT APPLICATION NUMBER: PCT/US01/10118  
; CURRENT FILING DATE: 2001-03-17  
; PRIOR APPLICATION NUMBER: US 60/192,537  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/203,567  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/215,895  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: phosphorothioate ISS-ODN  
PCT-US01-10118-3

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 7  
PCT-US01-11290-1  
; Sequence 1, Application PC/TUS0111290  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Takabayashi, Kenji  
; APPLICANT: Nguyen, Minh-Duc  
; TITLE OF INVENTION: Synergistic Improvements to  
; FILE REFERENCE: 6510-203WO  
; CURRENT APPLICATION NUMBER: PCT/US01/11290  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,890  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence  
PCT-US01-11290-1

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 8  
PCT-US01-14508-1  
; Sequence 1, Application PC/TUS0114508  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Lois, Augusto F.  
; APPLICANT: Takabayashi, Kenji  
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and  
; FILE REFERENCE: 06510/168WO1  
; CURRENT APPLICATION NUMBER: PCT/US01/14508  
; CURRENT FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/262,321  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/202,274  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ISS-ODN  
PCT-US01-14508-1

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 9  
PCT-US99-21203-19  
; Sequence 19, Application PC/TUS9921203



GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski L.L.P.  
STREET: 865 S. Figueroa Street, 29th Floor  
CITY: Los Angeles  
STATE: CA  
COUNTRY: US  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US99/21203  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/927,120  
FILING DATE: 05 September 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Berliner, Robert  
REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 5555-188  
TELEPHONE: 213-892-9200  
TELEFAX: 213-680-4518  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: non-coding oligonucleotides  
PCT-US99-21203-19

Query Match 100.0%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22  
|||||  
DB 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 10  
US-08-927-120-19  
Sequence 19, Application US/08927120  
GENERAL INFORMATION:  
APPLICANT: Raz, Eyal  
TITLE OF INVENTION: IMMUNIZATION-FREE METHODS  
TITLE OF INVENTION: FOR STIMULATING IMMUNE RESPONSIVENESS AND REDUCING  
INFLAMMATION IN A HOST  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,120

FILING DATE: 22-AUG-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Taylor, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/054001  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: non-coding oligonucleotides  
US-08-927-120-19

Query Match 100.0%; Score 22; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22  
|||||  
DB 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 11  
US-09-167-039-19  
Sequence 19, Application US/09167039  
GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: METHODS AND ADJUVANTS  
TITLE OF INVENTION: FOR STIMULATING MUCOSAL IMMUNITY  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 402 West Broadway, Suite 2300  
CITY: San Diego  
STATE: CA  
COUNTRY: US  
ZIP: 92101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/167,039  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/927,120  
FILING DATE: 05 September 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Taylor, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/063001  
TELEPHONE: 619-234-3510  
TELEFAX: 619-234-6655  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: non-coding oligonucleotides  
US-09-167-039-19

Query Match 100.0%; Score 22; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 TGACTGTGAACGTTCCGAGATGA 22

## RESULT 12

US-09-235-742-19  
; Sequence 19, Application US/09235742  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eval  
; TITLE OF INVENTION: Immunization-Free Methods for Treating  
; TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and  
; TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1  
; TITLE OF INVENTION: Phenotype  
; FILE REFERENCE: 6510-170CONA  
; CURRENT APPLICATION NUMBER: US/09/235,742  
; CURRENT FILING DATE: 1999-01-21  
; EARLIER APPLICATION NUMBER: 08/927,120  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 08/593,554  
; EARLIER FILING DATE: 1996-01-30  
; EARLIER APPLICATION NUMBER: 08/725,968  
; EARLIER FILING DATE: 1996-10-04  
; EARLIER APPLICATION NUMBER: 60/028,118  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Recombinant or Synthetic Sequence  
US-09-235-742-19

Query Match 100.0%; Score 22; DB 16; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

## RESULT 13

US-09-296-477-2  
; Sequence 2, Application US/09296477A  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, E.  
; APPLICANT: SCHWARTZ, D.  
; APPLICANT: ROMAN, M.  
; APPLICANT: DINA, D.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,  
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE  
; FILE REFERENCE: 37782000420  
; CURRENT APPLICATION NUMBER: US/09/296,477A  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: 09/092,329  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 60/048,793  
; EARLIER FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 22

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-296-477-2

Query Match 100.0%; Score 22; DB 16; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

## RESULT 14

US-09-308-036A-1  
; Sequence 1, Application US/09308036A  
; GENERAL INFORMATION:  
; APPLICANT: Carson, Dennis A.  
; APPLICANT: Raz, Eval  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Immunostimulatory  
; TITLE OF INVENTION: Polynucleotide/Immunomodulatory Molecule Conjugates  
; FILE REFERENCE: 6510-172CIP  
; CURRENT APPLICATION NUMBER: US/09/308,036A  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: PCT/US97/19004  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/028,118  
; PRIOR FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DY1018 polynucleotide  
US-09-308-036A-1

Query Match 100.0%; Score 22; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

## RESULT 15

US-09-324-191A-1  
; Sequence 1, Application US/09324191A  
; GENERAL INFORMATION:  
; APPLICANT: Schwartz, David  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH  
; TITLE OF INVENTION: MODIFIED BASES AND METHODS OF USE THEREOF  
; FILE REFERENCE: 37782000200  
; CURRENT APPLICATION NUMBER: US/09/324,191A  
; CURRENT FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: 60/080,310  
; PRIOR FILING DATE: 1998-06-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-324-191A-1

Query Match 100.0%; Score 22; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred No. 0.75;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22  
| | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

Search completed: October 9, 2001, 21:12:35  
Job time: 20060 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:20 ; Search time 1391.6 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-09-713-136-1

Perfect score: 22  
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq1:\*  
7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq2:\*  
8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	7 US-09-802-518-1	Sequence 1, Appli
2	22	100.0	22	7 US-09-802-359-1	Sequence 1, Appli
3	22	100.0	22	7 US-09-802-376-1	Sequence 1, Appli
4	21	95.5	22	7 US-09-802-518-7	Sequence 7, Appli
5	21	95.5	22	7 US-09-802-359-7	Sequence 7, Appli
6	21	95.5	22	7 US-09-802-376-7	Sequence 7, Appli
7	20.4	92.7	22	6 US-09-770-943-2	Sequence 2, Appli
8	20.4	92.7	22	7 US-09-802-518-2	Sequence 2, Appli
9	20.4	92.7	22	7 US-09-802-518-4	Sequence 4, Appli
10	20.4	92.7	22	7 US-09-802-359-2	Sequence 2, Appli
11	20.4	92.7	22	7 US-09-802-359-4	Sequence 4, Appli
12	20.4	92.7	22	7 US-09-802-376-2	Sequence 2, Appli
13	20.4	92.7	22	7 US-09-802-376-4	Sequence 4, Appli
14	20	90.9	22	7 US-09-802-518-8	Sequence 8, Appli
15	20	90.9	22	7 US-09-802-359-8	Sequence 8, Appli
16	20	90.9	22	7 US-09-802-376-8	Sequence 8, Appli
17	19.4	88.2	22	7 US-09-802-518-6	Sequence 6, Appli
18	19.4	88.2	22	7 US-09-802-359-6	Sequence 6, Appli
19	19.4	88.2	22	7 US-09-802-376-6	Sequence 6, Appli
20	18.8	85.5	22	6 US-09-770-943-1	Sequence 1, Appli
21	18.8	85.5	22	6 US-09-770-943-3	Sequence 3, Appli
22	18.8	85.5	22	6 US-09-770-943-10	Sequence 10, Appli
23	18.8	85.5	22	7 US-09-802-518-10	Sequence 10, Appli
24	18.8	85.5	22	7 US-09-802-518-11	Sequence 11, Appli
25	18.8	85.5	22	7 US-09-802-359-9	Sequence 9, Appli

Sequence 10, Appli  
Sequence 9, Appli  
Sequence 10, Appli  
Sequence 4, Appli  
Sequence 331, App  
Sequence 28028, A  
Sequence 47271, A  
Sequence 1286, Ap  
Sequence 21114, A  
Sequence 216, App  
Sequence 9048, Ap  
Sequence 14097, A  
Sequence 7849, Ap  
Sequence 19415, A  
Sequence 1014, Ap  
Sequence 10258, A  
Sequence 484, App  
Sequence 10235, A  
Sequence 10236, A

26 18.8 85.5 22 7 US-09-802-359-10  
27 18.8 85.5 22 7 US-09-802-376-9  
28 18.8 85.5 22 7 US-09-802-376-10  
29 17.2 78.2 22 6 US-09-770-943-4  
30 17.2 78.2 252 5 US-09-825-790-331  
31 16.8 76.4 252 7 US-09-540-213-28028  
32 16.8 76.4 285 7 US-09-540-213-47271  
33 16.8 76.4 649 7 US-09-902-340-1286  
34 16.2 73.6 427 6 US-09-909-629-21114  
35 16.2 73.6 442 6 US-09-836-472-216  
36 16.2 73.6 445 6 US-09-906-555-9048  
37 16.2 73.6 448 6 US-09-904-703-14097  
38 16.2 73.6 448 6 US-09-909-627-7849  
39 16.2 73.6 469 6 US-09-909-627-19415  
40 16.2 73.6 606 5 US-09-921-378-10527  
41 16.2 73.6 668 6 US-09-836-472-1014  
42 16.2 73.6 3713 8 US-60-278-232-10258  
43 16.2 73.6 82360 6 US-09-803-736-484  
44 15.8 24853 7 US-09-764-874-10235  
45 15.8 32212 7 US-09-764-874-10236

## ALIGNMENTS

RESULT 1  
US-09-802-518-1  
; Sequence 1, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802.518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-1

Query Match 100.0%; Score 22; DB 7; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2  
US-09-802-359-1  
; Sequence 1, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802.359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1

```
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match          100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match          100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 4
US-09-802-518-7
; Sequence 7, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-1

Query Match          100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7
```

Query Match 95.5%; Score 21; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.14;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaangttcgagatga 22

RESULT 7  
US-09-770-943-2  
; Sequence 2, Application US/09770943  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/770,943  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/092,314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-770-943-2

Query Match 92.7%; Score 20.4; DB 6; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.29;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgtttagatga 22

RESULT 8  
US-09-802-518-2  
; Sequence 2, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-2

Query Match 92.7%; Score 20.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.29;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22

Query Match 95.5%; Score 21; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.14;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 9  
US-09-802-518-4  
; Sequence 4, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-4

Query Match 92.7%; Score 20.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.29;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 10  
US-09-802-359-2  
; Sequence 2, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-359-2

Query Match 92.7%; Score 20.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.29;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 11  
US-09-802-359-4  
; Sequence 4, Application US/09802359  
; GENERAL INFORMATION:

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; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
; US-09-802-359-4

Query Match          92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 12
US-09-802-376-2
; Sequence 2, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
; US-09-802-376-2

Query Match          92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13
US-09-802-376-4
; Sequence 4, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
; US-09-802-376-4

Query Match          92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 14
US-09-802-518-8
; Sequence 8, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
; US-09-802-518-8

Query Match          90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 15
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-8

Query Match      90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
   ||||| ||| |||||
Db 1 tgactgtgaangttingagatga 22

Search completed: October 9, 2001, 21:35:59
Job time: 21219 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:18:18 ; Search time 2150.93 Seconds  
(without alignments)  
158.206 Million cell updates/sec

Title: US-09-713-136-2  
Perfect score: 22  
Sequence: 1 tgacggtgaacgttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba1:\*  
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4: gb\_in1:\*  
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6: gb\_in3:\*  
7: gb\_em:\*  
8: gb\_ov:\*  
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11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
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16: em\_ba1:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
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27: em\_htg\_hum6:\*  
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29: em\_htg\_hum8:\*  
30: em\_htg\_hum9:\*  
31: em\_htg\_inv1:\*  
32: em\_htg\_inv2:\*  
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37: em\_hum4:\*  
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53: gb\_sts1:\*  
54: gb\_sts2:\*  
55: gb\_sts3:\*  
56: gb\_sy:\*  
57: gb\_un:\*  
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59: gb\_v12:\*  
60: gb\_htg1:\*  
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62: gb\_htg3:\*  
63: gb\_htg4:\*  
64: gb\_htg5:\*  
65: gb\_htg6:\*  
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71: gb\_htg12:\*  
72: gb\_htg13:\*  
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74: gb\_htg15:\*  
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82: gb\_htg23:\*  
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84: gb\_htg25:\*  
85: gb\_pr1:\*  
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87: gb\_pr3:\*  
88: gb\_pr4:\*  
89: gb\_pr5:\*  
90: gb\_pr6:\*  
91: gb\_pr7:\*  
92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_rol:\*  
95: gb\_rod:\*  
96: gb\_in4:\*  
97: gb\_pr10:\*  
98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	10	AX083676 Sequence
2	20.4	92.7	22	9	AX036945 Sequence
3	20.4	92.7	22	9	AX046993 Sequence
4	20.4	92.7	22	10	AX083675 Sequence
5	19.4	88.2	22	10	AX083681 Sequence
6	18.8	85.5	22	9	AX036946 Sequence
7	18.8	85.5	22	10	AX083678 Sequence
8	18.4	83.6	22	10	AX083682 Sequence

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9 17.8 80.9 22 10 AX083680 Sequence
10 17.2 78.2 22 9 AX036944
11 17.2 78.2 22 9 AX036952
12 17.2 78.2 2079 5 AF025951 Dictyoste
13 16.8 76.4 111234 88 AC079157 Homo sapi
14 16.8 76.4 159072 74 AC073123
15 16.8 76.4 159072 74 AC073123
16 16.2 73.6 642 71 AC032512 Giardia i
17 16.2 73.6 781 71 AC035787 Giardia i
18 16.2 73.6 858 72 AC064490 Giardia i
19 16.2 73.6 1014 72 AC048567 Giardia i
20 16.2 73.6 1076 72 AC048568 Giardia i
21 16.2 73.6 1572 15 SCYJL043W
22 16.2 73.6 1736 9 A49990
23 16.2 73.6 3514 2 BPFHABDNA
24 16.2 73.6 3983 7 S57131
25 16.2 73.6 4880 15 SCYJL042W
26 16.2 73.6 6040 2 CTU32622
27 16.2 73.6 7031 94 AF320616
28 16.2 73.6 11830 2 BPFHAB1
29 16.2 73.6 11831 2 BPFHABFH
30 16.2 73.6 11883 10 I06606
31 16.2 73.6 12256 1 AF111796
32 16.2 73.6 93821 66 AC021596
33 16.2 73.6 136282 84 HSDU36889
34 16.2 73.6 145939 79 AL158143
35 16.2 73.6 149886 94 MMHC438N12
36 16.2 73.6 157647 26 AC069450 Homo sapi
37 16.2 73.6 165337 70 AC027442 Homo sapi
38 16.2 73.6 187237 86 AC007938 Homo sapi
39 16.2 73.6 189893 66 AC021165 Homo sapi
40 16.2 73.6 182271 76 AC080169 Mus muscu
41 16.2 73.6 185637 60 AC007979 Mus muscu
42 16.2 73.6 189706 75 AC073778 Mus muscu
43 16.2 73.6 200905 82 AL590619 Mus muscu
44 16.2 73.6 201214 75 AC074012 Homo sapi
45 16.2 73.6 209777 69 AC024934 Homo sapi

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## ALIGNMENTS

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RESULT 1
AX083676 28-FEB-2001
LOCUS AX083676 22 bp DNA
DEFINITION Sequence 2 from Patent WO0112223.
ACCESSION AX083676
VERSION AX083676.1 GI:13185408
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest, G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
JOURNAL Patent: WO 0112223-A 2 22-FEB-2001;
JOURNAL Dynavax Technologies Corporation (US)
FEATURES
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="synthetic construct"
BASE COUNT 6 a 4 c 7 g 5 t
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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
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Db 1 TGACCGTGAACGTTTCGAGATGA 22
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LOCUS AX036945 22 bp DNA
DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier, A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
JOURNAL ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
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Query Match 92.7%; Score 20.4; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
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Db 1 TGACTGTGAACGTTTCGAGATGA 22
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AX046993 15-DEC-2000
LOCUS AX046993 22 bp DNA
DEFINITION Sequence 2 from Patent WO0067787.
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss, R. B.
TITLE Hiv immunogenic compositions and methods
JOURNAL Patent: WO 0067787-A 2 16-NOV-2000;
JOURNAL THE IMMUNE RESPONSE CORPORATION (US)
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/db_xref="taxon:32630"
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Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
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Db 1 TGACTGTGAACGTTTCGAGATGA 22
RESULT 4
AX083675 28-FEB-2001
LOCUS AX083675 22 bp DNA
DEFINITION Sequence 1 from WO0112223.

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ACCESSION AX083675  
VERSION AX083675.1 GI:13185407  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Carpentier, A.  
TITLE Patent: FR 2790955-A 3 22-SEP-2000;  
JOURNAL ASSIST PUBL HOPITAUX DE PARIS (FR)  
FEATURES Location/Qualifiers  
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Best Local Similarity 95.5%; Pred. No. 1.2;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgaccgtgaacgttcgagatga 22  
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Db 1 TGAAGTGTGACGTTCCGAGATGA 22  
RESULT 5  
AX083681  
LOCUS AX083681 22 bp DNA PAT 28-FEB-2001  
DEFINITION Sequence 7 from Patent WO0112223.  
ACCESSION AX083681  
VERSION AX083681.1 GI:13185413  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 22)  
AUTHORS van Nest, G.  
TITLE Methods of modulating an immune response using immunostimulatory s  
sequences and compositions for use therein  
JOURNAL Patent: WO 011223-A 7 22-FEB-2001;  
Dynamax Technologies Corporation (US)  
FEATURES Location/Qualifiers  
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/organism="synthetic construct"  
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modified\_base 11  
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Best Local Similarity 90.9%; Pred. No. 4.4;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Db 1 TGAAGTGTGACGTTCCGAGATGA 22  
RESULT 6  
AX036946  
LOCUS AX036946 22 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 3 from Patent FR2790955.  
ACCESSION AX036946  
VERSION AX036946.1 GI:11226374  
KEYWORDS

SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Carpentier, A.  
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;  
ASSIST PUBL HOPITAUX DE PARIS (FR)  
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Best Local Similarity 90.9%; Pred. No. 9.7;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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RESULT 7  
AX083678  
LOCUS AX083678 22 bp DNA PAT 28-FEB-2001  
DEFINITION Sequence 4 from Patent WO0112223.  
ACCESSION AX083678  
VERSION AX083678.1 GI:13185410  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 22)  
AUTHORS van Nest, G.  
TITLE Methods of modulating an immune response using immunostimulatory s  
sequences and compositions for use therein  
JOURNAL Patent: WO 011223-A 4 22-FEB-2001;  
Dynamax Technologies Corporation (US)  
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Best Local Similarity 90.9%; Pred. No. 9.7;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 tgaccgtgaacgttcgagatga 22  
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Db 1 TGAAGTGTGACGTTCCGAGATGA 22  
RESULT 8  
AX083682  
LOCUS AX083682 22 bp DNA PAT 28-FEB-2001  
DEFINITION Sequence 8 from Patent WO0112223.  
ACCESSION AX083682  
VERSION AX083682.1 GI:13185414  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 22)  
AUTHORS van Nest, G.  
TITLE Methods of modulating an immune response using immunostimulatory s  
sequences and compositions for use therein

JOURNAL Patent: WO 0112223-A 8 22-FEB-2001;  
 Dynavax Technologies Corporation (US)  
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 ORIGIN

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 Db 1 TGA CTGTGAANGTTNGAGATGA 22

RESULT 9  
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 LOCUS AX083680 22 bp DNA PAT 28-FEB-2001  
 DEFINITION Sequence 6 from Patent WO0112223.  
 ACCESSION AX083680  
 VERSION AX083680.1 GI:13185412  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS van Nest,G.  
 TITLE Methods of modulating an immune response using immunostimulatory s  
 equences and compositions for use therein  
 JOURNAL Patent: WO 0112223-A 6 22-FEB-2001;  
 Dynavax Technologies Corporation (US)  
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RESULT 10  
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 DEFINITION Sequence 1 from Patent FR2790955.  
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 VERSION AX036944.1 GI:11226372  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Carpentier,A.

JOURNAL Patent: FR 2790955-A 1 22-SEP-2000;  
 ASSIST PUBL HOPITAUX DE PARIS (FR)  
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 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22  
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 Db 1 TGA CTGTGAAGGTTAGAGATGA 22

RESULT 11  
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 LOCUS AX036952 22 bp DNA PAT 16-NOV-2000  
 DEFINITION Sequence 9 from Patent FR2790955.  
 ACCESSION AX036952  
 VERSION AX036952.1 GI:11226380  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS Carpentier,A.  
 JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;  
 ASSIST PUBL HOPITAUX DE PARIS (FR)  
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 ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 78;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22  
 |||| |||| |||| |||| ||||  
 Db 1 TGA CTGTGAACGTTATAGATGA 22

RESULT 12  
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 LOCUS AF025951 2079 bp mRNA INV 26-OCT-1997  
 DEFINITION Dictyostellium discoideum heat-shock cognate protein 70 (hsc70)  
 ACCESSION AF025951  
 VERSION AF025951.1 GI:2564919  
 KEYWORDS  
 SOURCE Dictyostellium discoideum.  
 ORGANISM Dictyostellium discoideum  
 REFERENCE 1 (bases 1 to 2079)  
 AUTHORS Boves,H., Mintert,U., Dittrich,W., Faix,J. and Gerisch,G.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-SEP-1997) Cellbiology, Max-Planck-Institute of  
 Biochemistry, Am Klopferspitz 18a, Martinsried 82152, Germany  
 FEATURES Location/Qualifiers  
 source 1..2079  
 /organism="Dictyostellium discoideum"  
 /strain="AX3"  
 /db\_xref="taxon:44689"

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/cell_type="amoeba"
1..2079
/gene="hsc70"
123..2021
CDS
/gene="hsc70"
/note="chaperone; localized to filopodias and cortex;
hsc70"
/codon_start=1
/product="heat-shock cognate protein 70"
/protein_id="AA881865.1"
/db_xref="GI:2564920"
/translation="MSSSICIDLTGTYSCVGMQNDRVEIANDQGNRTTPSYAFNE
TERLIDAAKNOVAMPTNTIFDAKRLIGKFSDPVQSDMKHWPFKVIAKEDGKPHL
OVFEKGEVKTSPFEEVSSVLLKMKETAAYLGKTTINNAVITVPAYENDSOROATKDA
GATAKLVORINEPTAAAIAYGLEKKSOGERNILFDLGGTFDVSLLTIETGCVFEV
NATAGTHLGGEDFNRLVNHVFDEPKRHKHLDLMTNQRHRLRATACERAKRTLS
AQASIEIDLFEGIDFYTSITRAFELCADLFRGLDPVKLDSKDKDKTIHEIV
LVGSTRIPKVOQLLOHFNGLKNSINPDEAVAYGAQAAAILNSNEGAKVADILL
LDVAPLSMGLTAGGVTTLIPRNTIPCKKNOTFTSYSDNQTGVLVQVYVEGERAMTR
DNLLCKEELTNIPAPRGVPOIEVTFDIDANGILNVAEDKSTGNKHKITITNDKDR
LTAQIEKMKVMDKMPKQDQREYVESKNKLENYATVRSRTKDKKIAAKLSKEDR
KTVEEKSDKAINLWLANDSATKBEYEKAMKDLVACSPILSKYVQGGGNGPNFSGA
KTTVEEDLD"
BASE COUNT      682 a   459 c   372 g   566 t
ORIGIN
      1  tgacgtgaacgttcgagatga 22
      2  ||||| ||||| |||||
Db 1957 TGACCGTAAACTTTAGAGATGA 1936

Query Match      78.2%; Score 17.2; DB 5; Length 2079;
Best Local Similarity 86.4%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1  tgacgtgaacgttcgagatga 22
      1  ||||| ||||| |||||
Db 1957 TGACCGTAAACTTTAGAGATGA 1936

RESULT 13
AC079157      111234 bp      DNA      PRI      01-NOV-2000
LOCUS
DEFINITION      Homo sapiens clone RP11-1285C3, complete sequence.
ACCESSION      AC079157
VERSION      AC079157.3 GI:11067362
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston, R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 111234)
Waterston, R.H.
Direct Submission
Unpublished
Waterston, R.H.
Sequencing vector: pL3; 66%
Chemistry: Dye-terminator Big Dye; 34% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154864 bases at least Q40
Consensus quality: 156402 bases at least Q30
Consensus quality: 157217 bases at least Q20
Insert size: 162000; agarose-fp
Quality coverage: 8.21 in Q20 bases; agarose-fp
Quality coverage: 8.38 in Q20 bases; sum-of-contigs
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1142: contig of 1142 bp in length
* 1143 1242: gap of unknown length
* 1243 3083: contig of 1841 bp in length
* 3084 3183: gap of unknown length
* 3184 6171: contig of 2988 bp in length
* 6172 6271: gap of unknown length
* 6272 14837: contig of 8566 bp in length
* 14838 14937: gap of unknown length
* 14938 22486: contig of 7549 bp in length
* 22487 22586: gap of unknown length
* 22587 38878: contig of 16292 bp in length
```

```
Query Match      76.4%; Score 16.8; DB 88; Length 111234;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2  gaccgtgaacgttcgagatg 21
      1  ||||| ||||| |||||
Db 30683 GACCATGAACGTGGGAGATG 30702

RESULT 14
AC073123      159072 bp      DNA      HTG      30-AUG-2000
LOCUS
DEFINITION      Homo sapiens chromosome RPCI-11 clone RP11-614N3, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
ACCESSION      AC073123
VERSION      AC073123.6 GI:9945292
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston, R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 159072)
Waterston, R.H.
Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 30, 2000 this sequence version replaced gi:9690415.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0614N03
----- Summary Statistics -----
Sequencing vector: pL3; 66%
Chemistry: Dye-terminator Big Dye; 34%
Assembly program: Phrap; version 0.990319
Consensus quality: 154864 bases at least Q40
Consensus quality: 156402 bases at least Q30
Consensus quality: 157217 bases at least Q20
Insert size: 162000; agarose-fp
Quality coverage: 8.21 in Q20 bases; agarose-fp
Quality coverage: 8.38 in Q20 bases; sum-of-contigs
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1143 1242: gap of unknown length
* 1243 3083: contig of 1841 bp in length
* 3084 3183: gap of unknown length
* 3184 6171: contig of 2988 bp in length
* 6172 6271: gap of unknown length
* 6272 14837: contig of 8566 bp in length
* 14838 14937: gap of unknown length
* 14938 22486: contig of 7549 bp in length
* 22487 22586: gap of unknown length
* 22587 38878: contig of 16292 bp in length
```

\* 38979 38978: gap of unknown length  
\* 59379 59370: contig of 20392 bp in length  
\* 59371 59470: gap of unknown length  
\* 59471 88712: contig of 29242 bp in length  
\* 88713 88812: gap of unknown length  
\* 88813 159072: contig of 70260 bp in length.

FEATURES

source  
1. .159072  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="RP11-614N3"  
/clone="RP11-614N3"  
1. .1142  
/note="assembly\_name:Contig11"  
misc\_feature 1243..3083  
/note="assembly\_name:Contig12"  
misc\_feature 3184..6171  
/note="assembly\_name:Contig13"  
misc\_feature 6272..14837  
/note="assembly\_name:Contig14"  
misc\_feature 14938..22486  
/note="assembly\_name:Contig15"  
misc\_feature 22587..38878  
/note="assembly\_name:Contig16"  
misc\_feature 38979..59370  
/note="assembly\_name:Contig17"  
misc\_feature 59471..88712  
/note="assembly\_name:Contig18"  
misc\_feature 88813..159072  
/note="assembly\_name:Contig19  
clone\_end:SP6  
vector\_side:left"

BASE COUNT 48118 a 31947 c 32162 g 46044 t 801 others  
ORIGIN

Query Match 76.4%; Score 16.8; DB 74; Length 159072;  
Best Local Similarity 90.0%; Pred. No. 2.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gaccgtgaacgttcgagatg 21

||||| ||||| |||||

Db 82620 GACCATGACGTGCGAGATG 82639

RESULT 15

AC073123/c AC073123 159072 bp DNA HTG 30-AUG-2000  
LOCUS Homo sapiens chromosome RP11-614N3, WORKING DRAFT  
DEFINITION SQUENCE, 9 unordered pieces.

ACCESSION AC073123

VERSION AC073123.6 GI:9945292

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Waterston,R.H.

1 (bases 1 to 159072)

Unpublished

JOURNAL The sequence of Homo sapiens clone

REFERENCE 2 (bases 1 to 159072)

Waterston,R.H.

Direct Submission

Submitted (08-JUN-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Aug 30, 2000 this sequence version replaced gi:9690415.

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

Query Match 76.4%; Score 16.8; DB 74; Length 159072;  
Best Local Similarity 90.0%; Pred. No. 2.2e+02;

----- Project Information -----  
Center project name: H.NH0614N03  
----- Summary Statistics -----  
Sequencing vector: pBluescript, 34%  
Chemistry: Dye-terminator Big Dye, 34% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 154864 bases at least Q40  
Consensus quality: 156402 bases at least Q30  
Consensus quality: 157217 bases at least Q20  
Insert size: 162000; agarose-fp  
Quality coverage: 8.21 in Q20 bases; agarose-fp  
Quality coverage: 8.38 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 9 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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\* 1143 1242: gap of unknown length  
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\* 3084 3183: gap of unknown length  
\* 3184 6171: contig of 2988 bp in length  
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\* 6272 14837: contig of 8566 bp in length  
\* 14838 14937: gap of unknown length  
\* 14938 22486: contig of 7549 bp in length  
\* 22487 22586: gap of unknown length  
\* 22587 38878: contig of 16292 bp in length  
\* 38879 38978: gap of unknown length  
\* 38979 59370: contig of 20392 bp in length  
\* 59371 59470: gap of unknown length  
\* 59471 88712: contig of 29242 bp in length  
\* 88713 88812: gap of unknown length  
\* 88813 159072: contig of 70260 bp in length.

FEATURES

source

1. .159072  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="RP11-614N3"  
/clone="RP11-614N3"  
1. .1142  
/note="assembly\_name:Contig11"  
misc\_feature 1243..3083  
/note="assembly\_name:Contig12"  
misc\_feature 3184..6171  
/note="assembly\_name:Contig13"  
misc\_feature 6272..14837  
/note="assembly\_name:Contig14"  
misc\_feature 14938..22486  
/note="assembly\_name:Contig15"  
misc\_feature 22587..38878  
/note="assembly\_name:Contig16"  
misc\_feature 38979..59370  
/note="assembly\_name:Contig17"  
misc\_feature 59471..88712  
/note="assembly\_name:Contig18"  
misc\_feature 88813..159072  
/note="assembly\_name:Contig19  
clone\_end:SP6  
vector\_side:left"

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gaccgtgaacgttcgagatg 21

||||||| ||| |||||

Db 28703 GACCGTGACCTTCCAGATG 28684

Search completed: October 9, 2001, 16:18:29  
Job time: 2479 sec

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4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*  
12: gb\_est12.\*  
13: gb\_est13.\*  
14: gb\_est14.\*  
15: gb\_est15.\*  
16: gb\_est16.\*  
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18: gb\_est18.\*  
19: gb\_est19.\*  
20: gb\_est20.\*  
21: gb\_est21.\*  
22: gb\_est22.\*  
23: gb\_est23.\*  
24: gb\_est24.\*  
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28: gb\_est35.\*  
29: gb\_est37.\*  
30: gb\_est38.\*  
31: gb\_est39.\*  
32: gb\_est40.\*  
33: em\_estb.\*  
34: em\_estf.\*  
35: em\_esth1.\*  
36: em\_esth2.\*  
37: em\_esth3.\*  
38: em\_esth4.\*  
39: em\_esth5.\*  
40: em\_esth6.\*  
41: em\_esth7.\*  
42: em\_esth8.\*  
43: em\_esth9.\*



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216: em\_gss\_inv14:\*  
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218: em\_gss\_inv16:\*  
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254: em\_gss\_inv52:\*  
255: em\_gss\_inv53:\*  
256: em\_gss\_inv54:\*  
257: em\_gss\_inv55:\*  
258: em\_gss\_inv56:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17.4	79.1	531	13	AA898422	NC66H2T3
2	17.2	78.2	236	107	AU053757	AU053757
3	17.2	78.2	254	107	AU053032	AU053032
4	17.2	78.2	265	107	AU054169	AU054169
5	17.2	78.2	270	107	AU053754	AU053754
6	17.2	78.2	340	107	AU040059	AU040059
7	17.2	78.2	371	107	AU039239	AU039239
8	17.2	78.2	457	107	AU034234	AU034234
9	17.2	78.2	474	107	AU052381	AU052381
10	17.2	78.2	509	107	AU039788	AU039788
11	17.2	78.2	513	107	AU034515	AU034515
12	17.2	78.2	520	107	AU039823	AU039823
13	17.2	78.2	669	156	C22959	C22959
14	17.2	78.2	697	174	BG138405	EST478847
15	17.2	78.2	699	107	AU034932	AU034932
16	17.2	78.2	714	107	AU033417	AU033417
17	17.2	78.2	985	139	BE741976	601594215
18	16.8	76.4	526	245	AZ501799	1M0340J17
19	16.4	74.5	360	26	AV192496	AV192496
20	16.4	74.5	532	226	AQ270413	HS_2052_B
21	16.2	73.6	138	115	AW427585	63548 MAR
22	16.2	73.6	229	107	AU053807	AU053807
23	16.2	73.6	310	167	BE406273	WHE0409_H
24	16.2	73.6	323	148	BF386464	UT-R-CAL-
25	16.2	73.6	352	137	BE586027	Est#70sp6
26	16.2	73.6	398	167	BE428418	WTD006.G1
27	16.2	73.6	423	234	AQ815396	HS_5014_A
28	16.2	73.6	438	148	BF428883	WHE1710_E
29	16.2	73.6	439	229	AQ492115	V113G12 m
30	16.2	73.6	463	13	AA864966	oh36d12.s
31	16.2	73.6	474	167	BE419241	WNR021.G5
32	16.2	73.6	477	149	BF475131	WHE2111.B
33	16.2	73.6	497	229	AQ492226	V108A10 m
34	16.2	73.6	507	229	AQ460797	HS_5168_A
35	16.2	73.6	517	235	AQ874041	V102A7 mt
36	16.2	73.6	519	229	AQ501248	V24C11 mt
37	16.2	73.6	519	235	AQ875722	V128G1 mt
38	16.2	73.6	521	229	AQ501128	V27C2 mtTn
39	16.2	73.6	523	229	AQ500252	V34H4 mtTn
40	16.2	73.6	525	235	AQ875251	V121H4 mt
41	16.2	73.6	526	249	AZ764668	1M0561L12
42	16.2	73.6	527	167	BE429501	TAS000.G1
43	16.2	73.6	538	235	AQ876357	V98F5 mtTn
44	16.2	73.6	542	235	AQ873145	V60D4 mtTn
45	16.2	73.6	542	242	AZ385850	1M0144I02

## ALIGNMENTS

RESULT	1
AA898422	
LOCUS	NC66H2T3 Mycelial Neurospora crassa cDNA clone NM6H2 5' end, mRNA
DEFINITION	sequence.
ACCESSION	AA898422
VERSION	AA898422.1 GI:3044855
KEYWORDS	EST.
SOURCE	Neurospora crassa.
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
REFERENCE	1 (bases 1 to 531)
AUTHORS	Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L., Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, E., Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K., Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S., Trujillo, R.,

Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S. and Natvig, D.O.  
 Expressed sequences from conidial, mycelial, and sexual stages of *Neurospora crassa*  
 Fungal Genet. Biol. 21, 348-363 (1997)  
 97435549  
 Contact: Natvig, D.O./Nelson, M.A.  
 Department of Biology  
 University of New Mexico  
 Castetter Hall, Albuquerque, NM 87131, USA  
 Tel: 505 277 3411  
 Fax: 505 277 0304  
 Email: ngp@biology.unm.edu  
 Deposited in GDB at the National Center for Genome Resources with accession GDB:S1147294  
 Seq primer: T3.

## FEATURES

Location/Qualifiers  
 1..531  
 /organism="Neurospora crassa"  
 /strain="74-OR23-IV A (FGSC 2489)"  
 /db\_xref="taxon:5141"  
 /clone="NM6H2"  
 /clone\_lib="Mycelial"  
 /sex="Mating type A"  
 /tissue\_type="Mycelium"  
 /dev\_stage="Mycelium"  
 /lab\_host="E. coli"  
 /note="vector: pBluescript SK (-); Site1: EcoR I; Site2: Xho I; 2% sucrose for 24 hours. cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."  
 BASE COUNT 105 a 198 c 130 g 98 t  
 ORIGIN

Query Match 79.1% Score 17.4; DB 13; Length 531;  
 Best Local Similarity 94.7%; Pred. No. 60;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgaga 19  
 |||||  
 Db 192 TCACCGTGAACGTCGCGA 210

RESULT 2  
 AU053757/c mRNA EST 28-APR-1999  
 LOCUS AU053757 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium  
 DEFINITION AU053757 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium  
 ACCESSION AU053757  
 VERSION AU053757.1 GI:4702239  
 KEYWORDS EST.

SOURCE Dictyostelium discoideum.  
 ORGANISM Dictyostelium discoideum  
 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 REFERENCE 1 (bases 1 to 236)  
 YOSHINO, R., MORIO, T. and TANAKA, Y.  
 TITLE Developmental cDNA in Dictyostelium discoideum  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Hideko Urushihara  
 Institute of Biological Sciences  
 University of Tsukuba  
 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan  
 Email: d402hu@akura.cc.tsukuba.ac.jp  
 PROJECT = Dictyostelium discoideum cDNA project in Japan.

## FEATURES

Location/Qualifiers  
 1..236  
 /organism="Dictyostelium discoideum"  
 /strain="AX4"  
 /db\_xref="taxon:44689"  
 /clone="SLJ623"  
 /clone\_lib="Dictyostelium discoideum SL (H.Urushihara)"  
 /dev\_stage="slug"

BASE COUNT 91 a 42 c 36 g 64 t 3 others  
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 236;  
Best Local Similarity 86.4%; Pred. No. 69;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 104 TGACCGTAACCTTTAGAGATGA 83

RESULT 3  
AU053032/c  
LOCUS AU053032 254 bp mRNA EST 28-APR-1999  
DEFINITION AU053032 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium  
discoideum cDNA clone SLF551, mRNA sequence.  
ACCESSION AU053032  
VERSION AU053032.1 GI:4701515  
KEYWORDS EST.  
SOURCE Dictyostellium discoideum.  
ORGANISM Dictyostellium discoideum.  
REFERENCE Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.  
AUTHORS 1 (bases 1 to 254)  
TITLE Yoshino,R., Morio,T. and Tanaka,Y.  
JOURNAL Developmental cDNA in Dictyostellium discoideum  
COMMENT Unpublished (1997)  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan  
Email: d402huesakura.cc.tsukuba.ac.jp  
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES  
source  
1. .254  
/organism="Dictyostellium discoideum"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="SLF551"  
/clone\_lib="Dictyostellium discoideum SL (H.Urushihara)"  
/dev\_stage="slug"  
BASE COUNT 103 a 45 c 40 g 66 t  
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 254;  
Best Local Similarity 86.4%; Pred. No. 69;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 127 TGACCGTAACCTTTAGAGATGA 106

RESULT 4  
AU054169/c  
LOCUS AU054169 265 bp mRNA EST 28-APR-1999  
DEFINITION AU054169 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium  
discoideum cDNA clone SLR852, mRNA sequence.  
ACCESSION AU054169  
VERSION AU054169.1 GI:4702650  
KEYWORDS EST.  
SOURCE Dictyostellium discoideum.  
ORGANISM Dictyostellium discoideum.  
REFERENCE Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.  
AUTHORS 1 (bases 1 to 265)  
TITLE Yoshino,R., Morio,T. and Tanaka,Y.  
JOURNAL Developmental cDNA in Dictyostellium discoideum  
COMMENT Unpublished (1997)  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba

3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan  
Email: d402huesakura.cc.tsukuba.ac.jp  
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES  
source  
1. .265  
/organism="Dictyostellium discoideum"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="SLR852"  
/clone\_lib="Dictyostellium discoideum SL (H.Urushihara)"  
/dev\_stage="slug"  
BASE COUNT 108 a 48 c 42 g 67 t  
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 265;  
Best Local Similarity 86.4%; Pred. No. 70;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 134 TGACCGTAACCTTTAGAGATGA 113

RESULT 5  
AU053754/c  
LOCUS AU053754 270 bp mRNA EST 28-APR-1999  
DEFINITION AU053754 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium  
discoideum cDNA clone SLJ617, mRNA sequence.  
ACCESSION AU053754  
VERSION AU053754.1 GI:4702236  
KEYWORDS EST.  
SOURCE Dictyostellium discoideum.  
ORGANISM Dictyostellium discoideum.  
REFERENCE Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.  
AUTHORS 1 (bases 1 to 270)  
TITLE Yoshino,R., Morio,T. and Tanaka,Y.  
JOURNAL Developmental cDNA in Dictyostellium discoideum  
COMMENT Unpublished (1997)  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan  
Email: d402huesakura.cc.tsukuba.ac.jp  
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES  
source  
1. .270  
/organism="Dictyostellium discoideum"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="SLJ617"  
/clone\_lib="Dictyostellium discoideum SL (H.Urushihara)"  
/dev\_stage="slug"  
BASE COUNT 111 a 48 c 43 g 68 t  
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 270;  
Best Local Similarity 86.4%; Pred. No. 70;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 138 TGACCGTAACCTTTAGAGATGA 117

RESULT 6  
AU040059/c  
LOCUS AU040059 340 bp mRNA EST 29-MAR-1999  
DEFINITION AU040059 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium  
discoideum cDNA clone SLA335, mRNA sequence.  
ACCESSION AU040059  
VERSION AU040059.1 GI:4009299

```

KEYWORDS`
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum.

REFERENCE
AUTHORS Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
1 (bases 1 to 340)
Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostellium developmental cDNA project: generation and
analysis of expressed sequence tags from the first-finger stage of
development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostellium discoideum cDNA project in Japan'.

FEATURES
source
Location/Qualifiers
1..340
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLA335"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 136 a 55 g 82 t
ORIGIN
Query Match 78.2%; Score 17.2; DB 107; Length 340;
Best Local Similarity 86.4%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||| || |||||
Db 211 TGACCGTAACCTTTAGAGATGA 190

RESULT 7
LOCUS AU039239 371 bp mRNA EST 29-MAR-1999
DEFINITION AU039239 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLH241, mRNA sequence.
ACCESSION AU039239
VERSION AU039239.1 GI:4008220
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum.
REFERENCE Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostellium developmental cDNA project: generation and
analysis of expressed sequence tags from the first-finger stage of
development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostellium discoideum cDNA project in Japan'.

FEATURES
source
Location/Qualifiers
1..371
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLH241"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"

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BASE COUNT 153 a 68 c 61 g 89 t
ORIGIN
Query Match 78.2%; Score 17.2; DB 107; Length 371;
Best Local Similarity 86.4%; Pred. No. 73;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||| || |||||
Db 239 TGACCGTAAACTTTAGAGATGA 218

RESULT 8
LOCUS AU034234 457 bp mRNA EST 28-APR-1999
DEFINITION AU034234 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLC303, mRNA sequence.
ACCESSION AU034234
VERSION AU034234.1 GI:3799658
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum.
REFERENCE Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostellium developmental cDNA project: generation and
analysis of expressed sequence tags from the first-finger stage of
development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostellium discoideum cDNA project in Japan'.
POLYA-No.

FEATURES
source
Location/Qualifiers
1..457
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLC303"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 209 a 77 c 70 g 101 t
ORIGIN
Query Match 78.2%; Score 17.2; DB 107; Length 457;
Best Local Similarity 86.4%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||| || |||||
Db 282 TGACCGTAAACTTTAGAGATGA 261

RESULT 9
LOCUS AU052381 474 bp mRNA EST 28-APR-1999
DEFINITION AU052381 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLD225, mRNA sequence.
ACCESSION AU052381
VERSION AU052381.1 GI:4700865
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum.
REFERENCE Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

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REFERENCE	1 (bases 1 to 474)
AUTHORS	Yoshino,R., Morio,T. and Tanaka,Y.
TITLE	Developmental cDNA in Dictyostellium discoideum
JOURNAL	Unpublished (1997)
COMMENT	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-noda1, Tsukuba, Ibaraki 305, Japan Email: d402huesakura.cc.tsukuba.ac.jp PROJECT = Dictyostellium discoideum cDNA project in Japan.

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FEATURES
  source
    1. .474
    Location/Qualifiers
      /organism="Dictyostellium discoideum"
      /strain="AX4"
      /db_xref="taxon:44689"
      /clone="SLD235"
      /clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
      /dev_stage="slug"
      196 a 91 c 80 g 107 t
BASE COUNT
ORIGIN

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Query Match	78.28;	Score 17.2;	DB 107;	Length 474;
Best Local Similarity	86.44;	Pred. No. 76;		
Matches 19;	Conservative	0;	Mismatches	3;
Indels	0;	Gaps	0;	
Qy	1	tgacgtgaacgttcgagatga	22	
Db	342	TGACCGTAAACTTTAGAGATGA	321	

RESULT	10	
LOCUS	AU039788/c	
DEFINITION	AU039788 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium	29-MAR-1999
LOCUS	AU039788	509 bp mRNA EST
DEFINITION	AU039788 Dictyostelium discoideum cDNA clone SLG425, mRNA sequence.	
ACCESSION	AU039788	
VERSION	AU039788.1	GI:4009028
KEYWORDS	EST.	
SOURCE	Dictyostelium discoideum.	
ORGANISM	Dictyostelium discoideum	
	Eukaryota; Mycetozoa; Dictyosteliales; Dictyostelium.	

AUTHORS	Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B. N., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
TITLE	The Dictyostellium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development
JOURNAL	DNA Res. 5 (6), 335-340 (1998)
MEDLINE	99156227
COMMENT	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan Email: d402@huesakura.cc.tsukuba.ac.jp PROJECT = 'dictyostellium discoideum cDNA project in Japan'

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PROJECT = dictyostellium discoideum cDNA project in Japan
FEATURES
  source
    Location/Qualifiers
      1..509
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        /strain="AX4"
        /db_xref="taxon:44689"
        /clone="SLG435"
        /clone_11b="dictyostellium discoideum SL (H.Urushihara)"
        /dev_stage="slug"
BASE COUNT      207 a      99 c      88 g      115 t
ORIGIN
Query Match      78.2%; Score 17.2; DB 107; Length 509;
Best Local Similarity 86.4%; Pred. No. 77;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

## COMMENT

Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan  
Email: d402huesakura.cc.tsukuba.ac.jp  
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.  
Location/Qualifiers

## FEATURES

source  
1..520  
/organism="Dictyostelium discoideum"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="SLG510"  
/clone\_lib="dictyostelium discoideum SL (H.Urushihara)"  
/dev\_stage="slug"  
211 a 101 c 90 g 118 t

## BASE COUNT

ORIGIN  
211 a 101 c 90 g 118 t

Query Match 78.2%; Score 17.2; DB 107; Length 520;  
Best Local Similarity 86.4%; Pred. No. 77;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 393 TGACCGTAAACTTTAGAGATGA 372

## RESULT 13

C22959/c  
LOCUS C22959 669 bp mRNA EST 02-APR-1997  
DEFINITION C22959 Dictyostelium discoideum FC (H.Urushihara) Dictyostelium  
discoideum cDNA clone FC-AG10, mRNA sequence.

## ACCESSION

VERSION C22959.1 GI:1922108

## KEYWORDS

EST

## SOURCE

ORGANISM Dictyostelium discoideum.

REFERENCE Dictyostelium discoideum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

1 (bases 1 to 669)

AUTHORS Shimizu,H. and Urushihara,H.

TITLE Sexual-cDNA in CSM

JOURNAL Unpublished (1997)

COMMENT Contact: Hideko Urushihara

Institute of Biological Sciences

University of Tsukuba

3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan

Email: d402huesakura.cc.tsukuba.ac.jp.

## FEATURES

source  
1..669  
/organism="Dictyostelium discoideum"  
/strain="KAX3"  
/db\_xref="taxon:44689"  
/clone="FC-AG10"  
/clone\_lib="Dictyostelium discoideum FC (H.Urushihara)"  
270 a 131 c 114 g 154 t

## BASE COUNT

ORIGIN  
270 a 131 c 114 g 154 t

Query Match 78.2%; Score 17.2; DB 156; Length 669;  
Best Local Similarity 86.4%; Pred. No. 80;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 522 TGACCGTAAACTTTAGAGATGA 501

## RESULT 14

BG138405/c  
LOCUS BG138405 697 bp mRNA EST 31-JAN-2001  
DEFINITION BG138405 wild tomato pollen Lycopersicon pennellii cDNA clone  
EST478847 5' sequence, mRNA sequence.

## ACCESSION

BG138405

## VERSION

KEYWORDS BG138405.1 GI:12638593

## SOURCE

ORGANISM Lycopersicon pennellii.  
Lycopersicon pennellii.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.

## REFERENCE

AUTHORS 1 (bases 1 to 697)  
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,  
Hansen,C., Ronning,C. and Tanksley,S.

## TITLE

Generation of ESTs from wild tomato (L. pennellii) pollen

## JOURNAL

COMMENT Unpublished (2001)

## CONTACT

CUCI

## Clemson University Genomics Institute

## Clemson University

## 100 Jordan Hall, Clemson, SC 29634, USA

## Email: http://www.genome.clemson.edu/orders/index.html.

## FEATURES

source  
1..697  
/organism="Lycopersicon pennellii"  
/cultivar="TA56"  
/db\_xref="taxon:28526"  
/clone="clpp9118"  
/clone\_lib="wild tomato pollen"  
/tissue\_type="pollen"  
/dev\_stage="pollen collected from open flowers"  
/lab\_host="SOLK"  
/note="vector: paluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Pollen was collected from open flowers from  
L.pennellii TA56, and stored at -80 C until library  
construction."  
240 a 134 c 168 g 155 t

## BASE COUNT

ORIGIN  
240 a 134 c 168 g 155 t

## Query Match

Best Local Similarity 78.2%; Score 17.2; DB 174; Length 697;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 627 TGAACGTGAAGTTTGAGATGA 606

## RESULT 15

AU034932/c  
LOCUS AU034932 699 bp mRNA EST 28-APR-1999  
DEFINITION AU034932 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium  
discoideum cDNA clone SLE359, mRNA sequence.

## ACCESSION

VERSION AU034932.1 GI:3800356

## KEYWORDS

EST

## SOURCE

ORGANISM Dictyostelium discoideum.

REFERENCE Dictyostelium discoideum.

AUTHORS Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

1 (bases 1 to 699)

Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,

Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,

Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostelium developmental cDNA project: generation and

analysis of expressed sequence tags from the first-finger stage of

development

DNA Res. 5 (6), 335-340 (1998)

JOURNAL 99156227

MEDLINE

COMMENT Contact: Hideko Urushihara

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Email: d402huesakura.cc.tsukuba.ac.jp

PROJECT = 'Dictyostelium discoideum cDNA project in Japan'

POLYA=No.

FEATURES Location/Qualifiers

source 1. .699  
/organism="Dictyostellium discoideum"  
/strain="AX4"  
/db\_xref="taxon:4689"  
/clone="SLE359"  
/clone\_lib="Dictyostellium discoideum SL (H. Urushihara)"  
/dev\_stage="slug"  
BASE COUNT 267 a 145 c 120 g 167 t  
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 699;  
Best Local Similarity 86.4%; Pred. NO. 80;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
Db 567 TGACCGTAACCTTAGAGATGA 546

Search completed: October 9, 2001, 18:20:13  
Job time: 9783 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:47 ; Search time 515.84 Seconds  
(without alignments)  
26.779 Million cell updates/sec

Title: US-09-713-136-2

Perfect score: 22

Sequence: 1 tgaccggaacgttcgatga 22

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_0601.\*

- 1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.\*
- 2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.\*
- 8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT.\*
- 10: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.\*
- 11: /SID88/gcgdata/geneseq/geneseq/NA1990.DAT.\*
- 12: /SID88/gcgdata/geneseq/geneseq/NA1991.DAT.\*
- 13: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.\*
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- 17: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT.\*
- 18: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT.\*
- 19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
c 1	22	100.0	22	AAV80105
2	22	100.0	22	AAV80096
3	22	100.0	22	AAA38066
4	22	100.0	22	AAV77041
5	20.4	92.7	22	AAV32079
6	20.4	92.7	22	AAV36624
7	20.4	92.7	22	AAV80097
8	20.4	92.7	22	AAV80102
9	20.4	92.7	22	AAV80103
10	20.4	92.7	22	AAV64051
11	20.4	92.7	22	AAV96253

12	20.4	92.7	22	AAA90458	CpG adjuvant oligo
13	20.4	92.7	22	AAA14467	Immunostimulatory
14	20.4	92.7	22	AAA38065	Immunostimulatory
15	20.4	92.7	22	AAA38071	Immunostimulatory
16	20.4	92.7	22	AAA38072	Immunostimulatory
17	20.4	92.7	22	AZ55876	Immunomodulatory o
18	20.4	92.7	22	AAV77040	Immunomodulatory D
19	20.4	92.7	22	AAV29800	Cholera toxin immu
20	20.4	92.7	22	AAV82107	Oligonucleotide OD
21	20.4	92.7	22	AAV92377	CG motif and CFA c
22	19.6	89.1	22	AAV77046	Immunostimulatory
23	19.4	88.2	22	AZ55880	Immunomodulatory o
24	18.8	85.5	22	AAV80099	Immunomodulatory o
25	18.8	85.5	22	AAV80101	Immunomodulatory o
26	18.8	85.5	22	AAV96254	Sequence of a stab
27	18.8	85.5	22	AAA38068	Immunostimulatory
28	18.8	85.5	22	AAA38070	Immunostimulatory
29	18.8	85.5	22	AAV77043	Immunostimulatory
30	18.8	85.5	22	AAV77047	Immunostimulatory
31	18.4	83.6	22	AZ55881	Immunomodulatory o
32	18	81.8	22	AAV77045	Immunostimulatory
33	17.8	80.9	22	AZ55877	Immunomodulatory o
34	17.2	78.2	22	AAV32080	Nucleotide sequenc
35	17.2	78.2	22	AAV36625	ISS-ODN mutant Dv1
36	17.2	78.2	22	AAV55790	Immunostimulatory
37	17.2	78.2	22	AAV55797	Immunostimulatory
38	17.2	78.2	22	AAV55788	Immunostimulatory
39	17.2	78.2	22	AAV80106	Oligo used in expe
40	17.2	78.2	22	AAV80104	Oligo used in expe
41	17.2	78.2	22	AAC64052	Non-CpG control ph
42	17.2	78.2	22	AAV96252	Sequence of a stab
43	17.2	78.2	22	AAV96260	Sequence of a stab
44	17.2	78.2	22	AAA90459	CpG adjuvant oligo
45	17.2	78.2	22	AAV92378	CG motif and CFA c

ALIGNMENTS

RESULT 1

AAV80105/c  
ID AAV80105 standard; DNA; 22 BP.

XX AAV80105;

XX 12-MAR-1999 (first entry)

XX Oligo used in experiments for stimulation of cytokine production.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;



XX  
PS

Example 1; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AAGTTCC, AAGTTCCG,  
 CC GAGTTCC, and GAGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent  
 CC oligonucleotides that were tested for immunostimulatory activity. These  
 CC were used in experiments for the stimulation of cytokine production and  
 CC were found to lack immunostimulatory activity. The invention provides  
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX Sequence 22 BP; 5 A; 7 C; 4 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22

Db 22 TGACCGTGAACGTTTCGAGATGA 1

RESULT 2

AAV80096

ID AAV80096 standard; DNA; 22 BP.

XX AAV80096;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 7; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AAGTTCC, AAGTTCCG,

CC GAGTTCC, and GAGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22

Db 1 tgaccgtgaacgttcgagatga 22

RESULT 3

AAA38066

ID AAA38066 standard; DNA; 22 BP.

XX AAA38066;

XX 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #2.

XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
 KW development; ss.

XX Synthetic.

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual  
 XX Disclosure; Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunostimulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory composition which comprises a gp120  
 CC conjugated to it and not conjugated, is used for modulating or  
 CC stimulating a specific immune response against gp120 in an individual by  
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
 CC is also used for suppressing or delaying development of HIV infection in  
 CC an individual infected with HIV or an individual at risk of infection  
 CC with HIV, respectively. It is also used for treating an individual

CC infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 1 tgaccgtgaacgttcgagatga 22

RESULT 4

AAAF77041

ID AAF77041 standard; DNA; 22 BP.

XX

AC AAF77041;

XX

DT 15-MAY-2001 (first entry)

XX

DE Immunostimulatory DNA #1.

XX

KW Modulate; immune; antigen; immunostimulatory; ds.

XX

OS Synthetic.

XX

PN WO200112223-A2.

XX

PD 22-FEB-2001.

XX

PF 18-AUG-2000; 2000WO-US22835.

XX

PR 19-AUG-1999; 99US-0149768.

XX

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX

PI Van Nest G;

XX

DR WPI; 2001-211136/21.

XX

PT Modulating immune response to a second antigen in humans involves administering an immunostimulatory polynucleotide comprising an immunostimulatory sequence and a first antigen -

XX

PS Disclosure; Page 15; 63pp; English.

XX

CC The present invention relates to modulating an immune response to a second antigen in an individual, involving administering to the individual an immunomodulatory polynucleotide comprising an immunostimulatory sequence (ISS) and a first antigen.

XX

SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 22; DB 22; Length 22;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 1 tgaccgtgaacgttcgagatga 22

RESULT 5

AAV32079

ID AAV32079 standard; DNA; 22 BP.

XX

AC AAV32079;

XX

DT 09-SEP-1998 (first entry)

XX

DE Nucleotide sequence of DY1018.

XX DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;

XX immunisation; anaphylaxis; IgE; retinopathies; ss.

XX synthetic.

OS

PH Key Location/Qualifiers

FT modified\_base 1..22

FT /\*tag= a

FT /note= "phosphothioate backbone"

XX

PN WO9816247-A1.

XX

PD 23-APR-1998.

XX

PF 09-OCT-1997; 97WO-US19004.

XX

PR 11-OCT-1996; 96US-0028118.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Carson DA, Raz E, Roman M;

XX

DR WPI; 1998-261028/23.

XX

PT New immunomodulatory compositions - comprising an antigen conjugated to a polynucleotide that contains an immunostimulatory sequence

XX

PS Example 1; Page 36; 69pp; English.

XX

CC This is the nucleotide sequence of DY1018, which is conjugated to beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule (IMM), which comprises an antigen conjugated to a polynucleotide (PN) that contains at least one immunostimulatory nucleotide sequence (ISS). The conjugate synergistically boost the magnitude of the host immune response against an antigen to a level greater than the host immune response to either the IMM, antigen or ISS-PN alone. These responses to ISS-PN/IMM conjugates are particularly acute during the important early phase of the host immune response to an antigen. The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular (Th1 type) immune responses of the host. Thus, use of the method to boost the immune responsiveness of a host to subsequent challenge by a sensitising antigen without immunisation avoids the risk of CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE production in response to the antigen challenge. The conjugates can also be used to combat pathogenic infection and to stimulate CC therapeutic angiogenesis to treat conditions in which localised blood flow plays a significant etiological role, e.g. retinopathies.

XX

SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match

Best Local Similarity 92.7%; Score 20.4; DB 19; Length 22;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 1 tgaccgtgaacgttcgagatga 22

RESULT 6

AAAX36624

ID AAX36624 standard; DNA; 22 BP.

XX

AC AAX36624;

XX

DT 09-JUL-1999 (first entry)

XX

DE ISS-ODN DY1018 nucleotide sequence.

XX

KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;

KW granulocyte-mediated tissue inflammation; Th2 type immune response;  
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;  
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;  
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;  
 KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.

XX WO9911275-A2.

XX 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18382.

XX 05-SEP-1997; 97US-0927120.

XX (REGC ) UNIV CALIFORNIA.

XX Ray E;

XX WPI; 1999-312404/26.

XX Reducing antigen-stimulated granulocyte-mediated inflammation

XX Example 2; Page 30; 69pp; English.

XX This is the ISS-ODN DY1018 nucleotide sequence.  
 CC The invention relates to a method for preventing or reducing  
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:  
 CC (a) reduction in, or the absence of, a Th2 type immune response is  
 CC measured; or (b) there is a reduction or absence of other clinical signs  
 CC of inflammation in the host after antigen challenge. The method is used  
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
 CC and to modulate the host's immune responsiveness to an antigen,  
 CC particularly where the subject suffers from asthma, nasal polyposis,  
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
 CC antigen immunisation, the method is an antigen-independent method,  
 CC and avoids host production of both interleukin-4 (IL-4), which carries  
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
 CC adhesion to endothelia.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.21;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tgaccgtgaacgttcgagatga 22

||||| ||||||| |||||||

Db 1 tgactgtgaacgttcgagatga 22

RESULT 7

AAV80097

ID AAV80097 standard; DNA; 22 BP.

XX AAV80097;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.  
 XX Synthetic.

PN WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AAGGTTC, AAGGTTCG,  
 CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.21;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tgaccgtgaacgttcgagatga 22

||||| ||||||| |||||||

Db 1 tgactgtgaacgttcgagatga 22

RESULT 8

AAV80102

ID AAV80102 standard; DNA; 22 BP.

XX AAV80102;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.  
 XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 11

FT /\*tag= a

FT /note= "5-bromocytosine"

XX WO9855495-A2.

XX 10-DEC-1998.

XX

PF 05-JUN-1998; 98WO-US11578.  
 XX  
 PR 06-JUN-1997; 97US-0048793.  
 XX  
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX  
 PI Dina D, Roman M, Schwartz D;  
 XX  
 DR WPI; 1999-059898/05.  
 XX

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases  
 XX

PS Claim 23; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GAGGTTCC, and GAGGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.21;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgacgtgaacgttcgagatga 22  
 |||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 9  
 AAV80103  
 ID AAV80103 standard; DNA; 22 BP.

XX AC AAV80103;

XX DT 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
 XX  
 OS Synthetic.

XX Key modified\_base 11 Location/Qualifiers

FT /\*tag= a

FT /note= "5-bromocytosine"

XX W09B55495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Dina D, Roman M, Schwartz D;

DR WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases  
 XX

PS Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GAGGTTCC, and GAGGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.21;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgacgtgaacgttcgagatga 22  
 |||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 10

AAC64051

ID AAC64051 standard; DNA; 22 BP.

XX AC AAC64051;

XX DT 15-FEB-2001 (first entry)

XX Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.

XX CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;  
 KW enhanced antigen presentation; antigen-presenting cell; APC;  
 KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;  
 KW vaccine; ss.

XX OS Synthetic.

XX WO2000062787-A1.

XX 26-OCT-2000.

XX 11-APR-2000; 2000WO-US09664.

XX 15-APR-1999; 99US-0292278.

XX (REGC ) UNIV CALIFORNIA.

XX Raz E, Martin-Orozco E;

XX WPI; 2000-679548/66.

XX Enhancing antigen-presentation capabilities of T-cells for cancer  
 PT immunotherapy, by contacting cells with an immunostimulatory  
 PT oligonucleotide

XX PS Example 1; Page 18; 42pp; English.

XX CC The invention relates to a method of inducing activation of T-cells

CC to respond to an antigen, comprising contacting antigen-presenting cells

CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs

CC thus treated have enhanced antigen presenting capabilities compared to

CC antigen-activated APCs. APCs with enhanced antigen-presentation

CC capabilities then present the antigen to T-cells. The method is useful

CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour

CC antigen presenting capacity of tumour cells, thereby inducing T-cell

CC activation, and is therefore useful for treating tumours. Additionally,

CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.

CC ISS-ODN treated APCs are induced to take up antigen through upregulation

CC of Fc-receptor expression, to present antigen through upregulation of

CC major histocompatibility complex (MHC) Class I and II expression and

CC CD4 expression, to produce co-stimulatory factors (B7 and CD40), to

CC provide cell-to-cell adhesion through upregulation of intercellular

CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory

CC cytokine production, all at levels greater than that achieved through

CC contact of APC with antigen alone. The present sequence represents

CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the

CC invention.

XX CC

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.21;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22  
 ||||| ||||| ||||| |||||

Db 1 tgactgtgaacgttcgagatga 22

RESULT 11

AAA96253

ID AAA96253 standard; DNA: 22 BP.

XX AC AAA96253;

XX DT 08-FEB-2001 (first entry)

XX DE Sequence of a stabilised oligonucleotide with antitumour activity.

XX KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;

XX KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.

XX OS Synthetic.

XX PN WO200056342-A2.

XX PD 28-SEP-2000.

XX PF 17-MAR-2000; 2000WO-FR00676.

XX PR 19-MAR-1999; 99FR-0003433.

XX PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

XX PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX PI Carpentier A;

XX DR WPI: 2000-602192/57.

XX PT Use of stabilised oligonucleotides as antitumor agents, particularly

XX PT against nervous system tumors, have optimal activity and are not toxic

XX PS Example 2; Page 16; 57pp; French.

XX CC The present sequence represents a stabilised oligonucleotide which has

CC antitumour activity. The oligonucleotide comprises an octamer motif

CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where

CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are

CC immunostimulatory, and are not toxic. They may be adapted for use in

CC animals or humans. The stabilised oligonucleotides are used for

CC treating tumours, of any type and any degree of anaplasia, particularly

CC human tumours in the peripheral or central nervous systems, specifically

CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.

XX CC

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.21;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22  
 ||||| ||||| ||||| |||||

Db 1 tgactgtgaacgttcgagatga 22

RESULT 12

AAA90458

ID AAA90458 standard; DNA: 22 BP.

XX AC AAA90458;

XX DT 10-JAN-2001 (first entry)

XX DE CpG adjuvant oligonucleotide. SEQ ID NO:19.

XX KW

CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;

microemulsion; adsorbent microparticle; vaccine; Th1 immune response;

virial infection; bacterial infection; parasitic infection; HCV; HBV;

hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;

human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;

rabies virus; cholera; diphtheria; tetanus; pertussis;

Helicobacter pylori; Haemophilus influenzae; malaria; ss.

XX OS Synthetic.

XX PN WO200050006-A2.

XX PD 31-AUG-2000.

XX PF 09-FEB-2000; 2000WO-US03331.

XX PR 26-FEB-1999; 99US-0121858.

XX PR 29-JUL-1999; 99US-0146391.

XX PR 28-OCT-1999; 99US-0161997.

XX PA (CHIR) CHIRON CORP.

XX PI O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Uguzzoli M, Singh M;

XX PI Barackman J;

XX DR WPI: 2000-587123/55.

XX PT Microemulsion having an adsorbent surface comprising a microdroplet

PT emulsion consisting of a metabolizable oil and an emulsifying agent

PT which is a detergent, useful as a vaccine to treat bacterial, viral,

PT and parasitic infection

XX PS Claim 17; Page 40; 95pp; English.

XX CC The invention relates to a microdroplet emulsion (microemulsion) with an

CC adsorbent surface, and which comprises a metabolizable oil and an

CC emulsifying agent (a detergent). It also relates to a composition

CC comprising the microemulsion and a microparticle with an adsorbent

CC surface, where the microparticle comprises a polymer selected from a

CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a

CC polycaprolactone, a polyorthoester, a polyanhydride, and a

CC polycyanoacrylate, and a second detergent. The surface of the

CC microparticles efficiently adsorb biologically active macromolecules such  
 CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,  
 CC mediators of transcription or translation, metabolic intermediates and  
 CC adjuvants. Additionally, a second biologically active molecule may be  
 CC encapsulated within the microparticle. The microemulsion can be used in  
 CC methods of immunising a host animal, particularly a human, against a  
 CC viral, bacterial or parasitic infection, and in methods of increasing a  
 CC Th1 immune response. The microemulsions (having the appropriate antigens  
 CC adsorbed) may be particularly used as vaccines for hepatitis C virus  
 CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human  
 CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and  
 CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and  
 CC pertussis; Helicobacter pylori and Haemophilus influenzae; and  
 CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1  
 CC lymphocyte stimulating oligonucleotides containing at least one CpG motif  
 CC which are claimed for use as adjuvants in the compositions of the  
 CC invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.21;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

#### RESULT 13

AAA14467  
 ID AAA14467 standard; DNA; 22 BP.

XX AC AAA14467;

XX DT 21-AUG-2000 (first entry)

XX DE Immunostimulatory oligonucleotide (ISS-ODN) DY1018.

XX KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;  
 KW secretory immunoglobulin A production; siGa; Th1 phenotype; ds.

XX OS Synthetic.

XX PN WO200020039-A1.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-US21203.

XX PR 05-OCT-1998; 98US-0167039.

XX PA (RECC ) UNIV CALIFORNIA.

XX PI Raz E, Horner AA, Carson DA;

XX WPI; 2000-303647/26.

XX PT Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to  
 PT an antigen in a mammalian host through production of secretory  
 PT immunoglobulin A.

XX PS Claim 8; Page 21; 64pp; English.

XX CC The invention relates to a method of inducing mucosal immunity to an  
 CC antigen in a mammalian host, including the production of secretory  
 CC immunoglobulin A (siGa). Immune protection in the mucosa (the principal  
 CC site of entry of most foreign antigens) is mediated by mucosa-associated  
 CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory  
 CC cell sub-populations. The primary immune response which characterises  
 CC the induction of mucosal immunity to an antigen is siGa production by  
 CC activated B-cells. The method comprises introducing an immunostimulatory

CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the  
 CC sequence includes a core nucleotide sequence. The core nucleotide  
 CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific  
 CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A  
 CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used  
 CC as an adjuvant with an antigen for stimulating mucosal immunity. The  
 CC level of siGa production induced in the host is at least 3 times the  
 CC magnitude of siGa production achievable in response to introduction of  
 CC antigen alone into the mucosal tissue and is equivalent or greater than  
 CC the magnitude of siGa production achievable in response to introduction  
 CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The  
 CC host immune response is stimulated to antigen specific IgA production,  
 CC biased towards the Th1 phenotype while antigen-induced IgE production is  
 CC avoided. The adjuvant has little or no known toxicity in mammals and its  
 CC efficacy is comparable to that of cholera toxin which is used as a  
 CC mucosal adjuvant. The present sequence represents the immunostimulatory  
 CC oligonucleotide DY1018.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.21;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

#### RESULT 14

AAA38065  
 ID AAA38065 standard; DNA; 22 BP.

XX AC AAA38065;

XX DT 24-AUG-2000 (first entry)

XX DE Immunostimulatory sequence (ISS) #1.

XX KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
 KW development; ss.

XX OS Synthetic.

XX PN WO200021556-A1.

XX PD 20-APR-2000.

XX PF 08-OCT-1999; 99WO-US23677.

XX PR 09-OCT-1998; 98US-0103733.

XX PR 07-OCT-1999; 99US-0415186.

XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX PI Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX PT Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual.

XX PS Claim 3; Page 16; 65pp; English.

XX CC The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory composition which comprises a gp120  
 CC conjugated to an immunomodulatory polynucleotide, or is proximately

CC associated to it and not conjugated, is used for modulating or  
CC stimulating a specific immune response against gp120 in an individual by  
CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
CC is also used for suppressing or delaying development of HIV infection in  
CC an individual infected with HIV or an individual at risk of infection  
CC with HIV, respectively. It is also used for treating an individual  
CC infected with HIV in need of immune modulation.  
XX  
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
  
Query Match 92.7%; Score 20.4; DB 21; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.21;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
Db 1 tgactgtgaacgttcgagatga 22  
  
RESULT 15  
AAA38071  
ID AAA38071 standard; DNA; 22 BP.  
XX  
AC AAA38071;  
XX  
DT 24-AUG-2000 (first entry)  
XX  
DE Immunostimulatory sequence (ISS) #7.  
XX  
KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
KW development; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 11  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5-Bromocytosine"  
XX  
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XX  
PD 20-APR-2000.  
XX  
PF 08-OCT-1999; 99WO-US23677.  
XX  
PR 09-OCT-1998; 98US-0103733.  
PR 07-OCT-1999; 99US-0415186.  
XX  
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
PI Tighe H, Raz E, Schwartz D, Takabayashi K;  
XX  
DR WPI; 2000-317846/27.  
XX  
PT Anti-HIV composition comprises immunostimulatory polynucleotides and  
PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
PT response against HIV in an HIV infected individual  
XX  
PS Disclosure; Page 17; 65pp; English.  
XX  
CC The present invention relates to an immunostimulatory composition  
CC comprising a human immunodeficiency virus (HIV) antigen, and an  
CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
CC (ISS). This sequence represents an ISS that can be used in the  
CC composition. An immunostimulatory composition which comprises a gp120  
CC conjugated to an immunomodulatory polynucleotide, or is proximately  
CC associated to it and not conjugated, is used for modulating or  
CC stimulating a specific immune response against gp120 in an individual by  
CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
CC is also used for suppressing or delaying development of HIV infection in

CC an individual infected with HIV or an individual at risk of infection  
CC with HIV, respectively. It is also used for treating an individual  
CC infected with HIV in need of immune modulation.  
XX  
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
  
Query Match 92.7%; Score 20.4; DB 21; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.21;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Job time: 2977 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:35 ; Search time 10334.3 Seconds  
(without alignments)  
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Sequence: 1 tgacggtgacgttcgagatga 22  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues  
Total number of hits satisfying chosen parameters: 28310096

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Listing first 45 summaries

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5	22	100.0	22	28	US-09-713-136-2
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7	20.4	92.7	22	1	PCT-US00-35064-1
8	20.4	92.7	22	1	PCT-US01-03029-1
9	20.4	92.7	22	1	PCT-US01-06034-1
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38	19.4	88.2	22	17	US-09-324-191A-5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



## ALIGNMENTS

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; Sequence 1. Application US/09296477A  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, E.  
; APPLICANT: SCHWARTZ, D.  
; APPLICANT: ROMAN, M.  
; APPLICANT: DINA, D.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,  
; COMPOSITIONS THEREOF AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 37782000420  
; CURRENT APPLICATION NUMBER: US/09/296,477A  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: 09/092,329  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 60/048,793  
; EARLIER FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-296-477-1

Query Match 100.0%; Score 22; DB 16; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.51;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 tgaccgtgaacgttcgagatga 22

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; Sequence 5. Application US/09296477A  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, E.  
; APPLICANT: SCHWARTZ, D.  
; APPLICANT: ROMAN, M.  
; APPLICANT: DINA, D.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,  
; COMPOSITIONS THEREOF AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 37782000420  
; CURRENT APPLICATION NUMBER: US/09/296,477A  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: 09/092,329  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 60/048,793  
; EARLIER FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-296-477-5

Query Match 100.0%; Score 22; DB 16; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.51;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
DB 22 TGACCGTGAACGTTGAGATGA 1

RESULT 3  
US-09-415-186-2  
; Sequence 2. Application US/09415186  
; GENERAL INFORMATION:  
; APPLICANT: Tighe, Helen  
; APPLICANT: Raz, Eyal  
; APPLICANT: Schwartz, David  
; APPLICANT: Takabayashi, Kenji  
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 37782000700  
; CURRENT APPLICATION NUMBER: US/09/415,186  
; CURRENT FILING DATE: 1999-10-07  
; EARLIER APPLICATION NUMBER: 60/103,733  
; EARLIER FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-415-186-2

Query Match 100.0%; Score 22; DB 18; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.51;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
DB 1 tgaccgtgaacgttcgagatga 22

RESULT 4  
US-09-642-492-2  
; Sequence 2. Application US/09642492  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, G.  
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE  
; USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE  
; TITLE OF INVENTION: THEREIN  
; FILE REFERENCE: 37782000800  
; CURRENT APPLICATION NUMBER: US/09/642,492  
; CURRENT FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/149,768  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-642-492-2

Query Match 100.0%; Score 22; DB 25; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.51;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
DB 1 tgaccgtgaacgttcgagatga 22

APPLICANT: Horner, Anthony A.  
TITLE OF INVENTION: Method for Preventing an Anaphylactic  
REACTION  
FILE REFERENCE: 06510/201W01  
CURRENT APPLICATION NUMBER: PCT/US00/35064  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 60/171,830  
PRIOR FILING DATE: 1999-12-21  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Immunomodulatory nucleic acid molecule  
PCT-US00-35064-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
DB 1 tgactgtgaacgttcgagatga 22

RESULT 8  
PCT-US01-03029-1  
Sequence 1, Application PC/TUS0103029  
GENERAL INFORMATION:  
APPLICANT: Eyal Raz  
APPLICANT: Richard Kornbluth  
APPLICANT: Antonio Catanzaro  
APPLICANT: Tomoko Hayashi  
APPLICANT: Dennis A. Carson  
TITLE OF INVENTION: Immunomodulatory Polynucleotides in  
Treatment of Infection by an Intracellular Pathogen  
FILE REFERENCE: 06510/168W01  
CURRENT APPLICATION NUMBER: PCT/US01/03029  
CURRENT FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/179,353  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Immunomodulatory sequence  
PCT-US01-03029-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
DB 1 tgactgtgaacgttcgagatga 22

RESULT 9  
PCT-US01-06034-1  
Sequence 1, Application PC/TUS0106034  
GENERAL INFORMATION:  
APPLICANT: Raz, Eyal  
APPLICANT: Rachmilewitz, Daniel  
TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
Disease and Other Forms of Gastrointestinal Inflammation.  
FILE REFERENCE: 6510-202W0

US-09-713-136-2  
Sequence 2, Application US/09713136  
GENERAL INFORMATION:  
APPLICANT: Tuck, Stephen  
APPLICANT: Van Nest, Gary  
TITLE OF INVENTION: Immunomodulatory Compositions Containing  
An Immunostimulatory Sequence Linked To Antigen And Methods  
OF USE THEREOF  
FILE REFERENCE: 37782001500  
CURRENT APPLICATION NUMBER: US/09/713,136  
CURRENT FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: 60/165,467  
PRIOR FILING DATE: 1999-11-15  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic construct  
US-09-713-136-2

Query Match 100.0%; Score 22; DB 28; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.51;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
DB 1 tgaccgtgaacgttcgagatga 22

RESULT 6  
PCT-US00-18229-32  
Sequence 32, Application PC/TUS0018229  
GENERAL INFORMATION:  
APPLICANT: Raz, Eyal  
APPLICANT: Kobayashi, Hiroko  
TITLE OF INVENTION: Method for Enhancing an Immune Response  
FILE REFERENCE: 6510-189W01  
CURRENT APPLICATION NUMBER: PCT/US00/18229  
CURRENT FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 09/347,343  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
PCT-US00-18229-32

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
|||||  
DB 1 tgactgtgaacgttcgagatga 22

RESULT 7  
PCT-US00-35064-1  
Sequence 1, Application PC/TUS0035064  
GENERAL INFORMATION:  
APPLICANT: Raz, Eyal

; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
; OTHER INFORMATION: oligonucleotide primer  
; OTHER INFORMATION: oligonucleotide primer  
PCT-US01-06034-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgaccgtgaacgcttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgcttcgagatga 22

RESULT 10  
PCT-US01-10118-1  
; Sequence 1, Application PC/TUS0110118  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Cho, Hearn Jay  
; APPLICANT: Richman, Douglas  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T  
; FILE REFERENCE: 06510-18WO1  
; CURRENT APPLICATION NUMBER: PCT/US01/10118  
; CURRENT FILING DATE: 2001-03-17  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,537  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/203,567  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/215,895  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN  
; NAME/KEY: modified\_base  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: disulfide thymine  
PCT-US01-10118-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgaccgtgaacgcttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgcttcgagatga 22

RESULT 11  
PCT-US01-10118-3  
; Sequence 3, Application PC/TUS0110118  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Cho, Hearn Jay  
; APPLICANT: Richman, Douglas

; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T  
; FILE REFERENCE: 06510-18WO1  
; CURRENT APPLICATION NUMBER: PCT/US01/10118  
; CURRENT FILING DATE: 2001-03-17  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,537  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/203,567  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/215,895  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: phosphorothioate ISS-ODN  
PCT-US01-10118-3

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgaccgtgaacgcttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgcttcgagatga 22

RESULT 12  
PCT-US01-11290-1  
; Sequence 1, Application PC/TUS0111290  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Takabayashi, Kenji  
; APPLICANT: Nguyen, Minh-Duc  
; TITLE OF INVENTION: Synergistic Improvements to  
; FILE REFERENCE: 6510-203WO  
; CURRENT APPLICATION NUMBER: PCT/US01/11290  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,890  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence  
PCT-US01-11290-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgaccgtgaacgcttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgcttcgagatga 22

RESULT 13  
PCT-US01-14508-1  
; Sequence 1, Application PC/TUS0114508  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Lois, Augusto F.  
; APPLICANT: Takabayashi, Kenji

;; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and  
;; TITLE OF INVENTION: Methods of Use Thereof  
;; FILE REFERENCE: 06510/168WO1  
;; CURRENT APPLICATION NUMBER: PCT/US01/14508  
;; CURRENT FILING DATE: 2000-05-04  
;; PRIOR FILING DATE: 60/262,321  
;; PRIOR FILING DATE: 2001-01-17  
;; PRIOR APPLICATION NUMBER: 60/202,274  
;; PRIOR FILING DATE: 2000-05-05  
;; NUMBER OF SEQ ID NOS: 21  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 22  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: ISS-ODN  
PCT-US01-14508-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 14  
PCT-US99-21203-19  
;; Sequence 19, Application PC/TUS9921203  
;; GENERAL INFORMATION:  
;; APPLICANT: The Regents of the University of California  
;; TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING  
;; TITLE OF INVENTION: MUCOSAL IMMUNITY  
;; NUMBER OF SEQUENCES: 20  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fulbright & Jaworski L.L.P.  
;; STREET: 865 S. Figueroa Street, 29th Floor  
;; CITY: Los Angeles  
;; STATE: CA  
;; COUNTRY: US  
;; ZIP: 90017  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US99/21203  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/927,120  
;; FILING DATE: 05 September 1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Berliner, Robert  
;; REGISTRATION NUMBER: 20,121  
;; REFERENCE/DOCKET NUMBER: 5555-188  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 213-892-9200  
;; TELEFAX: 213-680-4518  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: non-coding oligonucleotides  
PCT-US99-21203-19

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 TGACTGTGAACGTTTCGAGATGA 22  
RESULT 15  
US-08-927-120-19  
;; Sequence 19, Application US/08927120  
;; GENERAL INFORMATION:  
;; APPLICANT: Raz, Eyal  
;; TITLE OF INVENTION: IMMUNIZATION-FREE METHODS  
;; TITLE OF INVENTION: FOR STIMULATING IMMUNE RESPONSIVENESS AND REDUCING  
;; TITLE OF INVENTION: INFLAMMATION IN A HOST  
;; NUMBER OF SEQUENCES: 20  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson, P.C.  
;; STREET: 4225 Executive Square, Suite 1400  
;; CITY: La Jolla  
;; STATE: CA  
;; COUNTRY: US  
;; ZIP: 92037  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/927,120  
;; FILING DATE: 22-AUG-1997  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Taylor, Stacy L.  
;; REGISTRATION NUMBER: 34,842  
;; REFERENCE/DOCKET NUMBER: 07340/054001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-678-5070  
;; TELEFAX: 619-678-5099  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: non-coding oligonucleotides  
US-08-927-120-19

Query Match 92.7%; Score 20.4; DB 13; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 TGACTGTGAACGTTTCGAGATGA 22

Search completed: October 9, 2001, 21:12:35  
Job time: 20060 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:35:59 ; Search time 1391.6 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-09-713-136-2  
Perfect score: 22  
Sequence: 1 tgaccgtgaacgttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New: \*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq: \*  
7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq: \*  
8: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	7 US-09-802-518-2	Sequence 2, Appli
2	22	100.0	22	7 US-09-802-359-2	Sequence 2, Appli
3	22	100.0	22	7 US-09-802-376-2	Sequence 2, Appli
4	20.4	92.7	22	7 US-09-802-518-1	Sequence 1, Appli
5	20.4	92.7	22	7 US-09-802-359-1	Sequence 1, Appli
6	20.4	92.7	22	7 US-09-802-376-1	Sequence 1, Appli
7	19.4	88.2	22	7 US-09-802-518-7	Sequence 7, Appli
8	19.4	88.2	22	7 US-09-802-359-7	Sequence 7, Appli
9	19.4	88.2	22	7 US-09-802-376-7	Sequence 7, Appli
10	18.8	85.5	22	7 US-09-770-943-2	Sequence 2, Appli
11	18.8	85.5	22	7 US-09-802-518-4	Sequence 4, Appli
12	18.8	85.5	22	7 US-09-802-359-4	Sequence 4, Appli
13	18.8	85.5	22	7 US-09-802-376-4	Sequence 4, Appli
14	18.4	83.6	22	7 US-09-802-518-8	Sequence 8, Appli
15	18.4	83.6	22	7 US-09-802-359-8	Sequence 8, Appli
16	18.4	83.6	22	7 US-09-802-376-8	Sequence 8, Appli
17	17.8	80.9	22	7 US-09-802-518-6	Sequence 6, Appli
18	17.8	80.9	22	7 US-09-802-359-6	Sequence 6, Appli
19	17.8	80.9	22	7 US-09-802-376-6	Sequence 6, Appli
20	17.2	78.2	22	6 US-09-770-943-1	Sequence 1, Appli
21	17.2	78.2	22	6 US-09-770-943-3	Sequence 3, Appli
22	17.2	78.2	22	6 US-09-770-943-10	Sequence 10, Appli
23	17.2	78.2	22	7 US-09-802-518-10	Sequence 10, Appli
24	17.2	78.2	22	7 US-09-802-518-11	Sequence 11, Appli
25	17.2	78.2	22	7 US-09-802-359-9	Sequence 9, Appli

26	17.2	78.2	22	7 US-09-802-359-10	Sequence 10, Appli
27	17.2	78.2	22	7 US-09-802-376-9	Sequence 9, Appli
28	17.2	78.2	22	7 US-09-802-376-10	Sequence 10, Appli
29	15.8	71.8	1407	6 US-09-894-844-35	Sequence 35, Appli
30	15.6	70.9	22	6 US-09-770-943-4	Sequence 4, Appli
31	15.6	70.9	189	8 US-60-253-652-21559	Sequence 21559, A
32	15.6	70.9	252	5 US-09-825-790-331	Sequence 331, App
33	15.6	70.9	333	6 US-09-803-110-7440	Sequence 7440, Ap
34	15.6	70.9	550	6 US-09-803-110-2557	Sequence 2557, Ap
35	15.6	70.9	768	5 US-09-543-681A-2526	Sequence 2526, Ap
36	15.6	70.9	813	1 PCT-US01-08656-2544	Sequence 1899, Ap
37	15.6	70.9	813	7 US-09-861-478-1899	Sequence 1899, Ap
38	15.6	70.9	821	7 US-09-861-478-1379	Sequence 1379, Ap
39	15.6	70.9	110684	6 US-09-803-736-1100	Sequence 1100, Ap
40	15.4	70.0	341	7 US-09-840-145-1568	Sequence 1568, Ap
41	15.4	70.0	207674	6 US-09-803-736-588	Sequence 588, App
42	15.2	69.1	252	7 US-09-540-213-28028	Sequence 28028, A
43	15.2	69.1	272	5 US-09-534-840-3533	Sequence 3533, Ap
44	15.2	69.1	285	7 US-09-540-213-47271	Sequence 47271, A
45	15.2	69.1	330	8 US-60-253-652-9623	Sequence 9623, Ap

## ALIGNMENTS

RESULT 1  
US-09-802-518-2  
; Sequence 2, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 37782001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-2

Query Match 100.0%; Score 22; DB 7; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22  
|||||  
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 2  
US-09-802-359-2  
; Sequence 2, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2

```
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-2

Query Match
Best Local Similarity 100.0%; Score 22; DB 7; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3
US-09-802-376-2
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-2

Query Match
Best Local Similarity 100.0%; Score 22; DB 7; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 4
US-09-802-518-1
; Sequence 1, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-1

Query Match
Best Local Similarity 92.7%; Score 20.4; DB 7; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match
Best Local Similarity 92.7%; Score 20.4; DB 7; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match
Best Local Similarity 92.7%; Score 20.4; DB 7; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match
Best Local Similarity 92.7%; Score 20.4; DB 7; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22
```

```
RESULT 7
US-09-802-518-7
; Sequence 7, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.47;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
   |||| |||| |||| |||| ||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 8
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.47;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
   |||| |||| |||| |||| ||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 9
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.47;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
   |||| |||| |||| |||| ||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 10
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match      85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
   |||| |||| |||| |||| ||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 11
US-09-802-518-4
; Sequence 4, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
```

```
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-4
```

```
Query Match      85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttccagatga 22
```

```
RESULT 12
US-09-802-359-4
; Sequence 4, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-4
```

```
Query Match      85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttccagatga 22
```

```
RESULT 13
US-09-802-376-4
; Sequence 4, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-4
```

```
Query Match      85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttccagatga 22
```

```
RESULT 14
US-09-802-518-8
; Sequence 8, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-8
```

```
Query Match      83.6%; Score 18.4; DB 7; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttngagatga 22
```

```
RESULT 15
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
```



; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-359-8

Query Match 83.6%; Score 18.4; DB 7; Length 22;  
Best Local Similarity 86.4%; Pred. No. 1.7;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22  
||| |||| || |||||  
Db 1 tgactgtgaangtngagatga 22

Search completed: October 9, 2001, 21:36:00  
Job time: 21220 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:41:58 ; Search time 217.64 Seconds  
(without alignments)  
19,136 Million cell updates/sec

Title: US-09-713-136-2  
Perfect score: 22  
Sequence: 1 tgaccgtgaacgttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.8	85.5	22	4	US-09-092-314-2
2	17.2	78.2	22	4	US-09-092-314-1
3	17.2	78.2	22	4	US-09-092-314-3
4	17.2	78.2	22	4	US-09-092-314-10
5	15.6	70.9	22	4	US-09-092-314-4
6	15.6	70.9	77	1	US-08-399-412A-58
7	14.6	66.4	440	1	US-07-998-003A-37
8	14.6	66.4	440	1	US-08-453-274B-37
9	14.6	66.4	440	1	US-08-453-695A-37
10	14.6	66.4	440	1	US-08-268-161A-37
11	14.6	66.4	440	2	US-08-453-702A-37
12	14.6	66.4	440	5	PCT-US93-12588-37
13	14.6	66.4	440	5	PCT-US95-08071-37
14	14.6	66.4	1553	1	US-09-217-490-1
15	14.6	66.4	1560	1	US-08-344-536-3
16	14.6	66.4	1560	3	US-08-920-562-3
17	14.4	65.5	31	4	US-09-070-408-110
18	14.2	64.5	906	6	5204252-3
19	14	63.6	22	4	US-09-092-314-5
20	14	63.6	22	4	US-09-092-314-7
21	14	63.6	22	4	US-09-092-314-8
22	14	63.6	73	1	US-08-434-001-33
23	14	63.6	73	1	US-08-434-585-33
24	14	63.6	73	1	US-08-434-425-33
25	14	63.6	73	2	US-08-437-667-33
26	14	63.6	73	3	US-08-906-955-33
27	14	63.6	73	3	US-08-945-909-33

28	14	63.6	73	5	PCT-US96-06060-33
29	14	63.6	76	1	US-08-442-572-42
30	14	63.6	76	1	US-08-361-795-42
31	14	63.6	76	5	PCT-US95-05600-125
32	14	63.6	538	1	US-08-840-683-5
33	14	63.6	538	2	US-08-555-722-5
34	14	63.6	1179	4	US-09-147-926-1
35	14	63.6	1352	1	US-07-714-819-1
36	14	63.6	1352	1	US-08-246-978A-1
37	14	63.6	1352	1	US-08-440-814A-1
38	14	63.6	1418	1	US-08-391-615-7
39	14	63.6	1484	1	US-08-485-618-102
40	14	63.6	1484	1	US-08-605-672-102
41	14	63.6	1484	2	US-08-482-293A-102
42	14	63.6	1484	2	US-08-943-363-102
43	14	63.6	1484	4	US-09-193-043-102
44	14	63.6	1635	4	US-09-178-252-10
45	14	63.6	1830	4	US-09-019-931-2

ALIGNMENTS

RESULT 1  
US-09-092-314-2  
; Sequence 2, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-2

Query Match 85.5%; Score 18.8; DB 4; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.3;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22  
||| ||||| ||||| ||||| |||||  
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 2  
US-09-092-314-1  
; Sequence 1, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-1

Query Match 78.2%; Score 17.2; DB 4; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| |||||  
DB 1 tgactgtgaagtttagatga 22

## RESULT 3

US-09-092-314-3  
; Sequence 3, Application US/09092314  
; Patent No. 6225292

; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal

; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory

; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292

; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314

; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794

; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3

; LENGTH: 22  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-3

Query Match 78.2%; Score 17.2; DB 4; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| |||||  
DB 1 tgactgtgaaccttagatga 22

## RESULT 4

US-09-092-314-10

; Sequence 10, Application US/09092314  
; Patent No. 6225292

; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal

; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory

; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292

; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314

; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794

; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10

; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-10

Query Match 78.2%; Score 17.2; DB 4; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| |||||  
DB 1 tgactgtgaagtttagatga 22

## RESULT 5

US-09-092-314-4

; Sequence 4, Application US/09092314  
; Patent No. 6225292

; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal

; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory

; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292

; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314

; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794

; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4

; LENGTH: 22  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-4

Query Match 70.9%; Score 15.6; DB 4; Length 22;  
Best Local Similarity 81.8%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22  
||||| ||||| ||||| |||||  
DB 1 tgactgtgaagcttagatga 22

## RESULT 6

US-08-399-412A-58

; Sequence 58, Application US/08399412A  
; Patent No. 5622828

; GENERAL INFORMATION:  
; APPLICANT: Parma, David

; APPLICANT: Gold, Larry  
; TITLE OF INVENTION: High-Affinity Oligonucleotide

; TITLE OF INVENTION: Ligands To Secretory Phospholipase  
; TITLE OF INVENTION: A2 (sPLA2)

; NUMBER OF SEQUENCES: 122  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood  
; STATE: Colorado

; COUNTRY: USA  
; ZIP: 80111

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

; COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,412A  
FILING DATE: 6-MARCH-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Julie L. Bernard  
REGISTRATION NUMBER: 36,450  
REFERENCE/DOCKET NUMBER: NEX27  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-399-412A-58

Query Match 70.9%; Score 15.6; DB 1; Length 77;  
Best Local Similarity 63.6%; Pred. No. 15;  
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22  
Db 42 UGCCACGACGACGUCGACGAUGA 63

RESULT 7  
US-07-998-003A-37  
Sequence 37, Application US/07998003A  
Patent No. 5643781  
GENERAL INFORMATION:  
APPLICANT: Suzuki, Shintaro  
TITLE OF INVENTION: Protocadherin Materials and Methods  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &  
ADDRESSER: Bicknell  
STREET: 20 South Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/998,003A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5643781and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 30903  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/346-5750  
TELEFAX: 312/984-9740

TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-07-998-003A-37

Query Match 66.4%; Score 14.6; DB 1; Length 440;  
Best Local Similarity 81.0%; Pred. No. 62;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatg 21  
Db 83 TGACCCTGACCCCTTCAAGATG 103

RESULT 8  
US-08-453-274B-37  
Sequence 37, Application US/08453274B  
Patent No. 5663300  
GENERAL INFORMATION:  
APPLICANT: Suzuki, Shintaro  
TITLE OF INVENTION: Protocadherin Materials and Methods  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,274B  
FILING DATE: 30-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5663300and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32660  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-453-274B-37

Query Match 66.4%; Score 14.6; DB 1; Length 440;  
Best Local Similarity 81.0%; Pred. No. 62;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatg 21  
Db 83 TGACCCTGACCCCTTCAAGATG 103

RESULT 9  
US-08-453-695A-37  
Sequence 37, Application US/08453695A

```

; Patent No. 5708143
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,695A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5708143and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32658
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-453-695A-37

Query Match 66.4%; Score 14.6; DB 1; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
||||| ||| ||| ||| |||
Db 83 TGACCCTGACCCCTCAAGATG 103

RESULT 10
US-08-268-161A-37
; Sequence 37, Application US/08268161A
; Patent No. 5798224
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,161A
; FILING DATE: June 27, 1994

```

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Young J. Suh
; REGISTRATION NUMBER: P-41,337
; REFERENCE/DOCKET NUMBER: 27866/32149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-268-161A-37

Query Match 66.4%; Score 14.6; DB 1; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
||||| ||| ||| ||| |||
Db 83 TGACCCTGACCCCTCAAGATG 103

RESULT 11
US-08-453-702A-37
; Sequence 37, Application US/08453702A
; Patent No. 5891706
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,702A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5891706and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32657
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-453-702A-37

Query Match 66.4%; Score 14.6; DB 2; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;

```

```
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
   ||||| ||| ||| |||||
Db 83 TGACCTGACCTTCAAGATG 103

RESULT 12
PCT-US93-12588-37
; Sequence 37, Application PC/TUS9312588
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12588
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/998,003
; FILING DATE: 29 DEC 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31811
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-12588-37

Query Match 66.4%; Score 14.6; DB 5; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
   ||||| ||| ||| |||||
Db 83 TGACCTGACCTTCAAGATG 103

RESULT 13
PCT-US95-08071-37
; Sequence 37, Application PC/TUS9508071
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
```

```
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08071
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12588
; FILING DATE: 23 DEC 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/998,003
; FILING DATE: 29 DEC 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-08071-37

Query Match 66.4%; Score 14.6; DB 5; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
   ||||| ||| ||| |||||
Db 83 TGACCTGACCTTCAAGATG 103

RESULT 14
US-09-217-490-1/c
; Sequence 1, Application US/09217490
; Patent No. 6165761
; GENERAL INFORMATION:
; APPLICANT: Schneider, Paile
; APPLICANT: Christensen, Soren
; APPLICANT: Dybdal, Lone
; APPLICANT: Fuglsang, Claus Crone
; APPLICANT: Xu, Feng
; APPLICANT: Golightly, Elizabeth
; TITLE OF INVENTION: Carbohydrate Oxidase And use Thereof In
; FILE REFERENCE: 5421.200-US
; CURRENT APPLICATION NUMBER: US/09/217,490
; CURRENT FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: PA 1997 01505
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: PA 1998 00763
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/068,717
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 60/088/725
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1553
```

TYPE: DNA  
ORGANISM: Microdochium nivale  
FEATURE:  
NAME/KEY: Intron  
LOCATION: (1012)..(1076)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1011)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1077)..(1553)  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: (67)..(1550)  
US-09-217-490-1

Query Match 66.4%; Score 14.6; DB 4; Length 1553;  
Best Local Similarity 81.0%; Pred. No. 73;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gaccgtgaacgttcgagatga 22  
||||| ||||| |||  
Db 529 GACCGTCATGTCGAGCTGA 509

RESULT 15  
US-08-344-536-3  
Sequence 3, Application US/08344536  
Patent No. 5674735  
GENERAL INFORMATION:  
APPLICANT: Onions, David E.  
APPLICANT: Nicolson, Lesley  
TITLE OF INVENTION: EHV-4 GLYCOPROTEIN VACCINE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: NO. 5674735th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,536  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/961,672  
FILING DATE: 05-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 1749-106  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 881-3140  
TELEFAX: (919) 881-3175  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 52..1506  
US-08-344-536-3

Query Match 66.4%; Score 14.6; DB 1; Length 1560;  
Best Local Similarity 81.0%; Pred. No. 73;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 tgaccgtgaacgttcgagatg 21  
||||| ||||| |||||  
Db 1088 TGCCGTAACGTTGAAGATG 1108

Search completed: October 9, 2001, 15:41:59  
Job time: 289 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:18:29 ; Search time 2150.93 Seconds  
(without alignments)  
165.397 Million cell updates/sec

Title: US-09-713-136-3  
Perfect score: 23  
Sequence: 1 tcattcgaacgtccacagtca 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba1:  
2: gb\_ba2:  
3: gb\_ba3:  
4: gb\_in1:  
5: gb\_in2:  
6: gb\_in3:  
7: gb\_om:  
8: gb\_ov:  
9: gb\_pat1:  
10: gb\_pat2:  
11: gb\_ph:  
12: gb\_pl1:  
13: gb\_pl2:  
14: gb\_pl3:  
15: gb\_pl4:  
16: em\_ba1:  
17: em\_ba2:  
18: em\_fun:  
19: em\_htgo\_hum:  
20: em\_htgo\_inv:  
21: em\_htgo\_rod:  
22: em\_htg\_hum1:  
23: em\_htg\_hum2:  
24: em\_htg\_hum3:  
25: em\_htg\_hum4:  
26: em\_htg\_hum5:  
27: em\_htg\_hum6:  
28: em\_htg\_hum7:  
29: em\_htg\_hum8:  
30: em\_htg\_inv1:  
31: em\_htg\_inv2:  
32: em\_htg\_other:  
33: em\_htg\_rod:  
34: em\_hum1:  
35: em\_hum2:  
36: em\_hum3:  
37: em\_hum4:  
38: em\_hum5:  
39: em\_hum6:  
40: em\_hum7:  
41: em\_in:  
42: em\_om:  
43: em\_or:

44: em\_ov:  
45: em\_pat:  
46: em\_ph:  
47: em\_pl:  
48: em\_ro:  
49: em\_sts:  
50: em\_sy:  
51: em\_un:  
52: em\_v1:  
53: gb\_sts1:  
54: gb\_sts2:  
55: gb\_sts3:  
56: gb\_sy:  
57: gb\_un:  
58: gb\_v1:  
59: gb\_v12:  
60: gb\_htg1:  
61: gb\_htg2:  
62: gb\_htg3:  
63: gb\_htg4:  
64: gb\_htg5:  
65: gb\_htg6:  
66: gb\_htg7:  
67: gb\_htg8:  
68: gb\_htg9:  
69: gb\_htg10:  
70: gb\_htg11:  
71: gb\_htg12:  
72: gb\_htg13:  
73: gb\_htg14:  
74: gb\_htg15:  
75: gb\_htg16:  
76: gb\_htg17:  
77: gb\_htg18:  
78: gb\_htg19:  
79: gb\_htg20:  
80: gb\_htg21:  
81: gb\_htg22:  
82: gb\_htg23:  
83: gb\_htg24:  
84: gb\_htg25:  
85: gb\_pr1:  
86: gb\_pr2:  
87: gb\_pr3:  
88: gb\_pr4:  
89: gb\_pr5:  
90: gb\_pr6:  
91: gb\_pr7:  
92: gb\_pr8:  
93: gb\_pr9:  
94: gb\_rol:  
95: gb\_ro2:  
96: gb\_in4:  
97: gb\_pr10:  
98: em\_ba3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	100.0	23	10	AX083677
C 2	18.4	80.0	160974	90	AL139330 Human DNA
C 3	17.2	74.8	213	94	U26223 Mus musculus
C 4	17.2	74.8	992	53	AL43316 T3 end of
C 5	17.2	74.8	1158	7	M19680 Bovine mito
C 6	17.2	74.8	1718	95	J05266 Rat mitocho
7	17.2	74.8	7015	6	AF101304 Caenorhab
8	17.2	74.8	34348	6	AF067944 Caenorhab



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c 9 17.2 74.8 46057 88 AC073276 Homo sapi
c 10 17.2 74.8 71441 86 AC007042 Homo sapi
c 11 17.2 74.8 72265 86 AC006516 Homo sapi
c 12 17.2 74.8 83287 13 AP000603 Arabidops
c 13 17.2 74.8 128289 86 AC007972 Homo sapi
c 14 17.2 74.8 132060 78 AC090898 Homo sapi
c 15 17.2 74.8 138698 60 AC008454 Homo sapi
c 16 17.2 74.8 157965 72 AC053498 Homo sapi
c 17 17.2 74.8 192276 79 AL355353 Homo sapi
c 18 17.2 74.8 195247 81 AL390717 Homo sapi
c 19 17.2 74.8 208287 67 AC022532 Homo sapi
c 20 17 73.9 49323 12 AC007109 Arabidops
c 21 16.8 73.0 664 72 AC058348 Giardia i
c 22 16.8 73.0 811 71 AC039842 Giardia i
c 23 16.8 73.0 877 76 AC081149 Giardia i
c 24 16.8 73.0 882 71 AC040526 Giardia i
c 25 16.8 73.0 897 74 AC070300 Giardia i
c 26 16.8 73.0 924 72 AC065824 Giardia i
c 27 16.8 73.0 939 74 AC070334 Giardia i
c 28 16.8 73.0 993 77 AC085260 Giardia i
c 29 16.8 73.0 1022 72 AC061054 Giardia i
c 30 16.8 73.0 1033 72 AC055301 Giardia i
c 31 16.8 73.0 1058 75 AC077153 Giardia i
c 32 16.8 73.0 1140 72 AC054342 Giardia i
c 33 16.8 73.0 38392 65 AC019553 Drosophil
c 34 16.8 73.0 110000 79 AL3553643 Continuation (4 of
c 35 16.8 73.0 150682 82 AL590378 Homo sapi
c 36 16.8 73.0 159103 69 AC025687 Homo sapi
c 37 16.8 73.0 177226 78 AC090496 Mus muscu
c 38 16.8 73.0 185054 77 AC090013 Homo sapi
c 39 16.8 73.0 309883 4 AE003479 Drosophil
c 40 16.6 72.2 1108 94 AF237817 Mus muscu
c 41 16.6 72.2 1731 13 AP000392 Oryza sat
c 42 16.6 72.2 2190 94 AF284380 Mus muscu
c 43 16.6 72.2 8355 94 AB047760 Mus muscu
c 44 16.6 72.2 31147 65 AC018318 Drosophil
c 45 16.6 72.2 31309 12 AB013387 Arabidops

```

## ALIGNMENTS

```

RESULT 1
LOCUS AX083677 23 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 3 from Patent WO0112223.
ACCESSION AX083677
VERSION AX083677.1 GI:13185409
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 23)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
JOURNAL Patent: WO 011223-A 3 22-FEB-2001.
JOURNAL Dynavax Technologies Corporation (US)
FEATURES
source Location/Qualifiers
1..23
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN
Query Match 100.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tcattctcgaaacgtttccacagtca 23
|||||

```

```

Db 1 TCATCTCGAAGCTTCCACAGTCA 23
RESULT 2
LOCUS AL139330/c
DEFINITION AL139330 160974 bp DNA PRI 19-MAR-2001
Human DNA sequence from clone RP11-266C7 on chromosome 6q25.2-26,
complete sequence.
ACCESSION AL139330
VERSION AL139330.17 GI:13398696
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 160974)
AUTHORS Sycamore,N.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On Mar 21, 2001 this sequence version replaced gi:13274265.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,
SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/projects/C-elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP11-266C7 is from the library RPi-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-266C7 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-266C7 is at 1 in this sequence. The
true left end of clone RP3-403L10 is at 160875 in this sequence.
The true right end of clone RPI-257C19 is at 72466 in this
sequence.
FEATURES
source Location/Qualifiers
1..160974
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="q25.2-26"
/clone="RP11-266C7"
/clone_lib="RP11-11.1"
misc_feature 17..541
/note="match: GSS: Em:AQ488081"
repeat_region 143..456
/note="Alusg repeat: matches 1..310 of consensus"
misc_feature 591..1015
/note="match: STS: Em:C37401"
misc_feature complement(689..1172)
/note="match: GSS: Em:AQ763085"
repeat_region 4594..4892
/note="Alusx repeat: matches 1..298 of consensus"

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```

repeat_region 5190..5524
/note="MER47A repeat: matches 1. .366 of consensus"
repeat_region 6295..6584
/note="AluSg repeat: matches 21. .308 of consensus"
repeat_region 6973..7265
/note="AluJb repeat: matches 1. .303 of consensus"
repeat_region 7266..7398
/note="AluJo repeat: matches 2. .138 of consensus"
repeat_region 7648..7985
/note="L1MB7 repeat: matches 5830. .6173 of consensus"
repeat_region 7986..8290
/note="AluY repeat: matches 2. .304 of consensus"
repeat_region 8291..8414
/note="L1MB7 repeat: matches 5718. .5830 of consensus"
repeat_region 8415..8722
/note="AluY repeat: matches 1. .309 of consensus"
repeat_region 8914..9225
/note="AluSx repeat: matches 1. .312 of consensus"
repeat_region 11473..11709
/note="AluJb repeat: matches 85. .312 of consensus"
repeat_region 11862..11885
/note="12 copies 2 mer aa 95% conserved"
misc_feature 12664..13070
/note="CpG island"
evidence-not_experimental
repeat_region 13947..14128
/note="MER5A repeat: matches 18. .189 of consensus"
repeat_region 14438..14733
/note="AluJb repeat: matches 1. .297 of consensus"
repeat_region 14926..15235
/note="AluSx repeat: matches 1. .303 of consensus"
repeat_region 16326..16818
/note="AluSx repeat: matches 1. .293 of consensus"
repeat_region 17079..17245
/note="AluSx repeat: matches 147. .302 of consensus"
repeat_region 17246..17550
/note="AluSg repeat: matches 2. .306 of consensus"
repeat_region 17551..17689
/note="AluSx repeat: matches 5. .147 of consensus"
repeat_region 17805..18138
/note="AluJo repeat: matches 1. .302 of consensus"
repeat_region 19067..19261
/note="L1MB3A repeat: matches 5556. .5743 of consensus"
repeat_region 19262..19564
/note="AluSx repeat: matches 1. .304 of consensus"
misc_feature 19527..19976
/note="match: STS: Em:HS355C7S"
repeat_region 19565..19661
/note="L1MB3A repeat: matches 5743. .5841 of consensus"
repeat_region 19836..19973
/note="L2 repeat: matches 2606. .2745 of consensus"
repeat_region 20097..20373
/note="AluSx repeat: matches 3. .298 of consensus"
repeat_region 20664..20969
/note="AluSx repeat: matches 1. .302 of consensus"
repeat_region 22067..22106
/note="20 copies 2 mer tt 82% conserved"
repeat_region 22465..22777
/note="AluSp repeat: matches 1. .312 of consensus"
repeat_region 23399..23521
/note="L2 repeat: matches 2582. .2708 of consensus"
repeat_region 23577..23800
/note="AluJb repeat: matches 50. .276 of consensus"
repeat_region 24106..24399
/note="AluSg repeat: matches 1. .296 of consensus"
repeat_region 24527..24834
/note="AluSx repeat: matches 1. .307 of consensus"
repeat_region 25811..25971
/note="MIR repeat: matches 6. .167 of consensus"
repeat_region 26053..26242
/note="MER3 repeat: matches 2. .203 of consensus"
repeat_region 26261..26562
/note="AluSx repeat: matches 1. .304 of consensus"

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repeat_region 26672..26970
/note="AluSx repeat: matches 1. .299 of consensus"
repeat_region 28552..28856
/note="AluSx repeat: matches 2. .303 of consensus"
repeat_region 32169..32208
/note="10 copies 4 mer caaa 80% conserved"
repeat_region 32440..32755
/note="AluSg repeat: matches 1. .313 of consensus"
repeat_region 36071..36364
/note="AluSg repeat: matches 16. .308 of consensus"
misc_feature complement(36336..36775)
/note="match: GSS: Em:AQ119669"
misc_feature complement(36340..36779)
/note="match: GSS: Em:B89745"
repeat_region 36519..36969
/note="MER82 repeat: matches 2. .441 of consensus"
repeat_region 37004..37094
/note="MER82 repeat: matches 556. .646 of consensus"
repeat_region 37503..37616
/note="2 copies 57 mer 87% conserved"
repeat_region 39904..40210
/note="AluSg repeat: matches 1. .307 of consensus"
repeat_region 40816..41111
/note="AluJo repeat: matches 3. .292 of consensus"
repeat_region 42185..42311
/note="MIR repeat: matches 89. .226 of consensus"
repeat_region 42393..42467
/note="3 copies 25 mer 90% conserved"
repeat_region 43657..43709
/note="Alu repeat: matches 254. .308 of consensus"
repeat_region 44222..44253
/note="16 copies 2 mer ac 100% conserved"
repeat_region 45307..45446
/note="L1MC4 repeat: matches 6867. .7005 of consensus"
repeat_region 45449..45692
/note="61 copies 4 mer gatg 82% conserved"
repeat_region 45479..45672
/note="97 copies 2 mer tg 55% conserved"
repeat_region 45693..45772
/note="20 copies 4 mer atgg 81% conserved"
repeat_region 45698..45937
/note="12 copies 20 mer 62% conserved"
repeat_region 45773..45944
/note="43 copies 4 mer ggat 77% conserved"
repeat_region 45945..46104
/note="8 copies 20 mer 80% conserved"
repeat_region 46099..46146
/note="12 copies 4 mer aggt 75% conserved"
repeat_region 46256..46972
/note="L1MC4 repeat: matches 7015. .7771 of consensus"
repeat_region 46973..47379
/note="MSTRB repeat: matches 1. .425 of consensus"
repeat_region 47415..47533
/note="L1MC4 repeat: matches 7853. .7974 of consensus"
repeat_region 47774..48093
/note="AluJb repeat: matches 1. .311 of consensus"
misc_feature 48660..49031
/note="match: GSS: Em:AQ032423"
repeat_region 49386..49555

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Query Match      80.0%; Score 18.4; DB 90; Length 160974;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 tcctctgaacgttcacag 20
        ||||| ||||| |||||
DB 131791 TCATCTAGACGTTCCACAG 131772

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```

RESULT      3
MMU26223/c  213 bp      RNA      ROD      09-FEB-1996
LOCUS      Mus musculus clone pmg7 nonsatellite RNA sequence.
DEFINITION

```

11152876  
PUBLISHED 3 (bases 1 to 992)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,  
JOURNAL 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT This STS is part of a random genomic sequencing program of thirteen  
yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*  
*exiguus*, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*,  
*Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces*  
*lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*  
*angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,  
*Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to  
5 kb were prepared and both extremities were sequenced. See  
keywords for description of this sequence and for the sequence of  
the other extremity of this insert.

FEATURES  
Location/Qualifiers  
1..992  
/organism="Pichia angusta"  
/strain="CBS 4732"  
/db\_xref="taxon:4905"  
/clone="BB0AA015F02"  
/clone\_lib="BB0AA"  
/note="end : T3"  
<1..>837  
/misc\_feature  
/note="similar to Saccharomyces cerevisiae ORF YNL101w [  
similarity to YKL146w ]"  
/evidence=not\_experimental

BASE COUNT 265 a 215 c 209 g 302 t 1 others  
ORIGIN

Query Match 74.8% Score 17.2: DB 53: Length 992;  
Best Local Similarity 86.4% Pred. No. 2.6e+02;  
Matches 19: Conservative 0: Mismatches 3: Indels 0: Gaps 0: Y

QY 1 tcattctggaacgtgtccacagtc 22  
||||| ||||| ||||| |||||  
Db 422 TGATCTTGAACTTCCACAGTC 443

RESULT 5  
BOVATPSAS/c  
LOCUS BOVATPSAS 1158 bp mRNA MAM 26-APR-1993  
DEFINITION Bovine mitochondrial ATP synthase alpha-subunit mRNA, 5' end.  
ACCESSION M19680  
VERSION M19680.1 GI:162718  
KEYWORDS ATP synthase alpha subunit.  
SOURCE Bovine liver, cDNA to mRNA.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 1158)  
Breen,G.A.M.  
Bovine liver cDNA clones encoding a precursor of the alpha-subunit  
of the mitochondrial ATP synthase complex  
JOURNAL Biochem. Biophys. Res. Commun. 152, 264-269 (1988)  
MEDLINE 89192643  
COMMENT Draft entry and computer-readable sequence for [1] kindly provided  
by G.A.M.Breen, 12-JUL-1988.

FEATURES  
Location/Qualifiers  
1..1158  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
82..210  
/note="ATP synthase alpha subunit signal peptide"  
82..>1158  
/note="ATP synthase alpha subunit precursor"  
/codon\_start=1  
/protein\_id="AAA30399.1"  
/db\_xref="GI:162719"

CDS

/translation="MLSVRIAAVARALPRRAGLVSKNALGSSFVCTRNLHASNTRLQ  
KGTAMSSILREILGADTSVDLESTGRVLSIGDGIARVHGLRNVAQAEVFESSGL  
KGMNLDPNVGVVFGNDKLIKEDIVKRTGAIVDPVPGDELGRVADALGNADIG  
KPGVSKIRRIIPRISVREPMTGKAVDSLVPVIGRQRELIIGDROTGK  
TSAIDTIIINQRFNDGTDEKKLYCIYVAIGOKRSTVAQLVKRLTDADAMKTYIVS  
ATASDAAPLOYLAPYSGCSMGVEFRDNGKHALIYDLSKQAVAYROMSLLLRPPGR  
EAYPGDVFVLSRLLEAAKMNDSF"  
mat\_peptide 211..1155  
/note="ATP synthase alpha subunit"  
BASE COUNT 259 a 296 c 329 g 274 t  
ORIGIN 55 bp upstream of PstI site.

Query Match 74.8%; Score 17.2; DB 7; Length 1158;  
Best Local Similarity 86.4%; Pred. No. 2.6e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 tcactctgaacgttccacagtc 22  
Db 359 TCAGCTTGAACGTTCCTCAGTC 338

RESULT 6  
RATATPSB/c  
LOCUS RATATPSB 1718 bp mRNA ROD 27-APR-1993  
DEFINITION Rat mitochondrial H+-ATP synthase alpha subunit mRNA, complete cds.  
ACCESSION J05266  
VERSION J05266.1 GI:203054  
KEYWORDS ATP synthase; nucleotide-binding protein.  
SOURCE Rat (Sprague-Dawley adult) liver, cDNA to mRNA.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 1718)  
AUTHORS Lee J.H., Garboczi D.N., Thomas P.J. and Pedersen P.L.  
TITLE Mitochondrial ATP synthase: cDNA cloning, amino acid sequence, overexpression, and properties of the rat liver alpha subunit  
JOURNAL J. Biol. Chem. 265, 4664-4669 (1990)  
MEDLINE 90170980  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by P.J.Thomas, 24-JAN-1990.  
FEATURES  
source location/Qualifiers  
1..1718  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
<1..99  
/note="ATP synthase alpha subunit signal peptide (put.)  
(EC 3.6.1.3); putative"  
CDS  
<1..1632  
/note="ATP synthase alpha subunit precursor (EC 3.6.1.3)"  
/codon\_start=1  
/protein\_id="AAA40784.1"  
/db\_xref="GI:203055"  
/translation="RRALPRRAGLVSKNALGSSFVCTRNLHASNTRLQKGTAEEMSSI  
LEERIGADTSVDLESTGRVLSIGDGIARVHGLRNVAQAEVFESSGLKGMNLDPNVGVVFGNDKLIKEDIVKRTGAIVDPVPGDELGRVADALGNADIGKPGVSKIRRIIPRISVREPMTGKAVDSLVPVIGRQRELIIGDROTGKTRSAIDTIIINQRFNDGTDEKKLYCIYVAIGOKRSTVAQLVKRLTDADAMKTYIVS  
ATASDAAPLOYLAPYSGCSMGVEFRDNGKHALIYDLSKQAVAYROMSLLLRPPGREAYPGDVFYL  
KIRPAIINQRFNDGTDEKKLYCIYVAIGOKRSTVAQLVKRLTDADAMKTYIVS  
HSRLLEAAKMNDSFVGGGSLTAPVETQAGDSAYIPTNVISITDQGFLETFELFK  
LSRGVRLTELLKQGYSPMAIEQVAVIYAGVIRGLDLEPKLEPKITKPFESAFLSHVQ  
HOSLLGNIRSDGKISEQSDAKLKEIVTNFLAGEP"  
mat\_peptide 399 a 414 c 470 g 435 t  
/note="ATP synthase alpha subunit (EC 3.6.1.3)"  
BASE COUNT 399 a 414 c 470 g 435 t  
ORIGIN

Query Match 74.8%; Score 17.2; DB 95; Length 1718;  
Best Local Similarity 86.4%; Pred. No. 2.5e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 tcactctgaacgttccacagtc 22  
Db 248 TCAGCTTGAACGTTCCTCAGTC 227  
RESULT 7  
CELCO2E11  
LOCUS CELCO2E11 7015 bp DNA INV 29-OCT-1998  
DEFINITION Caenorhabditis elegans cosmid C02E11.  
ACCESSION AF101304  
VERSION AF101304.1 GI:3806125  
KEYWORDS Caenorhabditis elegans.  
SOURCE Caenorhabditis elegans  
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 7015)  
AUTHORS Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kersey, J., Kirsten, J., Lalister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifkin, I., Roopra, A., Saunders, D., Showkneen, R., Smaildon, N., Smith, A., Sonnenmet, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohlman, P.  
TITLE 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans  
JOURNAL Nature 368 (6466), 32-38 (1994)  
MEDLINE 94150718  
REFERENCE 2 (bases 1 to 7015)  
AUTHORS Pauley, A. and Harper, M.  
TITLE The sequence of C. elegans cosmid C02E11  
JOURNAL Unpublished (1998)  
REFERENCE 3 (bases 1 to 7015)  
AUTHORS Waterston, R.  
TITLE Direct Submission  
JOURNAL Submitted (26-OCT-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
COMMENT Submitted by: Genome Sequencing Center  
Department of Genetics, Washington University, St. Louis, MO 63110, USA, and  
Sanger Centre, Hinxton Hall  
Cambridge CB10 1RQ, England  
e-mail: rw@nematoe.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

# NEIGHBORING COSMID INFORMATION:

The 5' cosmid is R09A1, 200 bp overlap; 3' cosmid is K10C9, 2700 bp overlap. Actual start of this cosmid is not known. Last known base of 5' overlap is at base position 11396 of CELR09A1; actual end is at 4319 of CELC02E11.

NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

```

FEATURES
  source
    Location/Qualifiers
      1..7015
        /organism="Caenorhabditis elegans"
        /strain="Bristol N2"
        /db_xref="taxon:6239"
        /clone="C02E11"
        /chromosome="V"
        complement(1574..7000)
        /gene="C02E11.1"
        complement(join(1574..1666,2444..3467,3517..4088,
        4579..5367,5417..5638,6124..6536,6892..7000))
        /gene="C02E11.1"
        /note="contains similarity to human Pm5 protein; coded for
        by C. elegans cDNA yk286h3.3; coded for by C. elegans cDNA
        yk4b11.3; coded for by C. elegans cDNA yk21f6.3; coded for
        by C. elegans cDNA yk7d11.3; coded for by C. elegans cDNA
        yk28c8.3; coded for by C. elegans cDNA yk390g6.3; coded
        for by C. elegans cDNA yk397a11.3; coded for by C. elegans
        cDNA yk332e1.3; coded for by C. elegans cDNA yk503b8.3;
        coded for by C. elegans cDNA yk395c7.3; coded for by C.
        elegans cDNA yk431b6.3; coded for by C. elegans cDNA
        yk395c7.5; coded for by C. elegans cDNA yk286h3.5; coded
        for by C. elegans cDNA yk39a8.5; coded for by C. elegans
        cDNA yk21f6.5; coded for by C. elegans cDNA yk4b11.5;
        coded for by C. elegans cDNA yk431b6.5; coded for by C.
        elegans cDNA yk7d11.5"
        /codon_start=1
        /protein_id="AAC69200.1"
        /db_xref="GI:3806126"
        /translation="MKHEEVNPSNGYEMIPVYKNGHYTLKVSAPAGYVEPDSIEIK
        IDGKTDCASLNEDLYHLTFSVRCYVDGAAAGLPLVLTENGQIAETKTEDGKMYEM
        RAPPGKTEVSTGAGASECISNGKTSVEVNAPVVPVFNFKISGQLEVHRTSEMPF
        VDAVMTLYATSSLDLNIKCVSEGLNVPSTHVKCSIGKTDPRGRSLVACVPSGEY
        YLAASHVNGPSINFPQPKVYVQAASAREFAVQATGRVVRTSKDPLSLGSEVLY
        NEKSGGKTSGQGLTKLENLDEHETITAKAPQTFSTVHANYKFKVEIQDVTQVKF
        DICGOVEKSPNGVLKLTFTFKDDKRSLEIQPKADGSCFQPSVGLFTIEPTDKTSL
        TPRLLEVEVLKNAVTLNLFTHFTKTNANVHLSICGACTATVSLFPGQTLVRVKGTD
        VFTFENAGDKQTLGARDNDGRGCEWSEMTLVVEQSNTOPTIHFKNQFPAQIEISHP
        AEIENSNADKQNGTSTKGVEISICVPTSGYDVSLSGCKYKFERQKFLQIEISHP
        VHKVAPASRGITDLENDKAAVSIRIKSAGDSREIQVPAIDNGRFTPEELPSSG
        EQLVIVPSKRLPEPTSKVSTVTGKICENAVKSNFRGIFLDGSKPAVEKAVKAV
        LKDKOVVIAISNKDGAFAKIGPKRVEDYDITLDGKFTPTSPGQSVKLSQL
        SIRVDEVTNAPLDGVLLSVGCKGAGSDRSNNVLDETAHKNVVALAPGEYFVRIL
        QEYKFSPTSTYVKGQENHVLKGRVSFAYGKMRSEKMDKDVIIIEALSEGCD
        LHQSEATTREDGYTRINGLLPDCEYQVHAKSYAGDSPHSPFRFTVSMTEADVKGL
        EPMATITAKTIDIAVEIGMDTLPEIQSVRVITKNNNDHVQASVVAPOHLHYLVNLP
        RDGEVAIRVEAKPPQAFKTVRVVADQAKVARVPLTSSKRANDVDISVGTFLSL
        PFVTLALVFENQNRVLELLGTFIDWARTFAPTADNHHRRK"
        repeat_region
        5704..5892
        /note="C. elegans telomere-like hexamer repeat"
BASE COUNT 2109 a 1486 c 1442 g 1978 t
ORIGIN

Query Match 74.88; Score 17.2; DB 6; Length 7015;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tcactcgacgcttccacagtc 22
||||||| ||||||| |||
Db 6339 TCATCTCGTACTTTCACCCGTC 6360

RESULT 8
LOCUS CELK10C9 34348 bp DNA INV 28-MAY-1998
DEFINITION Caenorhabditis elegans cosmid K10C9.
ACCESSION AF067944
VERSION AF067944.1 GI:3165551
KEYWORDS

```

## SOURCE

ORGANISM

Caenorhabditis elegans.

Eukaryota; Metazoa;

Nematoda; Chromadorea; Rhabditida;

Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

## REFERENCE

AUTHORS

1 (bases 1 to 34348)

Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roodra, A., Saunders, D., Showkneen, R., Smalton, N., Smith, A., Sonhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J., and Wohldman, P.

2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

## TITLE

elegans

Nature 368 (6466), 32-38 (1994)

## MEDLINE

94150718

2 (bases 1 to 34348)

The sequence of C. elegans cosmid K10C9

Unpublished (1998)

3 (bases 1 to 34348)

Direct Submission

Waterston, R.

Submitted (23-MAY-1998)

Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

Submitted by:

Genome Sequencing Center

Department of Genetics, Washington University,

St. Louis, MO 63110, USA, and

Sanger Centre, Hinxton Hall

Cambridge CB10 1RQ, England

e-mail: rwenematode.wustl.edu and jes@sanger.ac.uk

COMMENT

NOTICE: This sequence may not be the entire insert of this clone.

It may be shorter because we only sequence overlapping sections

once, or longer because we provide a small overlap between

neighboring submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded or sequenced with an alternate

chemistry; an attempt was made to resolve all sequencing problems,

such as compressions and repeats; all regions were covered by

sequence from more than one subclone

## NEIGHBORING COSMID INFORMATION:

The 5' cosmid is C02E11, 2700 bp overlap; 3' cosmid is Y50D48.  
Actual start of this cosmid is at base position 1 of CELK10C9;  
actual end is at 34348 of CELK10C9

## NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

## FEATURES

source

1..34348  
/organism="Caenorhabditis elegans"  
/strain="Bristol N2"  
/db\_xref="taxon:6239"  
/clone="K10C9"  
/chromosome="V"  
complement(4432..7320)  
/gene="K10C9.4"  
complement(join(4432..4599,5154..5405,5797..5995,  
7226..7320))  
/gene="K10C9.4"

gene

CDS

```
repeat_region
repeat_region
gene
CDS
complement(join(10854..13293)
/gene="K10C9.8")
complement(join(10854..10942,10995..11307,12060..12201,
12727..12831,12882..13048,13096..13293))
/gene="K10C9.8"
/notes="similar to C. elegans olfactory receptor ODR-10
(GB:U49449)"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17674.1"
/db_xref="GI:3165558"
/translation="MLGKQSDLLKLIQDVSAQSFSLIINTLLIFVLTKSPKOLGAYK
CLMIIYSVEIFSLDVLVLPQHYSHGSTFLVIGIKDKLFSPEVLLFSSCIWRCF
GSMAYFAHFVYRWLVYEAHLKFEKGKILWLFSPFYALTWICTGYILSAEN
KEYFELSDVYVGLPELYKKKENGTLTYIMPFYIGLIISSYIIIVVIGILC
YRLNLSFTVTMSNLRNLQRLQFLVLTQTVPFVLMHIPAVIMEAFVLOLDLGV
YSAVVSTIIYIPAVDPITPIVIVENRKTVLKFFGCFKTHQIGTWTIAPTQFASST
HVN"
15903..16372
/gene="K10C9.3"
join(15903..16186,16243..16372)
/gene="K10C9.3"
/notes="Similar to ribonuclease; K10C9.3"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17668.1"
/db_xref="GI:3165552"
/translation="MKLLLLCISCIPLAYSHDGEPEFDYLMFTTIYTAVCRADDDSV
PESCEIPSGTPQNSIHGLWPNFENGYPQNCRTGPRHEDENLIKSIEDRLVWVWPNLY
PKTIQSPWKEVDKHGCTCAQSEKLFESELAYTE"
complement(16894..18897)
/gene="K10C9.6"
complement(join(16894..16964,17009..17457,18410..18897))
/gene="K10C9.6"
/notes="similar to C. elegans olfactory receptor ODR-10
(GB:U49449)"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17673.1"
/db_xref="GI:3165557"
/translation="MRVLDSEICRKVGFYVAFSTNEVLWITVHFHAKLFGAYKKMI
IYISVLSTSGLEIMKPTTHYNGALLSNCLEINPLKIROIFILISQFLLVI
SFISQVYRILCVFNCKTKYDGLKTIWILYPLVWTFIALSHLCLGSDFTDS
YIRKAIFENALEVSELPYAWPYAAGSIRAKGIIFLLFAIVLISFSYCIIFTCV
QMRNMKELKKEFTQNKLEYQFFALVMQTIQGTIFLIPTGPIMLTPIAPIFEL
EVNMQTGNLSLVGFYFSDSIAPFMIVSEYKIFLKKVICRMMKNNTAVPSSAVAST
V"
19421..22162
/gene="K10C9.2"
join(19421..19570,19619..19774,22043..22162)
/gene="K10C9.2"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17670.1"
/db_xref="GI:3165554"
/translation="MKVFDSDIDVAGLKSVPSEKPIITSSDLKNALSGVTSKGTQFQH
CLRDKTKQFLGLDIRLCNLKDLTIRDCPTDGKHPNRVSRPERSIGNRRRGPPLPSFO
PCPAEFYVLPMSSSISKSDSTSPSIFGRINSAIKNIGN"
complement(20003..21979)
/gene="K10C9.7"
complement(join(20003..20197,20409..20591,20635..20779,
21642..21750,21802..21979))
/gene="K10C9.7"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17671.1"
/db_xref="GI:3165555"
/translation="MKRGLNHPQNRKKIIFRPPRLTKLSEKALFOICKTTLNERRK
MKSIQNTIDELRKLKLSAGKSEEVORLKKEMQKHSKMFGEIFGVGATVGKPKPKKEVK
VPTKEMTFEKKRLLETTFFPNKVTGQARAKRETNFIANNPEIYATASPDQPSKAK
TDPVSPOLNIISFSWPITSGSDWSPHGSEFNDLTAPRVGKLTTPVQWSDMKKSSLK
LGTEDNFSKNSYDPAYSNTTQSQSVTLLYNSTSPYYDDSDGLGFLPLTCVQ"
29577..30095
/gene="K10C9.1"
join(29577..29667,29862..29905,30015..30095)
/gene="K10C9.1"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17669.1"
/db_xref="GI:3165553"
/translation="MRVLAVLLLLINIVGAVSSPYVLRSSQSGAAIVQILNDFEIP
VWLKFLNITNFQKNFFQVYSRKLTM"
BASE COUNT 11109 a 6038 c 5959 g 11242 t
ORIGIN
Query Match 74.8%; Score 17.2; DB 6; Length 34348;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 tcattctgaacgtctccacagtc 22
||||||| || ||||| |||
Db 2024 TCATCTCGTACTTCCACCGTC 2045
RESULT 9
AC073276/c
LOCUS AC073276 46057 bp DNA PRI 08-DEC-2000
DEFINITION Homo sapiens clone RP11-634P5, complete sequence.
ACCESSION AC073276
VERSION AC073276.5 GI:11597181
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 46057)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 46057)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 46057)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 46057)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Dec 7, 2000 this sequence version replaced gi:10944507.
Center project name: H_NH0654p05.
FEATURES
source
1..46057
/organism="Homo sapiens"
```

```

/db_xref="taxon:9606"
/clone="RP11-654P5"
BASE COUNT 15064 a 8714 c 8650 g 13629 t
ORIGIN

Query Match 74.8%; Score 17.2; DB 88; Length 46057;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctcgaacgttcacagtca 23
| ||||| ||| ||||| |||||
Db 33363 CTTCTCAAACTTTCACAGTCA 33342

RESULT 10
AC007042 71441 bp DNA PRI 30-SEP-2000
LOCUS Homo sapiens BAC clone RP11-399H17 from Y, complete sequence.
AC007042
ACCESSION AC007042
VERSION AC007042.2 GI:7243920
KEYWORDS HTC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 71441)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
REFERENCE 2 (bases 1 to 71441)
AUTHORS Nelson, D., Wohlmann, P. and Harris, A.
TITLE The sequence of Homo sapiens BAC clone RP11-399H17
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 7 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 8 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 9 (bases 1 to 71441)
AUTHORS Waterston, R.

```

# TITLE JOURNAL COMMENT

Direct Submission  
Submitted (30-SEP-2000) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Mar 15, 2000 this sequence version replaced gi:4371303.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)  
----- Summary Statistics  
-----  
Center project name: H\_NHO399H17  
-----

NOTICE: This sequence may not represent the entire insert of this  
clone. It may be shorter because we only sequence overlapping  
clone sections once, or longer because we provide a small overlap  
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.

## MAPPING INFORMATION:

The position of this clone was established as part of a  
collaboration between the Human Chromosome Y Mapping Project  
(Tomoko Kawaguchi, Helen Skaletsky, Laura G. Brown, Steve Rozen,  
and David C. Page at the Whitehead Institute for Biomedical  
Research, Cambridge MA) and the Washington University Genome  
Sequencing Center, St. Louis MO.

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male  
donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E.,  
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998). An improved  
approach for construction of bacterial artificial chromosome  
libraries. Genomics 51:1-8. The clone may be obtained either from  
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong  
and coworkers at the Roswell Park Cancer Institute  
(<http://bacpac.med.buffalo.edu>)  
VECTOR: pBACe3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-462A19. Actual start of  
this clone is at base position 51511 of RP11-462A19; actual end is  
at base position 71441 of RP11-399H17.

The sequence RP11-399H17 contains a dinucleotide (GA) repeat from  
base position 25628 to 25795, in which the exact sequence is  
unknown. The size of the repeat is consistent with digest  
information and PCR from clone DNA.

The clone sequenced to the left is RP11-462A19, 200 bp overlap.  
Actual start of this clone is at base position 51511 of  
RP11-462A19; actual end is at base position 71441 of RP11-399H17.

## FEATURES

```

source
1..71441
    Location/Qualifiers
        db_xref="taxon:9606"
        /organism="Homo sapiens"
        /chromosome="Y"
        /map="Y"
        /clone="RP11-399H17"
        /clone_lib="RPCI-11"
        232..255
        /rpt_family="AT-rich"
        /rpt_family="(CA)n"
        1617..1655
        /rpt_family="(CA)n"
        1680..2091
        /rpt_family="MER2_type"
        2102..2140
        /rpt_family="GA-rich"
repeat_region
repeat_region
repeat_region
repeat_region

```

```

repeat_region 2138..2310
/rpt_family="TAGA)n"
repeat_region 2946..3067
/rpt_family="Alu"
repeat_region 3439..3929
/rpt_family="MER1_type"
repeat_region 4207..4424
/rpt_family="MER21-group"
repeat_region 5307..6287
/rpt_family="L1"
repeat_region 6354..6518
/rpt_family="MIR"
repeat_region 6679..6972
/rpt_family="Alu"
repeat_region 6986..7168
/rpt_family="GA-rich"
repeat_region 7169..7198
/rpt_family="GA-rich"
repeat_region 7200..7245
/rpt_family="(GGGA)n"
repeat_region 7364..7563
/rpt_family="GA-rich"
repeat_region 7857..8093
/rpt_family="MaLR"
repeat_region 8094..8123
/rpt_family="MaLR"
repeat_region 8124..8197
/rpt_family="MaLR"
repeat_region 8237..8300
/rpt_family="Alu"
repeat_region 10527..10644
/rpt_family="MIR"
repeat_region 10645..10676
/rpt_family="Alu"
repeat_region 10913..11162
/rpt_family="(TAA)n"
repeat_region 11338..11754
/rpt_family="CT-rich"
repeat_region 12042..18127
/rpt_family="L1"
repeat_region 18128..18164
/rpt_family="AT-rich"
repeat_region 19474..19775
/rpt_family="Alu"
repeat_region 19836..20116
/rpt_family="Alu"
repeat_region 20117..20144
/rpt_family="(CAAA)n"
repeat_region 21022..21053
/rpt_family="AT-rich"
repeat_region 21667..22969
/rpt_family="L1"
repeat_region 22971..24502
/rpt_family="L1"
repeat_region 24527..24602
/rpt_family="LTR52"
repeat_region 24603..24640
/rpt_family="(CA)n"
repeat_region 24641..24911
/rpt_family="LTR52"
repeat_region 24915..25177
/rpt_family="Alu"
repeat_region 25202..25362
/rpt_family="(GAAA)n"
repeat_region 25390..25567
/rpt_family="GA-rich"
repeat_region 25588..25768
/rpt_family="GA-rich"
repeat_region 25769..25824
/rpt_family="(GAAA)n"
repeat_region 25825..26383

```

Query Match

74.8%; Score 17.2; DB 86; Length 71441;

```

Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctcgacgttccacagtca 23
||||| ||| |||||
DB 60643 CATCTCCAAAGTTTCACAGTCA 60664

RESULT 11
AC006516/C
LOCUS
DEFINITION
AC006516 72265 bp DNA PRI 31-JUL-1999
Homo sapiens Xq28 BAC GSHB-557D6 (Genome Systems Human BAC Library)
complete sequence.
AC006516
VERSION AC006516.10 GI:5649182
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 72265)
Muzny, D., Arenson, A.D., Bouck, J., Brundage, E., Bunac, C., Chen, Z.,
Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Garcia, C.,
Gorrell, J.H., Gorrell, L.L., Hernandez, J., Jackson, L.,
Kondejewski, N., Leal, B., Lichtarge, O., Liu, W., Logan, L.,
Martinez, C., Oswal, G., Pampell, L.R., Parish, B.J., Perez, L.,
Rashid, N.D., Rives, C., Scherer, S.E., Shen, H., Simon, M., Vo, Q.,
Williamson, A., Worley, K.C., Yu, W., Zhou, X., Nelson, D. and
Gibbs, R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE
AUTHORS
2 (bases 1 to 72265)
Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE
AUTHORS
3 (bases 1 to 72265)
Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
REFERENCE
AUTHORS
4 (bases 1 to 72265)
Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT
ON Jul 29, 1999 this sequence version replaced gi:4584315.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-helpebcm.tmc.edu

```

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the features listing.

## ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum





## RESULT 12

AP000603 LOCUS 83287 bp DNA PLN 27-DEC-2000  
 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRP15.  
 AP000603 BA000014  
 AP000603.1 GI:6045158  
 Arabidopsis thaliana (strain:Columbia) DNA, clone\_lib:Mitsui P1  
 clone:MRP15.  
 ORGANISM  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II;  
 Brassicales; Brassicaceae; Arabidopsis.  
 1 (sites)  
 Kaneko,T., Kato,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.  
 Structural analysis of Arabidopsis thaliana chromosome 3. II.  
 Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC  
 and BAC clones  
 DNA Res. 7 (3), 217-221 (2000)  
 20363099  
 2 (bases 1 to 83287)  
 Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.  
 Direct Submission  
 Submitted (13-OCT-1999) Yasukazu Nakamura, Kazusa DNA Research  
 Institute, Department of Plant Gene Research; 1532-3, Yana,  
 Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,  
 Tel:81-438-52-3935, Fax:81-438-52-3934)  
 Address for correspondence: kaos@kazusa.or.jp  
 http://www.kazusa.or.jp/kaos/cgi-bin/agd.graph.cgi?c=MRP15  
 For the latest information on annotation of this clone, please see  
 'product' or 'note' qualifiers. Genes that have no significant  
 protein similarity are described as 'unknown protein'.  
 The software programs used to predict genes include: Grail  
 (Informatics Group, Oak Ridge National Laboratory,  
 http://compbio.ornl.gov/grail-1.3/),  
 GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),  
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of  
 Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and  
 SplicePredictor (Volker Brendel, Stanford University,  
 http://gremlini.zool.tastate.edu/cgi-bin/sp.cgi).  
 Genes encoding tRNAs are predicted by tRNAscan-SE  
 (Sean Eddy, Washington University School of Medicine, St. Louis,  
 http://genome.wustl.edu/eddy/tRNAscan-SE/).  
 This sequence may not be the entire insert of this clone. It may be  
 shorter because we remove overlaps between neighboring submissions.  
 The 5' clone is MD011 and the 3' clone is K20M4.  
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 KLAKKSSPSANKRITTVLDSNNRSEDEIPETFIADFPNSLAKHLDSNNVTGDS  
 RL3FGCENETISVSNQSDRFPVSLNCKLLETNLNRSNLKIPGDDYWGNE  
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 SGFCSLQSSVLEKLLIANNVLSCTVPVLEKCKSLKATIDLSFNALGLIPKEITLP  
 KLSLVVWNNLTKGIPESICVGGNLETILNLTGSPESISAKTNLWHLSS  
 NLLTGEIPVGIKLEKLIQLQGNLSLTGNIPISELGNCKNLIMLDLNSNLTGNLPGE

LASOAGLVMPGVSQKQFAFVRNEGTCRAGGLVEFEGIRAEIRLEHFFPMVHSCPKT  
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 EGGKAIQVLDLSHNDLQGLPGSLGSLFSLDLSVNNLTGPIPGGOLTFPLTR  
 YANNGLCGVLPPLPCSSGSRPTRSHAKPKKQSIATGNSAGIVSFHWCTYMLNALYNA  
 RKVKKKEKREKRYIESLPTSGSSSLVSHQESLINSINATFEPKPLKLTFAHLEATN  
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 LHSCIPHIIRDMKSNVLLDQDFVARVSDFGMARLVSAALDTHLSVSTLAGTPGVYP  
 PEYQSFRCTAKGDVYSYVILLESLSGKKPIDPESEGEDNNLVGNAKOLYREKRAE  
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 VRTVGLKTSNFRIONHKLKLVEMEGSHVLDVSDLVHVGQCYGTILTANQEA  
 DYMVASRFLKSVITTTGLRVEGGKGPASSQLPGPVGMAWSLNGFRFRNLTA  
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 /db\_xref="GI:9280290"  
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 TILINDWYAKSTALKNFDSDGRTLGSDGVLNGSKIGLNNAFLTMTKPGKTYK  
 RICNVGKSTLNFRIQGHMKLVEMEGSHVLDVSDLVHVGQCYGTILTANQEA  
 YMVASTRFLKKEVTVGMSYEGSNVQASDDIPKAPGVMAWSLNGFRFRNLTA  
 ARNPQGSVHYGKINTTRIKLVNTQGVKGLRVALNGVSHTDPTPLKLAEYFGS  
 EKVFYNIKDEPAKITTITVEPNVNLNITHTREIVVFENHEKSVQSWHLDDGYF  
 VASEPGMTPEKRNKNNLLDAVSRHTVQVYPKCHAAIILLTFCNCGMNVRSNSR  
 LGQQLYVSVLSPEKSLRDEYNMPTSLQCGYKGTGPNPYTA"  
 complement(join(16079. 16171,16360. 16571,16662. 16773,  
 16877. 17077,17202. 17264,17449. 17508,17605. 17707,  
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 /evidence=not\_experimental  
 /protein\_id="BAB01747.1"



\* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence.  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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*      24406: gap of unknown length
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*      27689: gap of unknown length
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*      46183: contig of 5226 bp in length
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*      70477: contig of 1409 bp in length
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*      75250: contig of 1943 bp in length
*      77193: gap of unknown length
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*      80573: gap of unknown length
*      80674: contig of 1319 bp in length
*      81993: gap of unknown length
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*      123030: contig of 1745 bp in length
*      123130: gap of unknown length
*      125712: contig of 2582 bp in length
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*      127531: contig of 1719 bp in length
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*      129750: contig of 2119 bp in length
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# FEATURES

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/db_xref="taxon:9606"
/chromosome="UNK"
/clone="RP11-522A4"

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4875..7061
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7162..9430
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9531..12918
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15521..18397
/note="assembly_name:Contig106"
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/note="assembly_name:Contig151"
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Query Match      74.8%  Score 17.2; DB 78; Length 132060;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 catctcgaaagcttcacagtc 23
||||| ||||| ||||| |||||
Db 96281 CATCTCCAAAGTTTCACAGTCA 96260

RESULT 15
AC008454
LOCUS
DEFINITION
Homo sapiens chromosome 5 clone CTC-345M13, WORKING DRAFT SEQUENCE,
16 unordered pieces.
ACCESSION
AC008454
VERSION
AC008454.3 GI:7708872
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 138698)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
REFERENCE
2 (bases 1 to 138698).
DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On May 5, 2000 this sequence version replaced gi:6601060.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 317959
Center clone name: CIT-HSPC_345M13
-----
Summary Statistics
Consensus quality: 114452 bases at least Q40
Consensus quality: 128842 bases at least Q30
Consensus quality: 131746 bases at least Q20
Estimated insert size: 142000; pulse-field gel estimation
Estimated insert size: 137198; sum-of-contigs estimation
Quality coverage: 4.16 in Q20 bases; pulse field gel estimation
Quality coverage: 4.31 in Q20 bases; sum-of-contigs estimation.

```

\* NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 10366: contig of 2309 bp in length
* 12674: gap of unknown length
* 12675: contig of 2001 bp in length
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* 14776: contig of 3446 bp in length
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* 18422: contig of 2779 bp in length
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* 21300: contig of 4473 bp in length
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* 25774: contig of 4465 bp in length
* 30339: gap of unknown length
* 30438: contig of 5944 bp in length
* 36383: gap of unknown length
* 36482: contig of 10810 bp in length
* 47293: gap of unknown length
* 47393: contig of 11962 bp in length
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* 59454: contig of 14919 bp in length
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* 74374: contig of 24441 bp in length
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* 98915: gap of unknown length
* 99015: contig of 39684 bp in length.

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#### FEATURES

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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-345M13"
/clone_lib="Caltech human BAC library C"
BASE COUNT 35193 a 28953 c 30941 g 42070 t 1541 others
ORIGIN

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Query Match      74.8%  Score 17.2; DB 60; Length 138698;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```
Qy 1 tcattctcgaaagcttcacagtc 22
||||| ||||| ||||| |||||

```

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Db 46730 TCCTCTAGAACGTCCACAGTC 46751

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Search completed: October 9, 2001, 16:18:53
Job time: 2503 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:13 ; Search time 6788.49 Seconds  
(without alignments)  
32.027 Million cell updates/sec

Title: US-09-713-136-3  
Perfect score: 23  
Sequence: 1 tcattcgaacgttcacagatca 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
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2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
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6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*  
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107: gb\_est30.\*  
108: gb\_est31.\*  
109: gb\_est32.\*  
110: gb\_est33.\*  
111: gb\_est34.\*  
112: gb\_est35.\*  
113: gb\_est36.\*  
114: gb\_est37.\*  
115: gb\_est38.\*  
116: gb\_est39.\*

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117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
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123: gb_est54:*
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125: gb_est56:*
126: gb_est57:*
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128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
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143: gb_est74:*
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145: gb_est76:*
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159: gb_est90:*
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162: gb_est93:*
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213: gb_est144:*
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215: gb_est146:*
216: gb_est147:*
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219: gb_est150:*
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221: gb_est152:*
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226: gb_est157:*
227: gb_est158:*
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255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	19.4	84.3	848	137	BE570879	601329225
C 2	17.2	74.8	245	161	BB591857	BB591857
C 3	17.2	74.8	307	158	H34259	EST111000 R
C 4	17.2	74.8	360	26	AV193020	AV193020
C 5	17.2	74.8	360	26	AV193064	AV193064
C 6	17.2	74.8	545	122	AW914126	EST345430
C 7	17.2	74.8	567	138	BE665364	154341 MA
C 8	17.2	74.8	678	240	A2240360	RPCI-23-3
C 9	17.2	74.8	879	247	A2669229	ENTN42TR
C 10	17.2	74.8	1471	233	AQ750993	HS_5574_B
C 11	16.8	73.0	239	164	BE198167	ug75e03_Y
C 12	16.8	73.0	269	162	BE031712	130355 MA
C 13	16.8	73.0	306	116	AW436470	76707 MAR
C 14	16.8	73.0	334	116	AW486759	76713 MAR
C 15	16.8	73.0	416	164	BE198756	ug82b12_Y
C 16	16.8	73.0	417	111	AW119653	sd50e05_Y
C 17	16.8	73.0	470	164	BE197776	ug75e03_X
C 18	16.8	73.0	559	224	AQ073038	EP(3)3586
C 19	16.8	73.0	623	18	AI292915	GHI5946.5
C 20	16.6	72.2	181	239	AZ193981	SP_1025_A
C 21	16.6	72.2	214	137	BE556613	sq07d11_Y
C 22	16.6	72.2	271	22	AI616514	rehn0187_Y
C 23	16.6	72.2	283	132	BB368590	BB368590
C 24	16.6	72.2	305	127	BB162497	BB162497
C 25	16.6	72.2	316	161	BB558391	BB558391
C 26	16.6	72.2	346	174	BG226875	kp99b04_Y
C 27	16.6	72.2	360	153	BG404581	602420727
C 28	16.6	72.2	369	147	BF328053	QV3-BN015
C 29	16.6	72.2	369	234	AQ847354	LMAJFV1.1
C 30	16.6	72.2	384	168	BF703470	MI-P-H1-a
C 31	16.6	72.2	399	223	AQ030039	RPCI111-37
C 32	16.6	72.2	418	237	AZ022893	RPCI-23-2
C 33	16.6	72.2	489	111	AW060925	UI-M-BH1-
C 34	16.6	72.2	528	229	AQ494321	HS_5146_B
C 35	16.6	72.2	566	232	AQ699515	HS_5569_B
C 36	16.6	72.2	591	149	BF478532	WHE2009_G
C 37	16.6	72.2	613	111	AW069158	Cr43b10.X
C 38	16.6	72.2	683	32	AV714759	AV714759
C 39	16.6	72.2	717	229	AQ489343	RPCI-11-2
C 40	16.6	72.2	779	251	AZ903022	RPCI-24-1
C 41	16.6	72.2	807	233	AQ740875	HS_2274_A
C 42	16.6	72.2	811	168	BF670945	602150746
C 43	16.6	72.2	890	137	BE603743	HVSMEH008
C 44	16.6	72.2	1186	144	BF099637	601751660
C 45	16.4	71.3	357	224	AQ085892	HS_2164_B

## ALIGNMENTS

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	19.4	84.3	848	137	BE570879	601329225
C 2	17.2	74.8	245	161	BB591857	BB591857
C 3	17.2	74.8	307	158	H34259	EST111000 R
C 4	17.2	74.8	360	26	AV193020	AV193020
C 5	17.2	74.8	360	26	AV193064	AV193064
C 6	17.2	74.8	545	122	AW914126	EST345430
C 7	17.2	74.8	567	138	BE665364	154341 MA
C 8	17.2	74.8	678	240	A2240360	RPCI-23-3
C 9	17.2	74.8	879	247	A2669229	ENTN42TR
C 10	17.2	74.8	1471	233	AQ750993	HS_5574_B
C 11	16.8	73.0	239	164	BE198167	ug75e03_Y
C 12	16.8	73.0	269	162	BE031712	130355 MA
C 13	16.8	73.0	306	116	AW436470	76707 MAR
C 14	16.8	73.0	334	116	AW486759	76713 MAR
C 15	16.8	73.0	416	164	BE198756	ug82b12_Y
C 16	16.8	73.0	417	111	AW119653	sd50e05_Y
C 17	16.8	73.0	470	164	BE197776	ug75e03_X
C 18	16.8	73.0	559	224	AQ073038	EP(3)3586
C 19	16.8	73.0	623	18	AI292915	GHI5946.5
C 20	16.6	72.2	181	239	AZ193981	SP_1025_A
C 21	16.6	72.2	214	137	BE556613	sq07d11_Y
C 22	16.6	72.2	271	22	AI616514	rehn0187_Y
C 23	16.6	72.2	283	132	BB368590	BB368590
C 24	16.6	72.2	305	127	BB162497	BB162497
C 25	16.6	72.2	316	161	BB558391	BB558391
C 26	16.6	72.2	346	174	BG226875	kp99b04_Y
C 27	16.6	72.2	360	153	BG404581	602420727
C 28	16.6	72.2	369	147	BF328053	QV3-BN015
C 29	16.6	72.2	369	234	AQ847354	LMAJFV1.1
C 30	16.6	72.2	384	168	BF703470	MI-P-H1-a
C 31	16.6	72.2	399	223	AQ030039	RPCI111-37
C 32	16.6	72.2	418	237	AZ022893	RPCI-23-2
C 33	16.6	72.2	489	111	AW060925	UI-M-BH1-
C 34	16.6	72.2	528	229	AQ494321	HS_5146_B
C 35	16.6	72.2	566	232	AQ699515	HS_5569_B
C 36	16.6	72.2	591	149	BF478532	WHE2009_G
C 37	16.6	72.2	613	111	AW069158	Cr43b10.X
C 38	16.6	72.2	683	32	AV714759	AV714759
C 39	16.6	72.2	717	229	AQ489343	RPCI-11-2
C 40	16.6	72.2	779	251	AZ903022	RPCI-24-1
C 41	16.6	72.2	807	233	AQ740875	HS_2274_A
C 42	16.6	72.2	811	168	BF670945	602150746
C 43	16.6	72.2	890	137	BE603743	HVSMEH008
C 44	16.6	72.2	1186	144	BF099637	601751660
C 45	16.4	71.3	357	224	AQ085892	HS_2164_B

## RESULT 1

## BE570879/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L1AM8791 row: b column: 08  
High quality sequence stop: 651.  
Location/Qualifiers  
1. 848  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3602983"  
/clone.lib="NCLCGAP\_Mam6"  
/sex="female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: Sali; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 202 a 210 c 238 g 198 t  
ORIGIN

Query Match 84.38; Score 19.4; DB 137; Length 848;  
Best Local Similarity 95.28; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcattctgaacgttccacagt 21  
|||||  
Db 149 TCATCTCGAATGTCACAGT 129  
|||||

RESULT 2  
BB591857 245 bp mRNA EST 30-NOV-2000  
LOCUS BB591857 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA  
DEFINITION clone B020004B03 5', mRNA sequence.  
ACCESSION BB591857.1 GI:11488459  
VERSION BB591857  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Alizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodozana, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sakai, D., Sato, K., Shibata, K., Shibata, Y., Shingagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, P., Tanaka, T., Tova, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Alizawa, K. et al. 2000)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Genome Exploration Research Group, Life Science Tsukuba Center,  
Genome Science Laboratory  
The Institute of Physical and Chemical Research (RIKEN), Genomic  
Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: +81-298-36-9013  
Fax: +81-298-36-9098  
Email: genome-res@tc.riken.go.jp/  
URL: <http://genome.rtc.riken.go.jp/>  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki





```

Query Match      74.8%; Score 17.2; DB 26; Length 360;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgtttccacagtc 22
||||| ||| ||||| |||
Db 215 TCATCTCGTACTTCCACCGTC 194

RESULT 5
AV193064/c 360 bp mRNA EST 22-JUL-1999
LOCUS AV193064 Yujii Kohara unpublished cDNA:Strain N2 hermaphrodite
DEFINITION embryo Caenorhabditis elegans cDNA clone yk612h9 5', mRNA sequence.
ACCESSION AV193064
VERSION AV193064.1 GI:5575216
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Mochizuki,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yujii Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykoha@lab.nig.ac.jp.
FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk612h9"
/clone_lib="Yujii Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 95 a 83 c 108 g 73 t 1 others
ORIGIN

Query Match      74.8%; Score 17.2; DB 26; Length 360;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgtttccacagtc 22
||||| ||| ||||| |||
Db 197 TCATCTCGTACTTCCACCGTC 176

RESULT 6
AW914126/c 545 bp mRNA EST 25-MAY-2000
LOCUS EST345430 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
DEFINITION RGI1A76 5' end, mRNA sequence.
ACCESSION AW914126
VERSION AW914126.1 GI:8079799
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 545)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
7712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 Reverse.
FEATURES
source
1..545
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGI1A76"
/clone_lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 129 a 116 c 176 g 124 t
ORIGIN

Query Match      74.8%; Score 17.2; DB 122; Length 545;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgtttccacagtc 22
||||| ||| ||||| |||
Db 165 TCAGCTGAACGTTCTCAGTC 144

RESULT 7
BE665364 567 bp mRNA EST 08-SEP-2000
LOCUS BE665364 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BE665364
ACCESSION BE665364.1 GI:10025864
VERSION EST.
KEYWORDS COW.
SOURCE Bos taurus
ORGANISM Bos taurus
REFERENCE 1 (bases 1 to 567)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keeler,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred 18
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 71 row: P column: 4
Seq primer: ATTAGGTGACACTATAG.
FEATURES
source
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/organism="Bos taurus"
/db_xref="taxon:9913"

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/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="Dh108"
/notes="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 20 and day 40
embryos."
BASE COUNT      121 a   180 c   97 g   168 t   1 others
ORIGIN

Query Match      74.8%; Score 17.2; DB 138; Length 567;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctgaacgttccacagtca 23
||||| ||| ||||| |||||
Db 332 CATCTGGAAGGTTCCAGTAGTCA 353

RESULT 8
A2240360 A2240360 678 bp DNA GSS 15-JUN-2000
LOCUS
DEFINITION RPCI-23-32H8.TVB RPCI-23 Mus musculus genomic clone RPCI-23-32H8,
DNA sequence.
ACCESSION A2240360
VERSION A2240360.1 GI:8553470
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Zhao S., Nierman W., Feldblyum T., Malek J., Shatsman S., Akinret
B., Levins M., McGann S., Isegaye G., Geer K., Kroi M., de Jong P.
and Fraser C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other GSSs: RPCI-23-32H8.TJB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac.ends/mouse/bac\_end\_intro.html
Plate: 32 row: H column: 8
Seq primer: T7
Class: BAC ends.
FEATURES
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Location/Qualifiers
1..678
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-32H8"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="Dh108"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
189 a 163 c 136 g 190 t
BASE COUNT
ORIGIN

```

```

Query Match      74.8%; Score 17.2; DB 240; Length 678;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctgaacgttccacagtca 23
||||| ||| ||||| |||||
Db 381 CATCTGGTACTTCCACAGTCA 402

RESULT 9
A2669229 A2669229 879 bp DNA GSS 14-DEC-2000
LOCUS
DEFINITION ENTHN42FR Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION A2669229
VERSION A2669229.1 GI:11806375
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica
REFERENCE Eukaryota; Entamoebidae; Entamoeba.
AUTHORS Loftus B., Van Aken S. and Fraser C.
TITLE Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 50
High quality sequence stop: 721.
FEATURES
source
Location/Qualifiers
1..879
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
325 a 101 c 158 g 295 t
BASE COUNT
ORIGIN

Query Match      74.8%; Score 17.2; DB 247; Length 879;
Best Local Similarity 86.4%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctgaacgttccacagtca 23
||||| ||| ||||| |||||
Db 862 CATCTGACGTGTTCCAAAGTCA 841

RESULT 10
AQ750993/c

```

```

LOCUS       A0750993       1471 bp      DNA          GSS              19-JUL-1999
DEFINITION  HS_5574_B1_G10_SP6_RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=1150 Col=19 Row=N, DNA sequence.
ACCESSION   A0750993
VERSION     A0750993.1  GI:5538151
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 1471)
AUTHORS    Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE       Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL     Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE     99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieder@resour.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 1150 row: N column: 19
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 1471.
FEATURES             source
     source          1..1471
     db_xref="taxon:9606"
     /clone="plate=1150 Col=19 Row=N"
     /clone_lib="RPCI-11 Human Male BAC Library"
     /sex="male"
     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
     Male blood DNA was isolated from one randomly chosen donor
     and partially digested with a combination of EcoRI and
     EcoRI Methylase. Size selected DNA was cloned into the
     pBACe3.6 vector at EcoRI sites"
BASE COUNT      385 a      366 c      374 g      324 t      22 others
ORIGIN
1 ctcctgaacgtttccacagtca 23
||||| ||||| ||||| |||||
Db 520 CATCTGGATCGTTCACATTCA 499

Query Match      74.8%; Score 17.2; DB 233; Length 1471;
Best Local Similarity 86.4%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 cctctgaacgtttccacagtca 23
||||| ||||| ||||| |||||
Db 520 CATCTGGATCGTTCACATTCA 499

RESULT 11
BE198167/c
LOCUS       BE198167       239 bp      mRNA          EST              26-JUN-2000
DEFINITION  uq75e03.y1 Soares_mammary_gland_NMLMG Mus musculus
            IMAGE:1548220 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR
            6 MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   BE198167
VERSION     BE198167.1  GI:8710336
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

LOCUS       BE198167       239 bp      mRNA          EST              09-JUL-2000
DEFINITION  130355 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BE031712
VERSION     BE031712.1  GI:8326721
KEYWORDS    EST.
SOURCE      pig.
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 269)
AUTHORS    Fahrénkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
TITLE       Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
JOURNAL     Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt.trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCACGATCAGCAGC
            Plate: 60 row: H column: 12

```

```

REFERENCE       1 (bases 1 to 239)
AUTHORS        NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
            Email: cgaaps@email.nih.gov
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:953568
            Seq primer: -40RP from Gibco
            High quality sequence stop: 230.
FEATURES             source
     source          1..239
     organism="Mus musculus"
     /db_xref="taxon:10090"
     /clone="IMAGE:1548220"
     /clone_lib="Soares_mammary_gland_NMLMG"
     /sex="female (lactating)"
     /tissue_type="mammary gland"
     /lab_host="DH10B"
     /note="Vector: pT73D-Pac (Pharmacia) with a modified
     polylinker; 1st strand cDNA was prepared from mammary
     gland tissue from a lactating female, and was then primed
     with a Not I - oligo(dT) primer. Double-stranded cDNA was
     ligated to Eco RI adaptors (Pharmacia), digested with Not
     I and cloned into the Not I and Eco RI sites of the
     modified pT73 vector. Library is normalized. Library
     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      63 a      47 c      66 g      63 t
ORIGIN
1 tctcgacgtttccacagtca 23
||||| ||||| ||||| |||||
Db 77 TCTCTAACATTCCACAGTCA 58

Query Match      73.0%; Score 16.8; DB 164; Length 239;
Best Local Similarity 90.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctcgacgtttccacagtca 23
||||| ||||| ||||| |||||
Db 77 TCTCTAACATTCCACAGTCA 58

RESULT 12
BE031712/c
LOCUS       BE031712       269 bp      mRNA          EST              09-JUL-2000
DEFINITION  130355 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BE031712
VERSION     BE031712.1  GI:8326721
KEYWORDS    EST.
SOURCE      pig.
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 269)
AUTHORS    Fahrénkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
TITLE       Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
JOURNAL     Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt.trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCACGATCAGCAGC
            Plate: 60 row: H column: 12

```

Seq primer: ATTTAGGTGACACTATAG.

## FEATURES

source

Location/Qualifiers

1. .269  
 /organism="Sus scrofa"  
 /db\_xref="taxon:9823"  
 /clone\_lib="MARC 2P1G"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="vector: pcMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled tissue from day 11, 13, 15, 20,  
 and 30 embryos."  
 BASE COUNT 134 a 47 c 53 g 34 t 1 others  
 ORIGIN

Query Match 73.0%; Score 16.8; DB 162; Length 269;  
 Best Local Similarity 90.0%; Pred. No. 3.6e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctcgaaacgttccacagtca 23

Db 70 TCTCGAACCTTCCAGAGTCA 51

## RESULT 13

AW436470/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 20

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

Plate: 31 row: M column: 10

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1. .306

/organism="Sus scrofa"

/db\_xref="taxon:9823"

/clone\_lib="MARC 2P1G"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="vector: pcMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled tissue from testis, ovary,  
 endometrium, hypothalamus, pituitary, and placenta."  
 BASE COUNT 70 a 99 c 66 g 71 t  
 ORIGIN

## Query Match

Best Local Similarity

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctcgaaacgttccacagtca 23

Db 222 TCTCGAACCTTCCAGAGTCA 203

## RESULT 14

AW486759/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 20

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

Plate: 31 row: N column: 10

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1. .334

/organism="Sus scrofa"

/db\_xref="taxon:9823"

/clone\_lib="MARC 2P1G"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="vector: pcMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled tissue from testis, ovary,  
 endometrium, hypothalamus, pituitary, and placenta."  
 BASE COUNT 86 a 102 c 68 g 74 t  
 ORIGIN

## Query Match

Best Local Similarity

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctcgaaacgttccacagtca 23

Db 222 TCTCGAACCTTCCAGAGTCA 203

## RESULT 15

BE198756/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 20

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

Plate: 31 row: M column: 10

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1. .306

/organism="Sus scrofa"

/db\_xref="taxon:9823"

/clone\_lib="MARC 2P1G"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="vector: pcMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled tissue from testis, ovary,  
 endometrium, hypothalamus, pituitary, and placenta."  
 BASE COUNT 70 a 99 c 66 g 71 t  
 ORIGIN

## Query Match

Best Local Similarity

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 416)

## AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

MGI:954211

Seq primer: -40RP from Gibco

High quality sequence stop: 380.

## FEATURES

Location/Qualifiers

## source

1..416

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone\_image="1548863"

/clone\_lib="Soares.mammary\_gland\_NMLMG"

/sex="female (lactating)"

/tissue\_type="mammary gland"

/lab\_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from mammary  
gland tissue from a lactating female, and was then primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT7T3 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

122 a 81 c 105 g 107 t

## ORIGIN

## Query Match

73.0%; Score 16.8; DB 164; Length 416;

Best Local Similarity 90.0%; Pred. No. 3.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 tctcgaacgttccacagtca 23

|||||

Db 78 TCTCTAACATTCCACAGTCA 59

Search completed: October 9, 2001, 18:20:16

Job time: 9786 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:47 ; Search time 515.84 Seconds  
(without alignments)  
27.997 Million cell updates/sec

Title: US-09-713-136-3  
Perfect score: 23  
Sequence: 1 tcactcgaacgttcacagtcac 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
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18: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	AAV80098	Immunomodulatory o
2	23	100.0	23	AAA38067	Immunostimulatory
3	23	100.0	23	AAF77042	Immunostimulatory
C 4	17.4	75.7	3491	AAV74428	Staphylococcus aur
C 5	17.2	74.8	1192	AAV37952	Arabidopsis thalia
C 6	17.2	74.8	2021	AAC51260	Arabidopsis thalia
C 7	16.6	72.2	23	AAV80109	Oligo used in expe
C 8	16.2	70.4	932	AAV53540	DNA encoding a p11
C 9	16.2	70.4	1735	AAV46985	Arabidopsis thalia
C 10	16.2	70.4	6623	AAV75251	Nucleotide sequenc
C 11	15.8	68.7	508	AAA44452	Human secreted exp

C 12	15.8	68.7	3365	11	ARQ05751	RNA 1 gene of CMV.
C 13	15.6	67.8	928	21	AAV42372	Arabidopsis thalia
C 14	15.6	67.8	2972	20	AAV24415	Human bladder tumor
C 15	15.6	67.8	3641	11	AAQ05752	Microspore-specific
C 16	15.6	67.8	3641	18	AAV48866	Brassica napus mic
C 17	15.6	67.8	6199	21	AAV75562	Human ORFX ORF117
C 18	15.6	67.8	9179	20	AAV13246	Enterococcus faeca
C 19	15.6	67.8	49999	20	AAV23904	Human LOBO homolog
C 20	15.2	66.1	611590	21	AAV22303	Arabidopsis thalia
C 21	15	65.2	22	19	AAV32079	Nucleotide sequenc
C 22	15	65.2	22	20	AAV36624	ISS-ODN DY1018 nuc
C 23	15	65.2	22	20	AAV80105	Oligo used in expe
C 24	15	65.2	22	20	AAV80096	Immunomodulatory o
C 25	15	65.2	22	20	AAV80097	Immunomodulatory o
C 26	15	65.2	22	20	AAV80102	Immunomodulatory o
C 27	15	65.2	22	20	AAV80103	Immunomodulatory o
C 28	15	65.2	22	21	AAV64051	Immunostimulatory
C 29	15	65.2	22	21	AAV6253	Sequence of a stab
C 30	15	65.2	22	21	AAV90458	CPG adjuvant oligo
C 31	15	65.2	22	21	AAV14467	Immunostimulatory
C 32	15	65.2	22	21	AAA38065	Immunostimulatory
C 33	15	65.2	22	21	AAA38066	Immunostimulatory
C 34	15	65.2	22	21	AAA38071	Immunostimulatory
C 35	15	65.2	22	21	AAA38072	Immunostimulatory
C 36	15	65.2	22	21	AAV55876	Immunomodulatory o
C 37	15	65.2	22	22	AAV77040	Immunomodulatory o
C 38	15	65.2	22	22	AAV77041	Immunostimulatory
C 39	15	65.2	22	22	AAV29800	Cholera toxin immu
C 40	15	65.2	22	22	AAV82107	Oligonucleotide OD
C 41	15	65.2	22	22	AAV92377	CG motif and CFA c
C 42	15	65.2	187	16	AAV20195	Human gene signatu
C 43	15	65.2	518	21	AAV77943	Human ORFX ORF3098
C 44	15	65.2	910	21	AAC51128	Arabidopsis thalia
C 45	15	65.2	913	21	AAC32622	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAV80098

ID AAV80098 standard; DNA; 23 BP.

XX AAV80098;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

PT Immunostimulatory oligonucleotides regulate the immune system - and  
PT contain an immune-stimulating octanucleotide sequence; for treating  
PT cancer, allergic and infectious diseases

XX Claim 6; Page 29; 63pp; English.

PS The invention relates to immunomodulatory oligonucleotides that comprise

CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,

CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat

CC patients needing immune regulation, such as those suffering from cancer,

CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the

CC oligonucleotide; and determining the relative amount of Th1-biased

CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent

CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

SQ

Query Match 100.0%; Score 23; DB 20; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.0078;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tcactctcgaacgttccacagtcga 23

|||||

Db 1 tcactctcgaacgttccacagtcga 23

RESULT 2

AAA38067

ID AAA38067 standard; DNA; 23 BP.

AC AAA38067;

XX

XX 24-AUG-2000 (first entry)

XX

XX Immunostimulatory sequence (ISS) #3.

XX

XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;

KW gp120; human immunodeficiency virus; HIV; immune response; infection;

KW development; ss.

XX

XX Synthetic.

XX

XX WO200021556-A1.

XX

XX 20-APR-2000.

XX

XX 08-OCT-1999; 99WO-US23677.

XX

XX 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

XX

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX

XX WPI; 2000-317846/27.

XX

XX Anti-HIV composition comprises immunostimulatory polynucleotides and

PT HIV glycoprotein gp120 useful for modulating, stimulating an immune

PT response against HIV in an HIV infected individual

XX

XX Disclosure; Page 16; 65pp; English.

XX

XX The present invention relates to an immunostimulatory composition

CC comprising a human immunodeficiency virus (HIV) antigen, and an

CC immunomodulatory polynucleotide comprising an immunostimulatory sequence

CC (ISS). This sequence represents an ISS that can be used in the

CC composition. An immunostimulatory composition which comprises a gp120

CC conjugated to an immunomodulatory polynucleotide, or is proximately

CC associated to it and not conjugated, is used for modulating or

CC stimulating a specific immune response against gp120 in an individual by

CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It

CC is also used for suppressing or delaying development of HIV infection in

CC an individual infected with HIV or an individual at risk of infection

CC with HIV, respectively. It is also used for treating an individual

CC infected with HIV in need of immune modulation.

XX

SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 23; DB 21; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.0078;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tcactctcgaacgttccacagtcga 23

|||||

Db 1 tcactctcgaacgttccacagtcga 23

RESULT 3

AAF77042

ID AAF77042 standard; DNA; 23 BP.

XX

XX AAF77042;

XX

XX 15-MAY-2001 (first entry)

DT

XX Immunostimulatory DNA #2.

DE

XX Modulate; Immune; antigen; immunostimulatory; ds.

KW

XX Synthetic.

OS

XX WO200112223-A2.

PN

XX 22-FEB-2001.

PD

XX 18-AUG-2000; 2000WO-US22835.

PF

XX 19-AUG-1999; 99US-0149768.

PR

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX

XX Van Nest G;

PI

XX WPI; 2001-211136/21.

DR

XX

XX Modulating immune response to a second antigen in humans involves

PT administering an immunostimulatory polynucleotide comprising an

PT immunostimulatory sequence and a first antigen

XX

XX Disclosure; Page 15; 63pp; English.

XX

XX The present invention relates to modulating an immune response to

CC a second antigen in an individual, involving

CC administering to the individual an immunomodulatory polynucleotide

CC comprising an immunostimulatory sequence (ISS) and a first antigen.

XX

SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 23; DB 22; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.0078;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tcactctcgaacgttccacagtcga 23

|||||

Db 1 tcactctcgaacgttccacagtcga 23

RESULT 4

AAV74428/c



ID AAV74428 standard; DNA; 3491 BP.  
AC AAV74428;  
XX  
DT 16-MAR-1999 (first entry)  
XX  
DE Staphylococcus aureus contig SEQ ID #117.  
XX  
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX  
OS Staphylococcus aureus.  
XX  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1741..1800  
FT /\*tag= a  
FT /note= "these bases represent a line of missing text in  
FT the sequence listing in the specification. They  
FT are included to maintain the nucleotide numbering  
FT given in the specification for this DNA sequence".  
XX  
XX  
PN EP786519-A2.  
XX  
XX 30-JUL-1997.  
XX  
XX  
PF 07-JAN-1997; 97EP-0100117.  
XX  
XX 05-JAN-1996; 96US-0009861.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;  
PI Rosen CA;  
PI  
XX  
DR WPI: 1997-374922/35.  
XX  
XX  
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus  
PT stored on computer readable medium and used in the production of  
PT anti-S.aureus vaccines  
XX  
XX  
PS Claim 1: Page 665-666; 327lpp; English.  
XX  
XX  
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
CC of the invention. The DNA sequences are recorded on a computer readable  
CC medium, preferably selected from a floppy or hard disk, random access  
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CC the S.aureus DNA sequences allows putative functions to be assigned so  
CC that protein-encoding or regulatory regions of commercial, therapeutic or  
CC industrial importance can be obtained. Specifically, sequences which are  
CC likely to encode antigens have been identified and these polypeptides can  
CC be used in a vaccine composition against S.aureus infection. The  
CC polypeptides can also be used in a kit for the immunodetection of  
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CC for recombinant production of the polypeptides. The new DNA sequences  
CC (and their fragments) are useful as primers or probes for isolating  
CC homologues of any of the S.aureus DNA sequences contained on the  
CC computer readable medium.  
XX  
SQ Sequence 3491 BP; 1321 A; 457 C; 679 G; 964 T; 70 other;

Query Match 75.7%; Score 17.4; DB 18; Length 3491;  
Best Local Similarity 85.7%; Pred. No. 11;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 atctcgaaacgtttccacgtca 23  
||||| ||||| ||||| |||||  
Db 1264 ATYTCGACGTTCAACAGTCA 1244

RESULT 5  
AAC37952/C  
ID AAC37952 standard; DNA; 1192 BP.  
XX  
XX AAC37952;  
AC  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 19256.  
XX  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
XX EP1033405-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0123180.  
XX 09-MAR-1999; 99US-0123548.  
XX 23-MAR-1999; 99US-0125788.  
XX 25-MAR-1999; 99US-0126264.  
XX 29-MAR-1999; 99US-0126785.  
XX 01-APR-1999; 99US-0127462.  
XX 06-APR-1999; 99US-0128234.  
XX 08-APR-1999; 99US-0128714.  
XX 16-APR-1999; 99US-0129845.  
XX 19-APR-1999; 99US-0130077.  
XX 21-APR-1999; 99US-0130449.  
XX 23-APR-1999; 99US-0130510.  
XX 23-APR-1999; 99US-0130891.  
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XX 30-APR-1999; 99US-0132048.  
XX 30-APR-1999; 99US-0132407.  
XX 04-MAY-1999; 99US-0132484.  
XX 05-MAY-1999; 99US-0132485.  
XX 06-MAY-1999; 99US-0132486.  
XX 06-MAY-1999; 99US-0132487.  
XX 07-MAY-1999; 99US-0132863.  
XX 11-MAY-1999; 99US-0134256.  
XX 14-MAY-1999; 99US-0134218.  
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XX 18-MAY-1999; 99US-0134768.  
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XX 20-MAY-1999; 99US-0135124.  
XX 21-MAY-1999; 99US-0135353.  
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XX 25-MAY-1999; 99US-0136021.  
XX 27-MAY-1999; 99US-0136392.  
XX 28-MAY-1999; 99US-0136782.  
XX 01-JUN-1999; 99US-0137222.  
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XX 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.  
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PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
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PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
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PR 24-JUN-1999; 99US-0140695.  
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PR 01-JUL-1999; 99US-0141842.  
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PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
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PR 28-JUL-1999; 99US-0145951.  
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PR 18-AUG-1999; 99US-0149426.

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PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
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PR 07-SEP-1999; 99US-0152363.  
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PR 15-SEP-1999; 99US-0154018.  
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PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
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PR 22-OCT-1999; 99US-0160980.  
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PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
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PR 29-OCT-1999; 99US-0162142.

Query Match 74.8%; Score 17.2; DB 21; Length 1192;  
Best Local Similarity 86.4%; Pred. No. 13;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcatctcgaacgtttccacgtc 22  
||| ||||| ||||| ||||| ||  
Db 683 TCAGATCGAACGTTCCACATC 662

RESULT 6  
AAC51260/C  
ID AAC51260 standard; DNA; 2021 BP.  
XX  
AC AAC51260;

XX	18-OCT-2000	(first entry)
DT		
XX	Arabidopsis thaliana	DNA fragment SEQ ID NO: 67861.
DE		
XX	Hybridisation assay; genetic mapping; gene expression control;	
KW	protein identification; signal transduction pathway;	
KW	metabolic pathway; promoter; termination sequence; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-0301439.	
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PR	25-FEB-1999;	99US-0121825.
PR	03-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0132548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
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PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
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PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
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PR 27-AUG-1999; 99US-0151065.  
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 PR 27-AUG-1999; 99US-0151080.  
 PR 30-AUG-1999; 99US-0151303.  
 PR 31-AUG-1999; 99US-0151438.  
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 PR 13-SEP-1999; 99US-0153758.  
 PR 15-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
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 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
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 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
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 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
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 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 74.8%; Score 17.2; DB 21; Length 2021;  
 Best Local Similarity 86.4%; Pred. No. 13;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgttccacagtc 22  
 DB 1511 TCAGATCGAACGTTCCACATTC 1490

RESULT 7  
 AAV80109/c  
 ID AAV80109 standard; DNA: 23 BP.

AC AAV80109;

XX 12-MAR-1999 (first entry)

DT Oligo used in experiments for stimulation of cytokine production.

DE Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;

KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
 OS Synthetic.  
 XX WO9855495-A2.  
 PN 10-DEC-1998.  
 XX 05-JUN-1998; 98WO-US11578.  
 PF 06-JUN-1997; 97US-0048793.  
 PR (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX Dina D, Roman M, Schwartz D;  
 PI WPI; 1999-059898/05.  
 XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases  
 XX Example 1; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent  
 CC oligonucleotides that were tested for immunostimulatory activity. These  
 CC were used in experiments for the stimulation of cytokine production and  
 CC were found to lack immunostimulatory activity. The invention provides  
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.  
 XX Sequence 23 BP; 7 A; 3 C; 7 G; 6 T; 0 other;

Query Match 72.2%; Score 16.6; DB 20; Length 23;  
 Best Local Similarity 82.6%; Pred. No. 16;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattcgaacgttccacagtc 23  
 DB 23 TCATCTCTAACGTTCCACGAGTCA 1

RESULT 8  
 AAV53540/c  
 ID AAV53540 standard; DNA: 932 BP.  
 XX AAV53540;  
 AC AAV53540;

DT 30-OCT-1998 (first entry)

XX DNA encoding a p115 protein.

XX Staphylococcus aureus protein; immune response induction; eye infection;  
 KW antibody production; T-cell immune response; gastrointestinal infection;  
 KW respiratory infection; inhibitor; bacterial infection; cardiac infection;  
 KW central nervous system; kidney infection; urinary tract infection;  
 KW antimicrobial compound identification; broad spectrum antibiotic;  
 KW therapy; ss.  
 XX Staphylococcus aureus.

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XX PN EP841394-A2.
XX PD 13-MAY-1998.
XX PF 24-SEP-1997; 97EP-0307485.
XX PR 24-SEP-1996; 96US-0027032.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX Black MT, Burnham MKR, Hodgson JE, Knowles DJC;
XX Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M;
XX Ward JM;
XX WPI; 1998-252940/23.
XX P-PSDB; AAW7752.
XX New nucleic acid sequences from Staphylococcus aureus WCHU29 -
XX useful in vaccines and for treatment of bacterial infections of e.g.
XX respiratory tract and central nervous system
XX Claim 1: Page 199; 390pp; English.
XX This sequence encodes a Staphylococcus aureus protein that (based on
XX homology with a Mycoplasma hyorhinis protein) is a Pil5 protein, and
XX represents a DNA sequence of the invention.
XX The DNA sequences were isolated from Staphylococcus aureus WCHU29 .
XX (NCIMB 40771). Host cells containing the DNA sequences are used to
XX produce polypeptides or fragments. The proteins are used in the treatment
XX of disease, for inducing an immune response by administering them, to
XX produce antibody and/or T-cell immune response. Antagonists of the
XX proteins are used for the inhibition of bacterial polypeptides.
XX Conditions which may be treated include bacterial infections, especially
XX respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
XX urinary tract, skin, bones and joints. The proteins can also be used to
XX identify antimicrobial compounds which are broad spectrum antibiotics,
XX especially useful in the treatment of H. pylori infection.
XX
XX Sequence 932 BP; 339 A; 129 C; 192 G; 272 T; 0 other;

Query Match 70.48; Score 16.2; DB 19; Length 932;
Best Local Similarity 85.74; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 atctcgaaacttcacagatca 23
||| ||||| |||||
Db 214 ATTTCGACGTTCAACAGTCA 194

RESULT 9
AAC46985/c
ID AAC46985 standard; DNA; 1735 BP.
XX AC AAC46985;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 52135.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.

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XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
XX 30-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 04-MAY-1999; 99US-0132407.
XX 05-MAY-1999; 99US-0132484.
XX 06-MAY-1999; 99US-0132485.
XX 07-MAY-1999; 99US-0132486.
XX 11-MAY-1999; 99US-0132863.
XX 14-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134221.
XX 18-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
XX 10-JUN-1999; 99US-0138847.
XX 14-JUN-1999; 99US-0139119.
XX 16-JUN-1999; 99US-0139452.
XX 16-JUN-1999; 99US-0139453.
XX 17-JUN-1999; 99US-0139492.
XX 18-JUN-1999; 99US-0139454.
XX 18-JUN-1999; 99US-0139455.
XX 18-JUN-1999; 99US-0139456.
XX 18-JUN-1999; 99US-0139457.
XX 18-JUN-1999; 99US-0139458.
XX 18-JUN-1999; 99US-0139459.
XX 18-JUN-1999; 99US-0139460.
XX 18-JUN-1999; 99US-0139461.
XX 18-JUN-1999; 99US-0139462.
XX 18-JUN-1999; 99US-0139463.
XX 18-JUN-1999; 99US-0139750.
XX 18-JUN-1999; 99US-0139763.
XX 21-JUN-1999; 99US-0139817.
XX 22-JUN-1999; 99US-0139899.
XX 23-JUN-1999; 99US-0140353.
XX 23-JUN-1999; 99US-0140354.
XX 24-JUN-1999; 99US-0140695.
XX 28-JUN-1999; 99US-0140823.
XX 29-JUN-1999; 99US-0140991.
XX 30-JUN-1999; 99US-0141287.
XX 01-JUL-1999; 99US-0141842.
XX 01-JUL-1999; 99US-0142154.
XX 02-JUL-1999; 99US-0142055.
XX 06-JUL-1999; 99US-0142390.
XX 08-JUL-1999; 99US-0142803.
XX 09-JUL-1999; 99US-0142920.

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PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 21-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145911.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 06-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.

PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161922.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.  
PR 29-OCT-1999; 99US-0162142.

Query Match 70.4%; Score 16.2; DB 21: Length 1735;  
Best Local Similarity 85.7%; Pred. No. 43;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tcattctcgaaacgtttccacagt 21  
| ||| ||||| |||||  
Db 402 TTATCTAGACGCTTCCACACT 382

RESULT 10  
AAT75251  
ID AAT75251 standard; DNA: 6623-BP.  
XX AC AAT75251;  
XX DT 21-DEC-1998 (first entry)  
XX DE Nucleotide sequence encoding human RAD50 intron 5, 3' end.  
XX KW ds; human; RAD50; DNA repair; tumour suppression; cancer; Septin-2;  
XX KW central nervous system.  
XX OS Homo sapiens.  
XX PN W09727284-A2.  
XX PD 31-JUL-1997.  
XX PF 24-JAN-1997; 97WO-US01299.  
XX PR 17-JUL-1996; 96US-0687080.  
XX PR 26-JAN-1996; 96US-0592126.  
XX PA (GENE-) GENELABS TECHNOLOGIES INC.  
XX PI Dolganov G;  
XX XX

DR WP2: 1997-393672/36.  
 XX Human tumour suppressor gene RAD50 - useful to detect  
 PT predisposition to, decrease risk of and treat cancer, also Septin-2  
 PT homologues  
 XX  
 PS Claim 1: Page 103-106; 195pp; English.  
 XX  
 CC The human RAD50 (hRAD50) is involved in DNA repair and has tumour  
 CC suppression activity, can be used to detect predisposition to, decrease  
 CC the risk of or treat cancers, e.g. acute myeloid leukaemia,  
 CC myelodysplastic syndrome, therapy related myelodysplastic syndrome,  
 CC therapy related acute myeloid leukaemia, refractory anaemia or refractory  
 CC anaemia with excess blasts. Also disclosed in this invention is Human  
 CC Septin-2 homologues of which may be used as targets for cancer therapies  
 CC and central nervous system directed treatment methods, and to measure the  
 CC proliferative potential of selected cell types.  
 XX  
 SQ Sequence 6623 BP; 1823 A; 1242 C; 1314 G; 2244 T; 0 other;

Query Match 70.4%; Score 16.2; DB 18; Length 6623;  
 Best Local Similarity 85.7%; Pred. No. 51;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tcattctgaacgttccacagt 21  
 ||||| ||| ||||| |||  
 DB 587 tcattctgaacgttccacagt 607

RESULT 11  
 AAA44452/C  
 ID AAA44452 standard; cDNA: 508 BP.  
 XX  
 AC AAA44452;  
 XX  
 DT 21-AUG-2000 (first entry)  
 XX  
 DE Human secreted expressed sequence tag SEQ ID NO:1027.  
 XX  
 KW Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;  
 KW expressed sequence tag; EST; probe; chemotactic; proliferative;  
 KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;  
 KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;  
 KW antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;  
 KW cerebroprotective; neuroprotective; neutropic; antipsoriatic;  
 KW vaccine; autolimmune disorder; antidepressant; gene therapy;  
 KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;  
 KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;  
 KW central nervous system disorder; Alzheimer's disease; stroke;  
 KW Parkinson's disease; Huntington's disease; coagulation disorder;  
 KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;  
 KW tumour; infection; depression; psoriasis; ss.

OS Homo sapiens.  
 XX  
 XX WO200021991-A1.  
 PN  
 XX  
 XX 20-APR-2000.  
 PD  
 XX  
 XX 15-OCT-1999; 99WO-US24206.  
 PF  
 XX  
 XX 15-OCT-1998; 98US-0104436.  
 PR  
 XX  
 XX (GENY ) GENETICS INST INC.  
 PA  
 XX  
 XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Bowman MR;  
 PI  
 XX  
 DR WPI: 2000-317938/27.  
 XX

PT Isolated polynucleotides, and encoded proteins, comprising secreted

PT expressed sequence tags (sESTs), useful for treating various disorders  
 XX such as autoimmune, infectious, and central nervous system disorders -  
 XX  
 PS Claim 1: Page 466; 803pp; English.  
 XX  
 CC AAA43426 to AAA45925 represent specifically claimed secreted expressed  
 CC sequence tags (sESTs), isolated from human, mouse, chicken and rat  
 CC tissue sources. The sESTs can have a range of activities depending on  
 CC the tissues they were isolated from. The activities include:  
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;  
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;  
 CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;  
 CC antiasthmatic; vulnerary; antitumor; osteopathic; neuroprotective;  
 CC notropic; antiparkinsonian; antipsoriatic; cerebroprotective;  
 CC anticonvulsant; and antidepressant. The sESTs can be used for gene  
 CC therapy and in vaccines. The sESTs are useful as probes for the  
 CC identification and isolation of full-length cDNAs and genomic DNA  
 CC molecules which correspond to the sESTs. Proteins encoded by the sESTs  
 CC are useful in assays for determining biological activity and raising  
 CC antibodies. They may be useful for treatment of autoimmune disorders  
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions  
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,  
 CC osteoporosis, osteoarthritis, central nervous system disorders  
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's  
 CC disease), tumours, bacterial, fungal or viral infections, depression and  
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 508 BP; 178 A; 102 C; 126 G; 102 T; 0 other;

Query Match 68.7%; Score 15.8; DB 21; Length 508;  
 Best Local Similarity 89.5%; Pred. No. 59;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 5 ctcgaacgttccacagtca 23  
 ||||| ||||| ||||| |||||  
 DB 232 CTCGAAGGTTCCACAGTCA 214

RESULT 12  
 AAQ05751  
 ID AAQ05751 standard; cDNA: 3365 BP.  
 XX  
 AC AAQ05751;  
 XX  
 DT 19-DEC-1990 (first entry)  
 XX  
 DE RNA 1 gene of CMV.  
 XX  
 KW CMV; RNA 1; ss.  
 XX  
 XX Cucurbit mosaic virus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 97..3075  
 FT /\*tag= a  
 XX  
 XX JP02167080-A.  
 PN  
 XX  
 XX 27-JUN-1990.  
 PD  
 XX  
 XX 19-DEC-1988; 88JP-0320015.  
 PF  
 XX  
 XX 19-DEC-1988; 88JP-0320015.  
 PR  
 XX  
 XX (NOGY-) NOGYO SEIBUFSU IDEN.  
 PA  
 XX  
 XX WPI: 1990-241950/32.  
 DR P-PSDB; AAR96531.  
 DR  
 XX  
 XX Genome RNA 1 gene for prepn. of cucumber mosaic virus - codes  
 PT

PT protein contg. specified sequence of 994 amino acids used in prepn.  
PT of resistant plants.

XX PS Claim 2; Page 2; 10pp; Japanese.

XX CC The gene can be used to prepare plants which are resistant to  
CC cucumber mosaic virus. The DNA was prep'd. from RNA isolated from  
CC CMV-O virus.

XX SQ Sequence 3365 BP; 850 A; 734 C; 810 G; 971 T; 0 other;

Query Match 68.7%; Score 15.8; DB 11; Length 3365;  
Best Local Similarity 89.5%; Pred. NO. 76;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tcattctgaaacgtttccaca 19  
||||| ||||| |||||

Db 548 tcattctgaaacgtttccaca 566

RESULT 13

AAC42372/C  
ID AAC42372 standard; DNA: 928 BP.

XX AC AAC42372;

XX DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35303.

XX KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;

XX KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 18-MAY-1999; 99US-0134370.

PR 19-MAY-1999; 99US-0134768.

PR 20-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
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PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
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PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
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PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
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PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
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PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.



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PR 02-AUG-1999; 99US-0146388.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
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PR 31-AUG-1999; 99US-0151438.
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PR 29-SEP-1999; 99US-0156596.
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PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 67.8%; Score 15.6; DB 21; Length 938;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tcattcgaacgttccacagtc 22
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Db 894 TCATCTCTAGCTTCAACAGTC 873

RESULT 14
AAZ24415
ID AAZ24415 standard; cDNA; 2972 BP.
XX
AC AAZ24415;
XX
DT 14-FEB-2000 (first entry)
XX
DE Human bladder tumour cDNA library derived EST 27.
XX
KW Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;
KW treatment; gene therapy; EST; ss.
XX
OS Homo sapiens.
XX
PN DE19818619-A1.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1998; 98DE-1018619.
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PR 21-APR-1998; 98DE-1018619.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
XX
DR WPI; 1999-612028/53.
XX
PT New nucleic acid sequences expressed in bladder tumor tissue, and
PT derived polypeptides, for treatment of bladder tumor and identification
PT of therapeutic agents.
XX
PS Claim 3; Page 81-82; 132pp; German.
XX
CC This invention describes novel polypeptide fragments (I) and the
CC polynucleotides (II) that encode them that are highly expressed in a
CC human bladder tumor and which have cytostatic activity. (II) are used
CC for recombinant expression of (I) and to isolate complete genes. (I) are
CC used to identify agents suitable for treatment of bladder cancer, to
CC directly treat this form of cancer (including expression from gene
CC therapy vectors) or are used in a preparation for cancer treatment. (I)
CC is also used for the generation of specific antibodies. (II) are
CC identified by assembling ESTs (expressed sequence tags) from a
CC particular tissue type before comparison of expression patterns. This
CC allows a significantly longer fragment of the gene to be revealed, and
CC therefore reduces the number of failures associated with the fact that
CC ESTs from different libraries may represent different parts of the same
CC unknown gene, distorting the estimated frequency of occurrence in a
CC particular tissue. AAZ43260-24309 represent expressed sequence tag (EST)
CC fragments isolated from a human bladder tumour cDNA library which encode
CC the proteins represented in AAY66143-Y66198.
XX
SQ Sequence 2972 BP; 710 A; 820 C; 773 G; 669 T; 0 other;

Query Match 67.8%; Score 15.6; DB 20; Length 2972;
Best Local Similarity 81.8%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 2171 catatcaaacgttgcacagaca 2192  
  
RESULT 15  
AAQ05752/c  
ID AAQ05752 standard; DNA; 3641 BP.  
XX  
AC AAQ05752;  
XX  
DT 02-JAN-1991 (first entry)  
XX  
DE Microspore-specific clone L10 from Brassica napus.  
XX  
KW Microspore; controllable male sterility; blocking pollen formation;  
XX anti-sense DNA; ss;  
XX Brassica napus spp. oleifera Westar.  
XX  
XX Key Location/Qualifiers  
FT TATA\_signal 759..762  
FT /\*tag= a  
FT prim\_transcript 790..2780  
FT /\*tag= b  
FT /\*note="includes 2 introns"  
FT /\*note="precise position of end not determined"  
FT exon 854..1104  
FT /\*tag= c  
FT /\*number=1  
FT intron 1105..1264  
FT /\*tag= d  
FT /\*number=1  
FT exon 1265..2374  
FT /\*tag= e  
FT intron 2375..2461  
FT /\*tag= f  
FT /\*number=2  
FT exon 2462..2780  
FT /\*tag= g  
FT /\*number=3  
FT promoter 1..726  
FT /\*tag= h  
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PN WO9008828-A.  
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XX 09-AUG-1990.  
XX  
XX 02-FEB-1990; 90WO-CA00037.  
XX  
XX 03-FEB-1989; 89EP-0301053.  
XX 02-FEB-1989; 89NZ-0227835.  
XX 03-FEB-1989; 89US-0306438.  
XX  
XX (PALA-) PALADIN HYBRIDS INC.  
XX  
XX Fabijanski S, Albani D, Robert LS, Arnison PG;  
XX  
XX WPI: 1990-260937/34.  
XX P-PSDB; AAR06518.  
XX  
XX Hybrid seed prodn. from plants with controllable male sterility -  
XX induced by insertion of anti-sense DNA which blocks formation of  
XX pollen.  
XX  
XX Claim 108; Page 159; 207pp; English.  
XX  
XX Clone L10 was identified as microspore-specific and critical to  
XX pollen formation and function. The promoter sequence may be cloned  
XX into a plasmid carrying a pollen-specific gene in the anti-sense  
XX orientation with respect to the promoter. The construct is

CC used to transform Brassica sp.  
CC In addition the plasmid carries a resistance gene to a chemical  
CC agent or stress. The sense and anti-sense genes are regulated such  
CC that they are expressed at about the same time as each other.  
CC Transfected plants are pollinated and selected according to  
CC presence of the resistance gene. The promoter is inducible so that  
CC plants are male-sterile only in the presence of the appropriate  
CC inducer.  
CC See also AAQ05749 and AAQ05753-Q05758.  
XX  
XX Sequence 3641 BP; 1094 A; 852 C; 673 G; 1012 T; 10 other;  
XX

Query Match 67.8%; Score 15.6; DB 11; Length 3641;  
Best Local Similarity 81.8%; Pred. No. 97;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tcattctogaacgttccacagtcc 22  
||| ||||| ||||| ||  
Db 2611 TCAGACGACGACGTTCCACATTC 2590

Search completed: October 9, 2001, 16:26:49  
Job time: 2979 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:35 ; Search time 10334.3 Seconds  
(without alignments)  
32.887 Million cell updates/sec

Title: US-09-713-136-3

Perfect score: 23

Sequence: 1 tcatctgaacgttcacagtcacgta 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	23	100.0	23	16	US-09-296-477-4
2	23	100.0	23	18	US-09-415-186-3
3	23	100.0	23	25	US-09-642-492-3
4	23	100.0	23	28	US-09-713-136-3
5	18.8	81.7	278	17	US-09-391-630-10240
6	18.8	81.7	278	25	US-09-654-617-60059
7	18.8	81.7	278	27	US-09-684-016-60059
8	18.8	81.7	278	46	US-60-144-084-9026
9	18.8	81.7	284	15	US-09-126-377-1868
10	17.8	77.4	1088	48	US-60-167-217-22953
11	17.8	77.4	3437	48	US-60-167-217-22952
12	17.4	75.7	612	16	US-09-270-849B-84639
13	17.4	75.7	3491	13	US-08-781-986A-117
14	17.4	75.7	3491	13	US-08-956-171-117
15	17.4	75.7	3491	13	US-08-956-171B-117
16	17.4	75.7	3491	13	US-08-956-171C-117
17	17.2	74.8	173	17	US-09-313-294A-3045
18	17.2	74.8	173	40	US-60-086-722-3045
19	17.2	74.8	310	45	US-60-138-103-17744
20	17.2	74.8	383	28	US-09-704-424-11573
21	17.2	74.8	395	19	US-09-521-640-8055
22	17.2	74.8	395	22	US-09-552-087-6707
23	17.2	74.8	407	28	US-09-704-424-13172
24	17.2	74.8	478	45	US-60-135-951-3244
25	17.2	74.8	506	25	US-09-654-617-409239
26	17.2	74.8	506	27	US-09-684-016-409239
27	17.2	74.8	516	28	US-09-704-424-10764
28	17.2	74.8	548	18	US-09-401-645-2094
29	17.2	74.8	571	17	US-09-371-508-3743
30	17.2	74.8	571	17	US-09-371-508-3743
31	17.2	74.8	571	29	US-09-747-508-3743
32	17.2	74.8	589	22	US-09-565-309A-34989
33	17.2	74.8	693	25	US-09-654-617-13602
34	17.2	74.8	693	27	US-09-684-016-13602
35	17.2	74.8	694	16	US-09-270-849B-157528
36	17.2	74.8	1509	25	US-09-654-617-385350
37	17.2	74.8	1509	27	US-09-684-016-385350
38	17.2	74.8	10734	56	US-60-242-679-145
39	17.2	74.8	13205	31	US-09-635-811-3
40	17.2	74.8	18471	24	US-09-620-392-52694
41	17.2	74.8	26773	24	US-09-620-392-10511
42	17.2	74.8	26773	28	US-09-702-134-28340
43	17.2	74.8	29666	24	US-09-620-392-17397
44	17.2	74.8	32417	53	US-60-212-413-106
45	17.2	74.8	32768	53	US-60-212-356-108

RESULT 5  
US-09-391-630-10240

; Sequence 10240, Application US/09391630  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Shukla, Hridayabhiramjam  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 38-21(15441)B  
; CURRENT APPLICATION NUMBER: US/09/391,630  
; CURRENT FILING DATE: 1999-09-08  
; NUMBER OF SEQ ID NOS: 18889  
; SEQ ID NO 10240  
; LENGTH: 278  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3049-022-Q1-E1-A8  
US-09-391-630-10240

Query Match 81.7%; Score 18.8; DB 17; Length 278;  
Best Local Similarity 90.9%; Pred. No. 31;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 140 catctctaccgttcacagtcga 161

## RESULT 6

US-09-654-617-60059  
; Sequence 60059, Application US/09654617  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong Annotated Plant Genes  
; TITLE OF INVENTION: 38-21(15097)D  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/654,617  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 60059  
; LENGTH: 278  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-654-617-60059

Query Match 81.7%; Score 18.8; DB 25; Length 278;  
Best Local Similarity 90.9%; Pred. No. 31;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 catctcgaaagcttcacagtcga 23  
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Db 140 catctctaccgttcacagtcga 161

## RESULT 7

US-09-684-016-60059  
; Sequence 60059, Application US/09684016  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong Annotated Plant Genes  
; TITLE OF INVENTION: 38-21(15097)D  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/684,016  
; CURRENT FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 463173  
; PRIOR FILING DATE: 2000-09-05  
; SEQ ID NO 60059  
; LENGTH: 278

; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-684-016-60059

Query Match 81.7%; Score 18.8; DB 27; Length 278;  
Best Local Similarity 90.9%; Pred. No. 31;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 catctcgaaagcttcacagtcga 23  
||||| | ||||| |||||  
Db 140 catctctaccgttcacagtcga 161

## RESULT 8

US-60-144-084-9026  
; Sequence 9026, Application US/60144084  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; APPLICANT: Buehler, Robert E.  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Coombs, Brian E.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Nelson, Donald E.  
; APPLICANT: Shukla, Hridayabhiramjam  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 38-21(15444)B  
; CURRENT APPLICATION NUMBER: US/60/144,084  
; CURRENT FILING DATE: 1999-07-16  
; NUMBER OF SEQ ID NOS: 47776  
; SEQ ID NO 9026  
; LENGTH: 278  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3049-022-Q1-E1-A8  
US-60-144-084-9026

Query Match 81.7%; Score 18.8; DB 46; Length 278;  
Best Local Similarity 90.9%; Pred. No. 31;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 catctcgaaagcttcacagtcga 23  
||||| | ||||| |||||  
Db 140 catctctaccgttcacagtcga 161

## RESULT 9

US-09-126-377-1868  
; Sequence 1868, Application US/09126377  
; GENERAL INFORMATION:  
; APPLICANT: Gooding, Douglas H.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Naughton, Rebecca E.  
; APPLICANT: Mullahy, Sara J.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM RAT ADRENAL GL  
; FILE REFERENCE: P2-0011 US  
; CURRENT APPLICATION NUMBER: US/09/126,377  
; CURRENT FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/054,913  
; EARLIER FILING DATE: 97-06-08  
; EARLIER APPLICATION NUMBER: 60/061,784  
; EARLIER FILING DATE: 97-07-10  
; NUMBER OF SEQ ID NOS: 2301  
; SOFTWARE: PERL Program  
; SEQ ID NO 1868  
; LENGTH: 284  
; TYPE: DNA

```

RESULT 13
US-08-781-986A-117/c
; Sequence 117, Application US/08781986A
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-117

```

Query Match 75.7%; Score 17.4; DB 11; Length 3491;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 atctcgacggttcacagtcga 23  
11:111 11111 1111111

DB 1264 ATYTCGCACGTTCAACAGTCA 1244

RESULT 14  
US-08-956-171-117/c  
Sequence 117, Application US/08956171  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3491 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-956-171-117

Query Match 75.7%; Score 17.4; DB 13; Length 3491;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 atctcgacggttcacagtcga 23  
11:111 11111 1111111

DB 1264 ATYTCGCACGTTCAACAGTCA 1244

RESULT 15  
US-08-956-171B-117/c  
Sequence 117, Application US/08956171B  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171B  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Kenley K.  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 610-5790  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3491 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 117:  
US-08-956-171B-117

Query Match 75.7%; Score 17.4; DB 13; Length 3491;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 atctcgacggttcacagtcga 23  
11:111 11111 1111111

DB 1264 ATYTCGCACGTTCAACAGTCA 1244

Search completed: October 9, 2001, 21:12:37  
Job time: 20062 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:00 ; Search time 1391.6 Seconds  
(without alignments)  
37.721 Million cell updates/sec

Title: US-09-713-136-3  
Perfect score: 23  
Sequence: 1 tcattcgaacgttccacagtca 23

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq1.\*  
7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq2.\*  
8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	23	7	US-09-802-518-3
2	23	100.0	23	7	US-09-802-359-3
3	23	100.0	23	7	US-09-802-376-3
4	18.8	81.7	284	5	US-09-534-852-4062
5	17.2	74.8	83287	6	US-09-803-736-413
6	17	73.9	52784	6	US-09-803-736-255
7	16.6	72.2	219	6	US-09-804-730-2192
8	16.6	72.2	348	7	US-09-540-213-6759
9	16.6	72.2	1699	8	US-60-278-561-11368
10	16.6	72.2	6058	6	US-09-764-891-5493
11	16.6	72.2	31309	6	US-09-803-736-895
12	16.6	72.2	60476	6	US-09-803-736-823
13	16.6	72.2	116149	6	US-09-803-736-163
14	16.6	72.2	138181	6	US-09-803-736-184
15	16.2	70.4	136	8	US-60-253-378-24945
16	16.2	70.4	305	8	US-60-253-456-28528
17	16.2	70.4	434	6	US-09-904-809-7140
18	16.2	70.4	437	5	US-09-921-378-13959
19	16.2	70.4	441	5	US-09-921-378-13608
20	16.2	70.4	443	5	US-09-921-378-13607
21	16.2	70.4	459	6	US-09-904-809-6627
22	16.2	70.4	537	6	US-09-796-692-8874
23	16.2	70.4	581	6	US-09-796-692-7189
24	16.2	70.4	648	6	US-09-757-031-676
25	16.2	70.4	700	7	US-09-735-271-526

C 26	16.2	70.4	700	7	US-09-735-271-527	Sequence 527, App
C 27	16.2	70.4	1089	1	PCT-US01-04926A-44	Sequence 44, Appl
C 28	16.2	70.4	1091	1	PCT-US01-04926A-388	Sequence 388, App
C 29	16.2	70.4	1441	6	US-09-764-872-875	Sequence 875, App
C 30	16.2	70.4	78369	6	US-09-803-736-817	Sequence 817, App
C 31	15.8	68.7	97	7	US-09-853-369-1419	Sequence 1419, Ap
C 32	15.8	68.7	361	6	US-09-823-301-1400	Sequence 1400, Ap
C 33	15.8	68.7	476	7	US-09-834-366-2692	Sequence 2692, Ap
C 34	15.8	68.7	727	6	US-09-758-456-112	Sequence 112, App
C 35	15.8	68.7	1982	8	US-60-278-561-10217	Sequence 10217, A
C 36	15.8	68.7	2978	1	PCT-US01-14827-4939	Sequence 4939, Ap
C 37	15.8	68.7	97798	6	US-09-803-736-1079	Sequence 1079, Ap
C 38	15.6	67.8	214	8	US-60-253-654-11535	Sequence 11535, A
C 39	15.6	67.8	214	8	US-60-255-592-11535	Sequence 11535, A
C 40	15.6	67.8	240	7	US-09-912-292-25501	Sequence 25501, A
C 41	15.6	67.8	240	7	US-09-540-213-12400	Sequence 12400, A
C 42	15.6	67.8	240	7	US-09-773-518-160	Sequence 160, App
C 43	15.6	67.8	251	7	US-09-855-807-5902	Sequence 5902, Ap
C 44	15.6	67.8	297	8	US-60-253-654-11282	Sequence 11282, A
C 45	15.6	67.8	297	8	US-60-255-592-11282	Sequence 11282, A

ALIGNMENTS

RESULT 1  
US-09-802-518-3  
; Sequence 3, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCES  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-3

Query Match 100.0%; Score 23; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 tcattcgaacgttccacagtca 23  
|||||  
Db 1 tcattcgaacgttccacagtca 23  
  
RESULT 2  
US-09-802-359-3  
; Sequence 3, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3





Query Match 73.9%; Score 17; DB 6; Length 52784;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 tctcgaaagcttccacag 20  
|||||  
Db 43475 TCTCGAAGCTTCCACAG 43459

RESULT 7  
US-09-804-730-2192  
; Sequence 2192, Application US/09804730  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Hammond-Kosack, Kim  
; APPLICANT: Masucci, James D.  
; APPLICANT: Urban, Martin  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51838)B  
; CURRENT APPLICATION NUMBER: US/09/804,730  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: US 60/189,657  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 22828  
; SEQ ID NO 2192  
; LENGTH: 219  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; OTHER INFORMATION: Clone ID: LIB3350-034-P1-K1-D4  
US-09-804-730-2192

Query Match 72.2%; Score 16.6; DB 6; Length 219;  
Best Local Similarity 82.6%; Pred. No. 53;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tcatctcgaaagcttccacagtc 23  
||| | |||||  
Db 126 tcaacctgaaagcttccacagaca 148

RESULT 8  
US-09-540-213-6759  
; Sequence 6759, Application US/09540213  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Delegeane, Angelo M.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Mullahy, Sara J.  
; APPLICANT: Naughton, Rebecca E.  
; TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS  
; FILE REFERENCE: PD-1031 CIP  
; CURRENT APPLICATION NUMBER: US/09/540,213  
; CURRENT FILING DATE: 2000-03-31  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 53844  
; SEQ ID NO 6759  
; LENGTH: 348  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: hu00312093  
; NAME/KEY: unsure  
; LOCATION: 23, 239, 283  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-540-213-6759

Query Match 72.2%; Score 16.6; DB 7; Length 348;

Best Local Similarity 82.6%; Pred. No. 57;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tcatctcgaaagcttccacagtc 23  
||||| ||||| ||||| ||  
Db 25 tcatatcaaacgtgtccacagaca 47

RESULT 9  
US-60-278-561-11368/c  
; Sequence 11368, Application US/60278561  
; GENERAL INFORMATION:  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Lal, Preeti  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms Identified Thereby  
; FILE REFERENCE: GX-0012-1 P  
; CURRENT APPLICATION NUMBER: US/60/278,561  
; CURRENT FILING DATE: 2001-03-23  
; NUMBER OF SEQ ID NOS: 15598  
; SOFTWARE: PERL Program  
; SEQ ID NO 11368  
; LENGTH: 1699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 404459.1  
; NAME/KEY: unsure  
; LOCATION: 1105-1155  
; OTHER INFORMATION: a, t, c, g, or other  
US-60-278-561-11368

Query Match 72.2%; Score 16.6; DB 8; Length 1699;  
Best Local Similarity 82.6%; Pred. No. 70;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tcatctcgaaagcttccacagtc 23  
||| ||||| ||||| |||||  
Db 192 TCTTCTCGAAGGTTCTCGAGTCA 170

RESULT 10  
US-09-764-891-5493  
; Sequence 5493, Application US/09764891  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC006  
; CURRENT APPLICATION NUMBER: US/09/764,891  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 10231  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5493  
; LENGTH: 6058  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-891-5493

Query Match 72.2%; Score 16.6; DB 6; Length 6058;  
Best Local Similarity 82.6%; Pred. No. 84;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tcatctcgaaagcttccacagtc 23  
||||| ||| | |||||  
Db 3334 tcatgtcaagtggtccacagtc 3356

RESULT 11  
US-09-803-736-895/c  
; Sequence 895, Application US/09803736  
; GENERAL INFORMATION:  
; APPLICANT: Bush, David F.  
; APPLICANT: Levin, Irena M.  
; APPLICANT: Norris, Susan R.  
; APPLICANT: Rounsley, Steven D.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof  
; FILE REFERENCE: 38-10(15493)D  
; CURRENT APPLICATION NUMBER: US/09/803,736  
; CURRENT FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 09/534,859  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 1582  
; SEQ ID NO 895  
; LENGTH: 31309  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-803-736-895

Query Match 72.2%; Score 16.6; DB 6; Length 31309;  
Best Local Similarity 82.6%; Pred. No. 1e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattctgaaagcttccacagtca 23  
||||| ||||||| |||||||  
Db 31244 TCCTCGAACCTTCCACAGTCA 31222

RESULT 12  
US-09-803-736-823  
; Sequence 823, Application US/09803736  
; GENERAL INFORMATION:  
; APPLICANT: Bush, David F.  
; APPLICANT: Levin, Irena M.  
; APPLICANT: Norris, Susan R.  
; APPLICANT: Rounsley, Steven D.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof  
; FILE REFERENCE: 38-10(15493)D  
; CURRENT APPLICATION NUMBER: US/09/803,736  
; CURRENT FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 09/534,859  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 1582  
; SEQ ID NO 823  
; LENGTH: 60476  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-803-736-823

Query Match 72.2%; Score 16.6; DB 6; Length 60476;  
Best Local Similarity 82.6%; Pred. No. 1.1e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattctgaaagcttccacagtca 23  
||||| ||||||| |||||||  
Db 45102 tcattctgaaagcttccacagtca 45124

RESULT 13  
US-09-803-736-163  
; Sequence 163, Application US/09803736  
; GENERAL INFORMATION:  
; APPLICANT: Bush, David F.

; APPLICANT: Levin, Irena M.  
; APPLICANT: Norris, Susan R.  
; APPLICANT: Rounsley, Steven D.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof  
; FILE REFERENCE: 38-10(15493)D  
; CURRENT APPLICATION NUMBER: US/09/803,736  
; CURRENT FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 09/534,859  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 1582  
; SEQ ID NO 163  
; LENGTH: 116149  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-803-736-163

Query Match 72.2%; Score 16.6; DB 6; Length 116149;  
Best Local Similarity 82.6%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattctgaaagcttccacagtca 23  
||||| ||||||| |||||||  
Db 25124 tcattctgaaagcttccacagtca 25146

RESULT 14  
US-09-803-736-184/c  
; Sequence 184, Application US/09803736  
; GENERAL INFORMATION:  
; APPLICANT: Bush, David F.  
; APPLICANT: Levin, Irena M.  
; APPLICANT: Norris, Susan R.  
; APPLICANT: Rounsley, Steven D.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof  
; FILE REFERENCE: 38-10(15493)D  
; CURRENT APPLICATION NUMBER: US/09/803,736  
; CURRENT FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 09/534,859  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 1582  
; SEQ ID NO 184  
; LENGTH: 138181  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-803-736-184

Query Match 72.2%; Score 16.6; DB 6; Length 138181;  
Best Local Similarity 82.6%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattctgaaagcttccacagtca 23  
||||| ||||||| |||||||  
Db 91835 TAATCTCGAACCTTCCGAAGTCA 91813

RESULT 15  
US-60-253-378-24945  
; Sequence 24945, Application US/60253378  
; GENERAL INFORMATION:  
; APPLICANT: Havukkala, Ilkka J  
; TITLE OF INVENTION: Polynucleotides isolated from plants  
; FILE REFERENCE: 1054P3  
; CURRENT APPLICATION NUMBER: US/60/253,378  
; CURRENT FILING DATE: 2000-11-27

; NUMBER OF SEQ ID NOS: 40367  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24945  
; LENGTH: 136  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-60-253-378-24945

Query Match 70.4%; Score 16.2; DB 8; Length 136;  
Best Local Similarity 85.7%; Pred. No. 81;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctcgaaagttccacagtc 22  
||| ||||| |||||  
Db 2 catttgaacgttccaaagtc 22

Search completed: October 9, 2001, 21:36:13  
Job time: 21233 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:41:59 ; Search time 217.64 Seconds  
(without alignments)  
20,006 Million cell updates/sec

Title: US-09-713-136-3

Perfect score: 23

Sequence: 1 tcatctcgacgttcacagtca 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.2	70.4	6623	2	US-08-687-080-68
2	15.8	68.7	719	4	US-08-998-416-626
3	15.6	67.8	3641	1	US-08-030-098-5
4	15.2	66.1	321	4	US-09-060-758-260
5	15	65.2	2265	3	US-08-906-865-2
6	15	65.2	3383	3	US-08-884-324-12
7	15	65.2	11464	3	US-08-884-324-13
8	15	65.2	28994	3	US-08-884-324-14
9	14.6	63.5	836	4	US-08-998-416-316
10	14.6	63.5	1041	1	US-08-842-540-1
11	14.6	63.5	1041	1	US-08-842-540-3
12	14.6	63.5	1041	1	US-08-690-413-1
13	14.6	63.5	1041	1	US-08-690-413-3
14	14.6	63.5	1853	1	US-08-553-110-2
15	14.6	63.5	4279	4	US-09-041-888-22
16	14.4	62.6	2350	1	US-08-843-871-1
17	14.4	62.6	2350	1	US-09-012-821-1
18	14.2	61.7	816	3	US-08-776-251-10
19	14.2	61.7	816	3	US-08-776-251-10
20	14.2	61.7	1596	6	5180813-1
21	14.2	61.7	1893	3	US-08-878-474-10
22	14.2	61.7	2039	3	US-09-276-531-45
23	14	60.9	76	1	US-08-447-169A-90
24	14	60.9	76	1	US-08-447-169A-100
25	14	60.9	76	2	US-08-233-012C-90
26	14	60.9	76	2	US-08-233-012C-100
27	14	60.9	836	2	US-08-967-364-4

28	14	60.9	836	3	US-09-368-408-4	Sequence 4, Appl
29	14	60.9	1229	2	US-08-790-572-2	Sequence 2, Appl
30	14	60.9	1229	2	US-09-213-398-2	Sequence 2, Appl
31	14	60.9	1613	2	US-08-812-204-1	Sequence 1, Appl
32	14	60.9	3182	1	US-08-595-559-6	Sequence 6, Appl
33	14	60.9	4118	1	US-08-119-125A-3	Sequence 3, Appl
34	14	60.9	4615	2	US-08-674-351-3	Sequence 3, Appl
35	14	60.9	12847	1	US-08-550-715-1	Sequence 1, Appl
36	14	60.9	13146	2	US-08-724-334D-3	Sequence 3, Appl
37	14	60.9	13146	3	US-09-270-984A-3	Sequence 3, Appl
38	13.8	60.0	361	6	5304466-1	Patent No. 5304466
39	13.8	60.0	4649	6	5183745-1	Patent No. 5183745
40	13.8	60.0	6443	6	5183745-5	Patent No. 5183745
41	13.8	60.0	11561	1	US-08-450-332-1	Sequence 1, Appl
42	13.8	60.0	11561	2	US-08-637-640-1	Sequence 1, Appl
43	13.8	60.0	11561	4	US-09-004-406C-1	Sequence 1, Appl
44	13.6	59.1	63	3	US-07-921-104D-36	Sequence 36, Appl
45	13.6	59.1	77	1	US-08-447-169A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1  
US-08-687-080-68  
; Sequence 68, Application US/08687080  
; Patent No. 5965427  
; GENERAL INFORMATION:  
; APPLICANT: Gregory Dolganov  
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof  
; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,080  
; FILING DATE: 17-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/592,126  
; FILING DATE: 26-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 4600-0111.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6623 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: 3' END OF INTRON 5 OF RAD50 GENOMIC  
; INDIVIDUAL ISOLATE: SEQUENCE  
US-08-687-080-68

Query Match 70.4% Score 16.2; DB 2; Length 6623;

```
Best Local Similarity 85.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgttcacagt 21
   ||||| ||| ||||| |||
Db 587 TCATCTCTAACCTCCAGAGT 607

RESULT 2
US-08-998-416-626
; Sequence 626, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippson, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 626:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1423UP
; US-08-998-416-626

Query Match 68.7%; Score 15.8; DB 4; Length 719;
Best Local Similarity 89.5%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tcattcgaacgttcacaga 19
   ||||| ||| ||||| |||
Db 498 TCATCCCGCAGCTTCCACA 516

RESULT 3
US-08-030-096-5/c
; Sequence 5, Application US/08030096
; Patent No. 5426041
; GENERAL INFORMATION:
; APPLICANT: Fabijanski, Steven F.
; APPLICANT: Arnison, Paul G.
; TITLE OF INVENTION: BINARY CRYPTOCYTOTOXIC METHOD OF HYBRID
; TITLE OF INVENTION: SEED PRODUCTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,096
; FILING DATE: 22-MAR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/556,917
; FILING DATE: 20-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA91/00255
; FILING DATE: 22-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/164/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(854...1105, 1266...2375, 2463...2779)
; US-08-030-096-5

Query Match 67.8%; Score 15.6; DB 1; Length 3641;
Best Local Similarity 81.8%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattcgaacgttcacagtc 22
   ||| ||||| ||||| |||
Db 2611 TCAGACGAACGTTCCACATTC 2590

RESULT 4
US-09-060-756-260/c
; Sequence 260, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
```

NUMBER OF SEQ ID NOS: 743  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 260  
LENGTH: 321  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (various positions within the sequence)  
OTHER INFORMATION: applicants are uncertain of bases designated as "n"  
US-09-060-756-260

Query Match 66.1%; Score 15.2; DB 4; Length 321;  
Best Local Similarity 85.0%; Pred. No. 30;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tcattcgaacgttccacag 20  
|||||  
Db 87 TCATCTCGAAGCTCGCGCAG 68

RESULT 5  
US-08-906-865-2  
Sequence 2, Application US/08906865  
Patent No. 6040168  
GENERAL INFORMATION:  
APPLICANT: Greengard, Paul  
APPLICANT: Porton, Barbara  
APPLICANT: Kao, Hung-Teh  
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
CITY: Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906.865  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-202  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
DESCRIPTION: /desc = "Synapsin III"  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-906-865-2

Query Match 65.2%; Score 15; DB 3; Length 2265;  
Best Local Similarity 78.3%; Pred. No. 51;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 tcattcgaacgttccacagtca 23  
|||||  
Db 15 TCATCTCCATCCATCCACAGCCA 37

RESULT 6  
US-08-884-324-12/c  
Sequence 12, Application US/08884324  
Patent No. 6060283  
GENERAL INFORMATION:  
APPLICANT: Takanori OKURA  
APPLICANT: Kakuji TORIGOE  
APPLICANT: Masahito KURIMOTO  
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
OF INDUCING THE PRODUCTION OF INTERFERON-  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/884,324  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 185,305/96  
FILING DATE: 27-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: OKURA-1  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3383 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: human  
TISSUE TYPE: placenta  
FEATURE:  
NAME/KEY: Intron  
LOCATION: 1..3383  
IDENTIFICATION METHOD: E  
US-08-884-324-12

Query Match 65.2%; Score 15; DB 3; Length 3383;  
Best Local Similarity 78.3%; Pred. No. 54;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tcattcgaacgttccacagtca 23  
|||||  
Db 1499 TCCACTAGGACGTTCCACAGACA 1477

RESULT 7  
US-08-884-324-13/c  
Sequence 13, Application US/08884324

Patent No. 6060283  
GENERAL INFORMATION:  
APPLICANT: Takanori OKURA  
APPLICANT: Kakuji TORIGOE  
APPLICANT: Masahi KURIMOTO  
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
OF INDUCING THE PRODUCTION OF INTERFERON-  
B  
NUMBER OF SEQUENCES: 35  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/884,324  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 185,305/96  
FILING DATE: 27-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: OKURA-1  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11464 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORGANISM: human  
TISSUE TYPE: placenta  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..3  
IDENTIFICATION METHOD: E  
NAME/KEY: leader peptide  
LOCATION: 4..82  
IDENTIFICATION METHOD: S  
NAME/KEY: Intron  
LOCATION: 83..1453  
IDENTIFICATION METHOD: E  
NAME/KEY: leader peptide  
LOCATION: 1454..1465  
IDENTIFICATION METHOD: S  
NAME/KEY: Intron  
LOCATION: 1466..4848  
IDENTIFICATION METHOD: E  
NAME/KEY: leader peptide  
LOCATION: 4849..4865  
IDENTIFICATION METHOD: S  
NAME/KEY: mat peptide  
LOCATION: 4866..4983  
IDENTIFICATION METHOD: S  
NAME/KEY: Intron  
LOCATION: 4984..6317  
IDENTIFICATION METHOD: E  
NAME/KEY: mat peptide  
LOCATION: 6318..6451  
IDENTIFICATION METHOD: S  
NAME/KEY: Intron

LOCATION: 6452..11224  
IDENTIFICATION METHOD: E  
NAME/KEY: mat peptide  
LOCATION: 11225..11443  
IDENTIFICATION METHOD: S  
NAME/KEY: 3'UTR  
LOCATION: 11444..11464  
IDENTIFICATION METHOD: E  
US-08-884-324-13  
Query Match 65.3%; Score 15; DB 3; Length 11464;  
Best Local Similarity 78.3%; Pred. No. 66;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Caps 0;  
QY 1 tcactcgaacgttcacagtca 23  
DB 2964 TCCACTAGGACGTTCCACAGACA 2942  
RESULT 8  
US-08-884-324-14/c  
Sequence 14, Application US/08884324  
Patent No. 6060283  
GENERAL INFORMATION:  
APPLICANT: Takanori OKURA  
APPLICANT: Kakuji TORIGOE  
APPLICANT: Masahi KURIMOTO  
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
OF INDUCING THE PRODUCTION OF INTERFERON-  
B  
NUMBER OF SEQUENCES: 35  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/884,324  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 185,305/96  
FILING DATE: 27-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: OKURA-1  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28994 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORGANISM: human  
TISSUE TYPE: placenta  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: 1..15606  
IDENTIFICATION METHOD: E  
NAME/KEY: leader peptide  
LOCATION: 15607..15685





```

;
; NAME/KEY: CDS
; LOCATION: 1..1041
US-08-842-540-1

Query Match      63.5%; Score 14.6; DB 1; Length 1041;
Best Local Similarity 81.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 atctcgaacgttcacagtca 23
Db 92 ATTACGACCGTTTCACAGTCA 112

RESULT 11
US-08-842-540-3
; Sequence 3, Application US/08842540
; Patent No. 5776695
; GENERAL INFORMATION:
; APPLICANT: Skatrud, Paul L.
; TITLE OF INVENTION: Biosynthetic Gene DDL From Streptococcus
; TITLE OF INVENTION: Pneumoniae
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690.413
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10556
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1041 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1041
US-08-690-413-1

Query Match      63.5%; Score 14.6; DB 1; Length 1041;
Best Local Similarity 81.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 atctcgaacgttcacagtca 23
Db 92 ATTACGACCGTTTCACAGTCA 112

RESULT 13
US-08-690-413-3
; Sequence 3, Application US/08690413
; Patent No. 5776733
; GENERAL INFORMATION:
; APPLICANT: Skatrud, Paul L.
; TITLE OF INVENTION: Biosynthetic Gene DDL From Streptococcus
; TITLE OF INVENTION: Pneumoniae
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842.540
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10556
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1041 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-842-540-3

Query Match      63.58; Score 14.6; DB 1; Length 1041;
Best Local Similarity 61.9%; Pred. No. 73;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 3 atctcgaacgttcacagtca 23
Db 92 AUUACGACCGUUUCACAGUCA 112

RESULT 12
US-08-690-413-1
; Sequence 1, Application US/08690413
; Patent No. 5776733
; GENERAL INFORMATION:

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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/690,413  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Webster, Thomas D.  
;; REGISTRATION NUMBER: 39,872  
;; REFERENCE/DOCKET NUMBER: X-10556  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 317-276-3334  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1041 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: mRNA  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
US-08-690-413-3

Query Match 63.5%; Score 14.6; DB 1; Length 1041;  
Best Local Similarity 61.9%; Pred. No. 73;  
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 atctcgaaacgttcacagtc 23  
I: ||| |||: |||||: ||  
Db 92 AUACGACCGUUCACAGUCA 112

## RESULT 14

US-08-553-110-2  
; Sequence 2, Application US/08553110  
; Patent No. 5723301

;; GENERAL INFORMATION:  
;; APPLICANT: Burke, James R.  
;; APPLICANT: Vance, Jeffrey M.  
;; APPLICANT: Enghild, Jan  
;; TITLE OF INVENTION: Therapeutics for Diseases Associated  
;; TITLE OF INVENTION: with CAG Trinucleotide Repeat Expansion  
;; NUMBER OF SEQUENCES: 2  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Kenneth D. Sibley  
;; STREET: P.O. Drawer 34009  
;; CITY: Charlotte  
;; STATE: No. 5723301th Carolina  
;; COUNTRY: United States of America  
;; ZIP: 28234

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION NUMBER: US/08/553,110  
;; FILING DATE:

;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sibley, Kenneth D.  
;; REGISTRATION NUMBER: 31,665  
;; REFERENCE/DOCKET NUMBER: 5405-117  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 919-420-2200  
;; TELEFAX: 919-881-3175  
;; INFORMATION FOR SEQ ID NO: 2:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1853 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide

US-08-553-110-2

Query Match 63.5%; Score 14.6; DB 1; Length 1853;  
Best Local Similarity 81.0%; Pred. No. 80;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 catctcgaaacgttcacagtc 22  
||||||| ||||| ||  
Db 368 CATCTCGAATGTTCCAGGCTC 388

## RESULT 15

US-09-041-886-22  
; Sequence 22, Application US/09041886  
; Patent No. 6235872

;; GENERAL INFORMATION:  
;; APPLICANT: Bredesen, Dale E.  
;; APPLICANT: Rabizadeh, Sharroz  
;; TITLE OF INVENTION: Proapoptotic Peptides, Dependence  
;; TITLE OF INVENTION: Polypeptides and Methods of Use  
;; NUMBER OF SEQUENCES: 72  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Campbell & Flores LLP  
;; STREET: 4370 La Jolla Village Drive, Suite 700  
;; CITY: San Diego

;; STATE: California  
;; COUNTRY: United States  
;; ZIP: 92122  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION NUMBER: US/09/041,886  
;; FILING DATE:

;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 2626  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 22:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4279 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 239..3794

US-09-041-886-22

Query Match 63.5%; Score 14.6; DB 4; Length 4279;  
Best Local Similarity 81.0%; Pred. No. 91;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 catctcgaaacgttcacagtc 22  
||||||| ||||| ||  
Db 843 CATCTCGAATGTTCCAGGCTC 863

Search completed: October 9, 2001, 15:42:02  
Job time: 292 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:18:53 ; Search time 2150.93 Seconds  
(without alignments)  
158.206 Million cell updates/sec

Title: US-09-713-136-4  
Perfect score: 22  
Sequence: 1 tgactgtgaacgttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

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GenEmbl:
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2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
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8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
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38: em_hum5:*
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42: em_om:*
43: em_or:*

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46: em_ph:*
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57: gb_un:*
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59: gb_v12:*
60: gb_htg1:*
61: gb_htg2:*
62: gb_htg3:*
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90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	9 AX036946	AX036946 Sequence
2	22	100.0	22	10 AX083678	AX083678 Sequence
3	21	95.5	22	10 AX083680	AX083680 Sequence
4	20.4	92.7	22	9 AX036945	AX036945 Sequence
5	20.4	92.7	22	9 AX046993	AX046993 Sequence
6	20.4	92.7	22	10 AX083675	AX083675 Sequence
7	19.4	88.2	22	10 AX083681	AX083681 Sequence
8	19.4	88.2	145939	79 AL158143	AL158143 Homo sapi

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9 18.8 85.5 22 9 AX036952
10 18.8 85.5 22 10 AX083676
11 18.4 83.6 22 10 AX083682
12 17.8 80.9 4334 85 AB033099
13 17.8 80.9 74992 74 AC069574
14 17.8 80.9 74992 74 AC069574
15 17.8 80.9 109120 79 AL157945
16 17.8 80.9 110762 81 AL391244
17 17.8 80.9 165010 93 HSD3839B4
18 17.8 80.9 186529 73 AC068363
19 17.8 80.9 197748 70 AC026283
20 17.8 80.9 197748 70 AC026283
21 17.4 79.1 108055 61 AC009521
22 17.4 79.1 168601 86 AC008123
23 17.4 79.1 169423 74 AC069309
24 17.4 79.1 169532 62 AC012513
25 17.2 78.2 22 9 AX036944
26 17.2 78.2 13302 1 AE001695
27 17.2 78.2 16854 1 AE001722
28 17.2 78.2 103785 13 ATE1116
29 17.2 78.2 146851 71 AC027697
30 17.2 78.2 152318 66 AC021766
31 17.2 78.2 158786 68 AC023337
32 17.2 78.2 166229 81 AL512601
33 17.2 78.2 190866 64 AC015954
34 17.2 78.2 193071 74 AC069535
35 17.2 78.2 193167 94 AC026767
36 17.7 77.3 7131 14 PPMASAS
37 16.8 76.4 1754 4 AB029058
38 16.8 76.4 102798 78 AL138730
39 16.8 76.4 111234 88 AC079157
40 16.8 76.4 135714 90 AL160037
41 16.8 76.4 142172 69 AC025957
42 16.8 76.4 151992 61 AC009939
43 16.8 76.4 153241 88 AC023510
44 16.8 76.4 157996 94 AC019026
45 16.8 76.4 159072 74 AC073123
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## ALIGNMENTS

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RESULT 1
AX036946
LOCUS AX036946 22 bp DNA
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION AX036946
VERSION AX036946.1 GI:11226374
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodeoxynucleotide"
6 a 4 c 6 g
BASE COUNT 6 a 4 c 6 g
ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
Oy 1 tgactgtgaacgttcacatga 22
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Db 1 TGACTGTGAACGTTCCAGATGA 22
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AX036952
LOCUS AX036952 22 bp DNA
DEFINITION Sequence 4 from Patent WO0112223.
ACCESSION AX036952
VERSION AX036952.1 GI:13185410
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Patent: WO 0112223-A 4 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 4 c 6 g
BASE COUNT 6 a 4 c 6 g
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Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
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|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22
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AX083676
LOCUS AX083676 22 bp DNA
DEFINITION Sequence 4 from Patent WO0112223.
ACCESSION AX083676
VERSION AX083676.1 GI:13185410
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Patent: WO 0112223-A 4 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 4 c 6 g
BASE COUNT 6 a 4 c 6 g
ORIGIN
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
Oy 1 tgactgtgaacgttcacatga 22
|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22
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AX083680
LOCUS AX083680 22 bp DNA
DEFINITION Sequence 6 from Patent WO0112223.
ACCESSION AX083680
VERSION AX083680.1 GI:13185412
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Patent: WO 0112223-A 6 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5-bromocytosine"
6 a 3 c 6 g 1 others
BASE COUNT 6 a 3 c 6 g 1 others
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Best Local Similarity 95.5%; Pred. No. 2.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0:
Oy 1 tgactgtgaacgttcacatga 22
|||||
Db 1 TGACTGTGAANGTTCCAGATGA 22
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AX036945
LOCUS AX036945 22 bp DNA
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226374
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
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source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodeoxynucleotide"
6 a 4 c 6 g
BASE COUNT 6 a 4 c 6 g
ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
Oy 1 tgactgtgaacgttcacatga 22
|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22
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LOCUS AX036945 22 bp DNA 16-NOV-2000  
DEFINITION Sequence 2 from Patent FR2790955.  
ACCESSION AX036945  
VERSION AX036945.1 GI:11226373  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequence.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Carpentier A.  
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;  
ASSIST PUBL HOPITAUX DE PARIS (FR)  
FEATURES Location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="oligodeoxynucleotide"  
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Query Match 92.7%; Score 20.4; DB 9; Length 22;  
Best Local Similarity 95.5%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaacggtccagatga 22  
|||||  
Db 1 TGAAGTGAACGTTTCGAGATGA 22  
RESULT 5  
AX046993  
LOCUS AX046993 22 bp DNA 15-DEC-2000  
DEFINITION Sequence 2 from Patent WO0067787.  
ACCESSION AX046993  
VERSION AX046993.1 GI:11876420  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequence.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Moss, R.B.  
JOURNAL HIV Immunogenic compositions and methods  
THE IMMUNE RESPONSE CORPORATION (US)  
FEATURES Location/Qualifiers  
source 1..22  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="phosphorothioate-modified synthetic oligodeoxynucleotide"  
BASE COUNT 6 a 3 c 7 g 6 t  
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Query Match 92.7%; Score 20.4; DB 9; Length 22;  
Best Local Similarity 95.5%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaacggtccagatga 22  
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Db 1 TGAAGTGAACGTTTCGAGATGA 22  
RESULT 6  
AX083675  
LOCUS AX083675 22 bp DNA 28-FEB-2001  
DEFINITION Sequence 1 from Patent WO0112223.  
ACCESSION AX083675  
VERSION AX083675.1 GI:13185407  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM

artificial sequence.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS van Nest, G.  
TITLE Methods of modulating an immune response using immunostimulatory sequences and compositions for use therein  
JOURNAL Patent: WO 0112223-A 1 22-FEB-2001;  
Dynavax Technologies Corporation (US)  
FEATURES Location/Qualifiers  
source 1..22  
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BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN  
Query Match 92.7%; Score 20.4; DB 10; Length 22;  
Best Local Similarity 95.5%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaacggtccagatga 22  
|||||  
Db 1 TGAAGTGAACGTTTCGAGATGA 22  
RESULT 7  
AX083681  
LOCUS AX083681 22 bp DNA 28-FEB-2001  
DEFINITION Sequence 7 from Patent WO0112223.  
ACCESSION AX083681  
VERSION AX083681.1 GI:13185413  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequence.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS van Nest, G.  
TITLE Methods of modulating an immune response using immunostimulatory sequences and compositions for use therein  
JOURNAL Patent: WO 0112223-A 7 22-FEB-2001;  
Dynavax Technologies Corporation (US)  
FEATURES Location/Qualifiers  
source 1..22  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="5-bromocytosine"  
BASE COUNT 6 a 2 c 7 g 6 t 1 others  
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Query Match 88.2%; Score 19.4; DB 10; Length 22;  
Best Local Similarity 90.9%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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|||||  
Db 1 TGAAGTGAACGTTTCGAGATGA 22  
RESULT 8  
AL158143  
LOCUS AL158143 145939 bp DNA HTG 08-APR-2001  
DEFINITION Homo sapiens chromosome X clone RP5-1074I8, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 17 unordered pieces.  
ACCESSION AL158143  
VERSION AL158143.12 GI:13567909  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 145939)  
Mclay, K.  
Direct Submission  
Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On Apr 9, 2001 this sequence version replaced gi:9931672.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: dj107418  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: pBlasmid; L08752; 100% of reads  
Chemistry: Dye-terminator ET-amersham; 7% of reads Chemistry:  
Dye-terminator Big Dye; 92% of reads  
Consensus quality: 137464 bases at least Q40  
Consensus quality: 141229 bases at least Q30  
Consensus quality: 143037 bases at least Q20  
Insert size: 144339; sum-of-contigs  
Insert size: 111741; 30.4% error; agarose-fp  
Quality coverage: 6.03x in Q20 bases; sum-of-contigs Quality  
coverage: 9.27x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 17 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
\* 3025 3124: gap of 100 bp  
\* 3125 10834: contig of 7710 bp in length  
\* 10835 10934: gap of 100 bp  
\* 10935 13595: contig of 2661 bp in length  
\* 13596 13695: gap of 100 bp  
\* 13696 16092: contig of 2397 bp in length  
\* 16093 16192: gap of 100 bp  
\* 16193 22530: contig of 6338 bp in length  
\* 22531 22630: gap of 100 bp  
\* 22631 27253: contig of 4623 bp in length  
\* 27254 27353: gap of 100 bp  
\* 27354 30261: contig of 2908 bp in length  
\* 30262 30361: gap of 100 bp  
\* 30362 33611: contig of 3250 bp in length  
\* 33612 33711: gap of 100 bp  
\* 33712 38262: contig of 4551 bp in length  
\* 38263 38362: gap of 100 bp  
\* 38363 40615: contig of 2253 bp in length  
\* 40616 40715: gap of 100 bp  
\* 40716 44299: contig of 3584 bp in length  
\* 44300 44399: gap of 100 bp  
\* 44400 47229: contig of 2830 bp in length  
\* 47230 47329: gap of 100 bp  
\* 47330 52776: contig of 5447 bp in length  
\* 52777 52876: gap of 100 bp  
\* 52877 60226: contig of 7350 bp in length  
\* 60227 60326: gap of 100 bp  
\* 60327 62930: contig of 2604 bp in length  
\* 62931 63030: gap of 100 bp  
\* 63031 67418: contig of 4389 bp in length  
\* 67420 67519: gap of 100 bp  
\* 67520 145939: contig of 78420 bp in length.  
Location/Qualifiers  
1. 145939

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="X"

/clone="RP5-107418"  
/clone\_lib="rpci-5"  
1. 3024  
/note="assembly\_fragment:00567  
vector\_end:SP6  
vector\_side:left"  
3125. 10834  
/note="assembly\_fragment:00921  
fragment\_chain:1"  
10935. 13595  
/note="assembly\_fragment:01789  
fragment\_chain:1"  
13696. 16092  
/note="assembly\_fragment:01424  
fragment\_chain:2"  
16193. 22530  
/note="assembly\_fragment:01022  
fragment\_chain:2"  
22631. 27253  
/note="assembly\_fragment:00011"  
27354. 30261  
/note="assembly\_fragment:00127"  
30362. 33611  
/note="assembly\_fragment:00247"  
33712. 38262  
/note="assembly\_fragment:00335"  
38363. 40615  
/note="assembly\_fragment:00495"  
40716. 44299  
/note="assembly\_fragment:00561"  
44400. 47229  
/note="assembly\_fragment:00700"  
47330. 52776  
/note="assembly\_fragment:00832"  
52877. 60226  
/note="assembly\_fragment:00912"  
60327. 62930  
/note="assembly\_fragment:01119"  
63031. 67419  
/note="assembly\_fragment:01935"  
67520. 145939  
/note="assembly\_fragment:02239"  
BASE COUNT 45121 a 27951 c 28095 g 43161 t 1611 others  
ORIGIN

Query Match 88.28; Score 19.4; DB 79; Length 145939;  
Best Local Similarity 95.2%; Pred. No. 19;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttccagatga 22  
||||||| |||||||  
Db 37628 GACTGTGAATGTTCCAGATGA 37648

RESULT 9  
LOCUS AX036952 22 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 9 from Patent FR2790955.  
ACCESSION AX036952  
VERSION AX036952.1 GI:11226380  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct.  
synthetic construct  
artificial sequence.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Carpentier, A.  
JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;  
ASSIST PUBL HOPITAUX DE PARIS (FR)  
FEATURES  
source  
1. 22  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 7 a 2 c 6 g 7 t  
 ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 35;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttccagatga 22  
 ||||| ||||| ||||| |||||  
 Db 1 TGACTGTGAACGTTATAGATGA 22

## RESULT 10

AX083676 22 bp DNA PAT 28-FEB-2001  
 LOCUS  
 DEFINITION Sequence 2 from Patent WO0112223.  
 ACCESSION AX083676  
 VERSION AX083676.1 GI:13185408  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS van Nest,G.  
 TITLE Methods of modulating an immune response using immunostimulatory s  
 JOURNAL sequences and compositions for use therein  
 Patent: WO 011223-A 2 22-FEB-2001;  
 Dynavax Technologies Corporation (US)  
 FEATURES Location/Qualifiers  
 source 1..22  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Synthetic construct" 5 t

BASE COUNT 6 a 4 c 7 g  
 ORIGIN

Query Match 85.5%; Score 18.8; DB 10; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 35;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttccagatga 22  
 ||||| ||||| ||||| |||||  
 Db 1 TGACCGTGAACGTTTCGAGATGA 22

## RESULT 11

AX083682 22 bp DNA PAT 28-FEB-2001  
 LOCUS  
 DEFINITION Sequence 8 from Patent WO0112223.  
 ACCESSION AX083682  
 VERSION AX083682.1 GI:13185414  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS van Nest,G.  
 TITLE Methods of modulating an immune response using immunostimulatory s  
 JOURNAL sequences and compositions for use therein  
 Patent: WO 011223-A 8 22-FEB-2001;  
 Dynavax Technologies Corporation (US)  
 FEATURES Location/Qualifiers  
 source 1..22  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="5-bromocytosine" 11  
 modified\_base 15  
 /mod\_base="OTHER"  
 modified\_base 15  
 /note="5-bromocytosine"

BASE COUNT 6 a 1 c 7 g 6 t 2 others  
 ORIGIN

Query Match 83.6%; Score 18.4; DB 10; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 57;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttccagatga 22  
 ||||| ||||| ||||| |||||  
 Db 1 TGACTGTGAANGTTNGAGATGA 22

## RESULT 12

AB033099/c 4334 bp mRNA PRI 11-NOV-1999  
 LOCUS  
 DEFINITION Homo sapiens mRNA for KIAA1273 protein, partial cds.  
 ACCESSION AB033099  
 VERSION AB033099.1 GI:6382027  
 KEYWORDS  
 SOURCE Homo sapiens brain cDNA to mRNA, clone\_lib:pBluescriptII SK plus  
 clone:hK09394.  
 ORGANISM  
 REFERENCE 1 (sites)  
 AUTHORS Ohara,O., Ishikawa,K., Kikuno,R., Hirose,M., Nomura,N. and  
 Nagase,T.,  
 TITLE Prediction of the coding sequences of unidentified human genes. XV.  
 The complete sequences of 100 new cDNA clones from brain which code  
 for large proteins in vitro  
 JOURNAL DNA Res. 6 (5), 337-345 (1999)  
 MEDLINE 20039619  
 REFERENCE 2 (bases 1 to 4334)  
 AUTHORS Ohara,O., Nagase,T. and Kikuno,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-OCT-1999) to the DDBJ/EMBL/GenBank databases. Osamu  
 Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology;  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:cdna@info.kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/,  
 Tel:++81-438-52-3913, Fax:++81-438-52-3914)

FEATURES  
 source 1..4334  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="hK09394"  
 /clone\_lib="pBluescriptII SK plus"  
 /tissue\_type="brain"  
 463..2283  
 /gene="KIAA1273"  
 <463..2283  
 /gene="KIAA1273"  
 /note="Start codon is not identified."  
 /codon\_start=1  
 /product="KIAA1273 protein"  
 /protein\_id="BAA86587.1"  
 /db\_xref="GI:6382028"

gene

CDS

BASE COUNT 860 a 1275 c 1363 g 836 t  
 ORIGIN



```

Query Match      80.9%; Score 17.8; DB 85; Length 4334;
Best Local Similarity 90.5%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgcactgtgacaggtccagatg 21
    ||||| | |||||
Db 3337 TGACTGTGACAGGTCCAGATG 3317

RESULT 13
AC069574 74992 bp DNA HTG 03-JUN-2000
LOCUS Homo sapiens chromosome 4 clone RP11-267H10 map 4, LOW-PASS
SEQUENCE SAMPLING.
AC069574
VERSION AC069574.1 GI:8225556
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74992)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campoliano,A., Castelle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,K., Jones,C., Kann,L., Karatas,A.,
Klein,J., Laroque,K., Lamazares,R., Landers,T., Lehoczkzy,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (03-JUN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W18R
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L9895
Center clone name: 267_H_10
-----
* NOTE: This record contains 86 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

```

```

* 32171 32270: gap of 100 bp
* 32271 33039: contig of 769 bp in length
* 33040 33139: gap of 100 bp
* 33140 33913: contig of 774 bp in length
* 33914 34013: gap of 100 bp
* 34014 34795: contig of 782 bp in length
* 34796 34895: gap of 100 bp
* 34896 35664: contig of 769 bp in length
* 35665 35764: gap of 100 bp
* 35765 36518: contig of 754 bp in length
* 36519 36618: gap of 100 bp
* 36619 37380: contig of 762 bp in length
* 37381 37480: gap of 100 bp
* 37481 38255: contig of 775 bp in length
* 38256 38355: gap of 100 bp
* 38356 39130: contig of 775 bp in length
* 39131 39230: gap of 100 bp
* 39231 40008: contig of 778 bp in length
* 40009 40108: gap of 100 bp
* 40109 40880: contig of 772 bp in length
* 40881 40980: gap of 100 bp
* 40981 41764: contig of 784 bp in length
* 41765 41864: gap of 100 bp
* 41865 42636: contig of 772 bp in length
* 42637 42736: gap of 100 bp
* 42737 43501: contig of 765 bp in length
* 43502 43601: gap of 100 bp
* 43602 44371: contig of 770 bp in length
* 44372 44471: gap of 100 bp
* 44472 45253: contig of 782 bp in length
* 45254 45353: gap of 100 bp
* 45354 46125: contig of 772 bp in length
* 46126 46225: gap of 100 bp
* 46226 46999: contig of 774 bp in length
* 47000 47099: gap of 100 bp
* 47100 47864: contig of 765 bp in length
* 47865 47964: gap of 100 bp
* 47965 48747: contig of 783 bp in length
* 48748 48847: gap of 100 bp
* 48848 49618: contig of 771 bp in length
* 49619 49718: gap of 100 bp
* 49719 50525: contig of 807 bp in length
* 50526 50625: gap of 100 bp
* 50626 51401: contig of 776 bp in length
* 51402 51501: gap of 100 bp
* 51502 52267: contig of 766 bp in length
* 52268 52367: gap of 100 bp
* 52368 53155: contig of 788 bp in length
* 53156 53255: gap of 100 bp
* 53256 54024: contig of 769 bp in length
* 54025 54124: gap of 100 bp
* 54125 54904: contig of 780 bp in length
* 54905 55004: gap of 100 bp
* 55005 55795: contig of 791 bp in length
* 55796 55895: gap of 100 bp
* 55896 56653: contig of 757 bp in length
* 56653 56752: gap of 100 bp
* 56753 57525: contig of 773 bp in length
* 57526 57625: gap of 100 bp
* 57626 58402: contig of 777 bp in length
* 58403 58502: gap of 100 bp
* 58503 59282: contig of 780 bp in length
* 59283 59382: gap of 100 bp
* 59383 60160: contig of 778 bp in length
* 60161 60260: gap of 100 bp

```

```

Query Match      80.98; Score 17.8; DB 74; Length 74992;
Best Local Similarity 90.5%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```
Oy 2 gactgtgaacgtctccagatga 22
|||||||

```

```
Db 12039 GACTGTGAACATTCACAGATAA 12059

```

# RESULT 14 AC069574/c

## LOCUS DEFINITION

Homo sapiens chromosome 4 clone RP11-267H10 map 4, LOW-PASS  
SEQUENCE SAMPLING.

## ACCESSION VERSION

AC069574.1 GI:8225556

## KEYWORDS SOURCE

HTG; HTGS\_PHASE0.  
human.

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 74992)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,

Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehotzky, J.,

Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marguis, N.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,

Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,

Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,

Young, G., Zainoun, J., Zimmer, A. and Zody, M.

## TITLE JOURNAL

Submitted (03-JUN-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

## COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

Center project name: L9895

Center clone name: 267\_H\_10

\* NOTE: This record contains 86 individual

\* sequencing reads that have not been assembled into

\* contigs. Runs of N are used to separate the reads

\* and the order in which they appear is completely

\* arbitrary. Low-pass sequence sampling is useful for

\* identifying clones that may be gene-rich and allows

\* overlap relationships among clones to be deduced.

\* However, it should not be assumed that this clone

\* will be sequenced to completion. In the event that

\* the record is updated, the accession number will

\* be preserved.

\* 1 784: contig of 784 bp in length

\* 785 884: gap of 100 bp

\* 885 1672: contig of 788 bp in length

\* 1673 1772: gap of 100 bp

\* 1773 2548: contig of 776 bp in length

\* 2549 2648: gap of 100 bp

\* 2649 3432: contig of 784 bp in length

AC069574 74992 bp DNA HTG 03-JUN-2000  
Homo sapiens chromosome 4 clone RP11-267H10 map 4, LOW-PASS  
SEQUENCE SAMPLING.

AC069574.1 GI:8225556  
HTG; HTGS\_PHASE0.  
human.

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74992)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 4, clone RP11-267H10  
Unpublished

2 (bases 1 to 74992)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,  
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S.,  
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehotzky, J.,  
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marguis, N.,  
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (03-JUN-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu  
Center project name: L9895  
Center clone name: 267\_H\_10

\* NOTE: This record contains 86 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads

\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows

\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that

\* the record is updated, the accession number will  
\* be preserved.

\* 1 784: contig of 784 bp in length  
\* 785 884: gap of 100 bp  
\* 885 1672: contig of 788 bp in length

\* 1673 1772: gap of 100 bp  
\* 1773 2548: contig of 776 bp in length  
\* 2549 2648: gap of 100 bp  
\* 2649 3432: contig of 784 bp in length

```
* 3433 3532: gap of 100 bp
* 3533 4305: contig of 773 bp in length
* 4306 4405: gap of 100 bp
* 4406 5157: contig of 752 bp in length
* 5158 5257: gap of 100 bp
* 5258 6018: contig of 761 bp in length
* 6019 6118: gap of 100 bp
* 6119 6891: contig of 773 bp in length
* 6892 6991: gap of 100 bp
* 6992 7756: contig of 765 bp in length
* 7757 7856: gap of 100 bp
* 7857 8620: contig of 764 bp in length
* 8621 8720: gap of 100 bp
* 8721 9505: contig of 785 bp in length
* 9506 9605: gap of 100 bp
* 9606 10384: contig of 779 bp in length
* 10385 10484: gap of 100 bp
* 10485 11254: contig of 770 bp in length
* 11255 11354: gap of 100 bp
* 11355 12129: contig of 775 bp in length
* 12130 12229: gap of 100 bp
* 12230 13000: contig of 771 bp in length
* 13001 13100: gap of 100 bp
* 13101 13865: contig of 765 bp in length
* 13866 14736: contig of 771 bp in length
* 14737 14836: gap of 100 bp
* 14837 15571: contig of 735 bp in length
* 15572 15671: gap of 100 bp
* 15672 16429: contig of 758 bp in length
* 16430 16529: gap of 100 bp
* 16530 17310: contig of 781 bp in length
* 17311 17410: gap of 100 bp
* 17411 18185: contig of 775 bp in length
* 18186 18285: gap of 100 bp
* 18286 19057: contig of 772 bp in length
* 19058 19157: gap of 100 bp
* 19158 19932: contig of 775 bp in length
* 19933 20032: gap of 100 bp
* 20033 20809: contig of 777 bp in length
* 20810 20909: gap of 100 bp
* 20910 21678: contig of 769 bp in length
* 21679 21778: gap of 100 bp
* 21779 22561: contig of 783 bp in length
* 22562 22661: gap of 100 bp
* 22662 23431: contig of 770 bp in length
* 23432 23531: gap of 100 bp
* 23532 24314: contig of 783 bp in length
* 24315 24414: gap of 100 bp
* 24415 25199: contig of 785 bp in length
* 25200 25299: gap of 100 bp
* 25300 26057: contig of 758 bp in length
* 26058 26157: gap of 100 bp
* 26158 26919: contig of 762 bp in length
* 26920 27019: gap of 100 bp
* 27020 27795: contig of 776 bp in length
* 27796 27895: gap of 100 bp
* 27896 28659: contig of 764 bp in length
* 28660 28759: gap of 100 bp
* 28760 29545: contig of 786 bp in length
* 29546 29645: gap of 100 bp
* 29646 30428: contig of 782 bp in length
* 30429 30527: gap of 100 bp
* 30528 31300: contig of 773 bp in length
* 31301 31400: gap of 100 bp
* 31401 32170: contig of 770 bp in length
* 32171 32270: gap of 100 bp
* 32271 33039: contig of 769 bp in length
* 33040 33139: gap of 100 bp
* 33140 33913: contig of 774 bp in length
* 33914 34013: gap of 100 bp
* 34014 34795: contig of 782 bp in length
* 34796 34895: gap of 100 bp
```

```
* 34896 35664: contig of 769 bp in length
* 35665 35764: gap of 100 bp
* 35765 36518: contig of 754 bp in length
* 36519 36618: gap of 100 bp
* 36619 37380: contig of 762 bp in length
* 37381 37480: gap of 100 bp
* 37481 38255: contig of 775 bp in length
* 38256 38355: gap of 100 bp
* 38356 39130: contig of 775 bp in length
* 39131 39230: gap of 100 bp
* 39231 40008: contig of 778 bp in length
* 40009 40108: gap of 100 bp
* 40109 40880: contig of 772 bp in length
* 40881 40980: gap of 100 bp
* 40981 41764: contig of 784 bp in length
* 41765 41864: gap of 100 bp
* 41865 42636: contig of 772 bp in length
* 42637 42736: gap of 100 bp
* 42737 43501: contig of 765 bp in length
* 43502 43601: gap of 100 bp
* 43602 44371: contig of 770 bp in length
* 44372 44471: gap of 100 bp
* 44472 45253: contig of 782 bp in length
* 45254 45353: gap of 100 bp
* 45354 46125: contig of 772 bp in length
* 46126 46225: gap of 100 bp
* 46226 46999: contig of 774 bp in length
* 47000 47099: gap of 100 bp
* 47100 47864: contig of 765 bp in length
* 47865 47964: gap of 100 bp
* 47965 48747: contig of 783 bp in length
* 48748 48847: gap of 100 bp
* 48848 49618: contig of 771 bp in length
* 49619 49718: gap of 100 bp
* 49719 50525: contig of 807 bp in length
* 50526 50625: gap of 100 bp
* 50626 51401: contig of 776 bp in length
* 51402 51501: gap of 100 bp
* 51502 52267: contig of 766 bp in length
* 52268 52367: gap of 100 bp
* 52368 53155: contig of 788 bp in length
* 53156 53255: gap of 100 bp
* 53256 54024: contig of 769 bp in length
* 54025 54124: gap of 100 bp
* 54125 54904: contig of 780 bp in length
* 54905 55004: gap of 100 bp
* 55005 55795: contig of 791 bp in length
* 55796 55895: gap of 100 bp
* 55896 56652: contig of 757 bp in length
* 56653 56752: gap of 100 bp
* 56753 57525: contig of 773 bp in length
* 57526 57625: gap of 100 bp
* 57626 58402: contig of 777 bp in length
* 58403 58502: gap of 100 bp
* 58503 59282: contig of 780 bp in length
* 59283 59382: gap of 100 bp
* 59383 60160: contig of 778 bp in length
* 60161 60260: gap of 100 bp
```

Query Match 80.9%; Score 17.8; DB 74; Length 74992;  
Best Local Similarity 90.5%; Pred. No. 1.3e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaacgttccagatga 22

||||||| ||||| |

Db 57162 GACTGTGAACATTCAGATAA 57142

RESULT 15

AL157945

LOCUS

DEFINITION

AL157945 109120 bp DNA

Homo sapiens chromosome 1 clone RP4-628J24 map p36.31-36.33, \*\*\*

SEQUENCING IN PROGRESS \*\*\*, 2 unordered pieces.

HTG

08-APR-2001

ACCESSION: AL157945  
VERSION: AL157945.15 GI:11610971  
KEYWORDS: HTG; HTGS\_PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE: human.  
ORGANISM: Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 109120)  
Frankland, J.  
Direct Submission  
Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk  
On Dec 9, 2000 this sequence version replaced gi:11414491.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: DJ628J24  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: M13; M7815; 1% of reads  
Sequencing vector: plasmid; L08752; 98% of reads  
Chemistry: Dye-terminator ABI; 1% of reads  
Chemistry: Dye-terminator Big Dye; 79% of reads  
Chemistry: Dye-terminator ET-amersham; 18% of reads  
Quality: 108774 bases at least Q40  
Consensus quality: 108884 bases at least Q30  
Consensus quality: 108962 bases at least Q20  
Insert size: 109020; sum-of-contigs  
Insert size: 109409; 10.4% error; agarose-fp  
Quality coverage: 10.62x in Q20 bases; sum-of-contigs Quality  
coverage: 10.72x in Q20 bases; agarose-fp  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 25559: contig of 25559 bp in length  
\* 25360 25659: gap of 100 bp  
\* 25660 109120: contig of 83461 bp in length.  
FEATURES  
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1..109120  
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/chromosome="1"  
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/clone\_lib="RPCI-4"  
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/note="assembly\_fragment:00655"  
misc\_feature  
25660..109120  
/note="assembly\_fragment:03347"  
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vector\_side:right  
23801 a 31255 c 31398 g 22566 t 100 others  
ORIGIN

Query Match 80.9% Score 17.8; DB 79; Length 109120;  
Best Local Similarity 90.5% Pred. No. 1.1e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 tgactgtgacgttccagatg 21  
|||||||  
Db 69219 TGACTGTGCAGTTCACATG 69239

Search completed: October 9, 2001, 16:19:04  
Job time: 2514 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:16 ; Search time 6788.49 seconds  
(without alignments)  
30.635 Million cell updates/sec

Title: US-09-713-136-4  
Perfect score: 22  
Sequence: 1 tgactgtgaacgttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*  
10: gb\_est10: \*  
11: gb\_est11: \*  
12: gb\_est12: \*  
13: gb\_est13: \*  
14: gb\_est14: \*  
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256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	88.2	961	172	BF971856 602240444
2	18.4	83.6	105	2	AA094019 cl1619.se
3	17.8	80.9	401	165	BE275964 601120704
4	17.8	80.9	441	22	AI597068 vj44e09.x
5	17.8	80.9	457	166	BE367478 P11_8_F04
6	17.8	80.9	473	188	R83554 Yq12d03.r1
7	17.8	80.9	514	240	AZ265882 RPCI-23-1
8	17.8	80.9	537	118	AW610890 un13e10.y
9	17.8	80.9	542	107	AU017198 AU017198
10	17.8	80.9	555	165	BE284315 601807423
11	17.8	80.9	563	173	BG070885 H3091D05-
12	17.8	80.9	572	248	AZ699837 RPCI-23-2
13	17.8	80.9	615	117	AW564152 LGL_285.H
14	17.8	80.9	666	137	BE582546 1-10C-WY
15	17.8	80.9	681	175	BG295408 602392719
16	17.8	80.9	705	145	BF178492 601807652
17	17.8	80.9	792	150	BF582440 602094391
18	17.8	80.9	803	235	AQ876162 V152A11.m
19	17.2	78.2	478	236	AQ966996 LERIN76TR
20	17.2	78.2	528	138	BE676474 7f30C08.X
21	17.2	78.2	602	104	AI996030 701549720
22	17.2	78.2	664	256	B77405 T31A1TFC.TA
23	17.2	78.2	669	256	B77406 T31A2TFC.TA
24	17.2	78.2	672	153	BG454943 NF110G04L
25	17.2	78.2	688	247	AZ644355 LM0508G15
26	17.2	78.2	996	220	CNS027GD Tetraodon
27	17.2	78.2	1021	222	CNS055HF Tetraodon
28	17.2	78.2	1061	221	CNS03DC2 Tetraodon
29	16.8	76.4	384	103	AI898251 EST267694
30	16.8	76.4	472	256	AZ930534 474_dh255
31	16.8	76.4	526	245	AZ501799 LM0340J17
32	16.8	76.4	531	256	AZ930854 474_dh259
33	16.8	76.4	559	21	AI489944 EST248283
34	16.8	76.4	801	234	AQ858141 nbe00012G
35	16.8	76.4	1228	144	BF128350 601810203
36	16.4	74.5	214	246	AZ578289 21b05.Sho
37	16.4	74.5	240	2	AA102862 mo10f10.r
38	16.4	74.5	373	14	AI006564 uc14405.Y
39	16.4	74.5	457	146	BF270840 GA_Eb000
40	16.4	74.5	500	155	BG578016 df04b10.Y
41	16.4	74.5	534	256	B75188 RPCI11-13P4
42	16.4	74.5	595	230	AQ383172 RPCI-11-4
43	16.4	74.5	675	106	AL583992 AL583992
44	16.4	74.5	980	218	AF075829 AF075829
45	16.2	73.6	150	31	AV626891 AV626891

ALIGNMENTS

RESULT	1
BF971856	BF971856 961 bp mRNA 22-JAN-2001
LOCUS	602240444F1 NIH_MGC_46 Homo sapiens cdna clone IMAGE:4328890 5', mRNA sequence.
DEFINITION	BF971856
ACCESSION	BF971856
VERSION	EST.
KEYWORDS	human.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 961)
AUTHORS	NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
CDNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1189 row: h column: 11  
High quality sequence stop: 555.  
Location/Qualifiers  
1. .901  
/organism="Homo sapiens"  
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/clone\_lib="NIH\_MGC\_46"  
/tissue\_type="leiomyosarcoma cell line"  
/lab\_host="DHI08 (phage-resistant)"  
/note="Organ: uterus; Vector: pORF7; Site: 1; XhoI; Site: 2; EGOR1; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 205 a 225 c 240 g 291 t  
ORIGIN

Query Match 88.2% Score 19.4; DB 172; Length 961;  
Best Local Similarity 95.2%; Pred. No. 35;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 gactgtgaacgtccagatga 22  
|||||  
Db 650 GACTGTGAACGTCGGATGA 670  
RESULT 2  
LOCUS AA094019 105 bp mRNA EST 25-OCT-1996  
DEFINITION cl1619.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens  
CDNA 5', mRNA sequence.  
ACCESSION AA094019  
VERSION AA094019.1 GI:1639612  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 105)  
AUTHORS Liew,C.C.  
TITLE CDNAs from fetal heart (1996)  
JOURNAL Unpublished (1996)  
COMMENT Contact: Liew CC  
Department of Laboratory Medicine and Pathobiology  
University of Toronto  
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5  
Tel: 4169788758  
Fax: 4169785650  
Email: liewccc@utcc.utoronto.ca  
PCR Primers  
FORWARD: 5' GCCAAGCTCGAATTACCCCTCACTAAAGG 3'  
BACKWARD: 5' CCAATGAATGTAGTACGACTCACTATAGGCG 3'  
Seq primer: 5' GAATTAACCCCTCACTAAAGG 3'.  
Location/Qualifiers  
1. .105  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human fetal heart, Lambda ZAP Express"  
/lab\_host="E. coli XL1-Blue"

/note=vector: Lambda ZAP Express; Site\_1: EcoRI; Site\_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested Lambda ZAP Express."

BASE COUNT  
ORIGIN

Query Match 83.6%; Score 18.4; DB 2; Length 105;  
Best Local Similarity 95.0%; Pred. No. 77;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgcgtgtgaacgttccagat 20  
|||||  
Db 43 TGAAGTGTGAACCTTCAGAT 62

RESULT 3

BE275964 401 bp mRNA EST 13-JUL-2000  
LOCUS 601120704F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:2967576 5',  
DEFINITION mRNA sequence.  
ACCESSION BE275964  
VERSION BE275964.1 GI:9150926  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 401)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: L12C72 row: g column: 01  
High quality sequence start: 32  
High quality sequence stop: 321.

FEATURES

Location/Qualifiers  
1..401  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NIH\_MGC\_20"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 124 a 94 c 77 g 106 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 165; Length 401;  
Best Local Similarity 90.5%; Pred. No. 1.9e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaacgttccagatga 22  
|||||  
Db 264 GACTGGGAACGTTTCAGATGA 284

RESULT 4

AI597068/c  
LOCUS  
DEFINITION

AI597068 441 bp mRNA EST 21-APR-1999  
VJ44609.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone  
IMAGE:931912 3', mRNA sequence.

ACCESSION AI597068

VERSION AI597068.1 GI:4606116

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 441)  
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person  
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter  
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

TITLE

JOURNAL

COMMENT

Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:536832

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

High quality sequence stop: 427.

FEATURES

source

1..441  
/organism="Mus musculus"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone\_image="931912"  
/clone\_lib="Stratagene mouse skin (#937313)"  
/sex="females"  
/tissue\_type="whole skin"  
/dev\_stage="11 weeks old"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI  
; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT. Whole skin from 11 week old C57BL/6 female mice.  
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'  
adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor  
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

BASE COUNT 103 a 144 c 111 g 82 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 22; Length 441;  
Best Local Similarity 90.5%; Pred. No. 1.9e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaacgttccagatga 22

|||||

Db 116 GCCTGTGAATGTTCCAGATGA 96

RESULT 5

BE367478

LOCUS

DEFINITION

BE367478 457 bp mRNA EST 20-JUL-2000

P11.8.F04.bl.A002 Pathogen induced 1 (P11) Sorghum bicolor cDNA,

mRNA sequence.

ACCESSION BE367478

VERSION BE367478.1 GI:9309035

KEYWORDS EST.

SOURCE sorghum.



ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.  
REFERENCE 1 (bases 1 to 457)  
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and Pratt L.H.  
An EST database from Sorghum: pathogen-induced plants  
Unpublished (2000)  
CONTACT: Cordonnier-Pratt MM  
Department of Botany  
The University of Georgia  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 542 1805  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.  
Seq primer: JEN REV  
High quality sequence stop: 456  
POLYA-No.

## FEATURES

source

## Location/Qualifiers

1..457  
/organism="Sorghum bicolor"  
/db\_xref="taxon:4558"  
/clone\_lib="Pathogen induced 1 (PIL)"  
/note="Organ: Anthracnose-infected leaves from two-week-old sorghum plants 48 hr after inoculation; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; Two-week-old sorghum plants (B7X 623 cultivar) were infected with pathogen (isolate FRM421 of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptibility to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."

BASE COUNT 89 a 137 c 148 g 83 t

## ORIGIN

Query Match 80.9%; Score 17.8; DB 166; Length 457;  
Best Local Similarity 90.5%; Pred. No. 1.9e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaacgttcagatga 22  
||||| ||||||| ||

Db 38 GACTGTGACCGTCCAGAAGA 58

## RESULT 6

R83554 473 bp mRNA EST 04-AUG-1995  
LOCUS yq12d03.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:196709 5', mRNA sequence.

Qy 2 gactgtgaacgttcagatga 22  
||||| ||||||| ||

Db 38 GACTGTGACCGTCCAGAAGA 58

## RESULT 6

R83554 473 bp mRNA EST 04-AUG-1995  
LOCUS yq12d03.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:196709 5', mRNA sequence.

Qy 2 gactgtgaacgttcagatga 22  
||||| ||||||| ||

Db 38 GACTGTGACCGTCCAGAAGA 58

R., Williamson,A., Wohldmann,P. and Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)  
CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 958  
High quality sequence stops: 332  
Source: IMAGE Consortium, LUNL  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 958 Std Error: 0.00  
Seq primer: M3Rpl  
High quality sequence stop: 332.

## FEATURES

source

## Location/Qualifiers

1..473  
/organism="Homo sapiens"  
/db\_xref="GDB:3765759"  
/db\_xref="taxon:9606"  
/clone="IMAGE:196709"  
/clone\_lib="Soares fetal liver spleen INFLS"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: p7T73D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGCAAGATTAATTAAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p7T73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 144 a 94 c 120 g 110 t

## ORIGIN

Query Match 80.9%; Score 17.8; DB 188; Length 473;  
Best Local Similarity 90.5%; Pred. No. 1.9e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaacgttcagatga 22  
||||| ||||||| ||

Db 319 GACTCTGAACGTCCAGCTGA 339

## RESULT 7

AZ265882 514 bp DNA GSS 26-JUL-2000  
LOCUS RPCI-23-143A3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-143A3, DNA sequence.

Qy 2 gactgtgaacgttcagatga 22  
||||| ||||||| ||

Db 319 GACTCTGAACGTCCAGCTGA 339

## RESULT 7

AZ265882 514 bp DNA GSS 26-JUL-2000  
LOCUS RPCI-23-143A3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-143A3, DNA sequence.

Qy 2 gactgtgaacgttcagatga 22  
||||| ||||||| ||

Db 319 GACTCTGAACGTCCAGCTGA 339

## RESULT 7

AZ265882 514 bp DNA GSS 26-JUL-2000  
LOCUS RPCI-23-143A3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-143A3, DNA sequence.

Qy 2 gactgtgaacgttcagatga 22  
||||| ||||||| ||

Db 319 GACTCTGAACGTCCAGCTGA 339

## RESULT 7

AZ265882 514 bp DNA GSS 26-JUL-2000  
LOCUS RPCI-23-143A3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-143A3, DNA sequence.

```

/dev_stage="two-cell stage embryo"
BASE COUNT      147 a      160 c      122 g      103 t      10 others
ORIGIN

Query Match      80.9% ; Score 17.8; DB 107; Length 542;
Best Local Similarity 90.5% ; Pred. No. 2e+02;

```

```

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaacgttccagatga 22
  ||||| ||||| ||||| |||||
Db 439 GGCTGTGAATGTTCCAGATGA 419

RESULT 10
BE284315 555 bp mRNA 26-OCT-2000
LOCUS 601087423F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3482308 5',
DEFINITION mRNA sequence.
ACCESSION BE284315
VERSION H3091D05.3 GI:9161168
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM8511 row: n column: 05
High quality sequence stop: 545.
FEATURES
Location/Qualifiers
source 1..555
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3482308"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 107 a 135 c 184 g 129 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 165; Length 555;
Best Local Similarity 90.5%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaacgttccagatga 22
  ||||| ||||| ||||| |||||
Db 406 GGCTGTGAATGTTCCAGATGA 426

RESULT 11
BG070885/c 563 bp mRNA 26-JAN-2001
LOCUS H3091D05-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
DEFINITION H3091D05.3, mRNA sequence.
ACCESSION BG070885
VERSION BG070885.1 GI:12553377
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 563)
Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka
, T.S., Carter, M.G. and Ko, M.S.H.
Verification and initial annotation of NIA mouse 15K cDNA clone set
Unpublished (2001)
Other_ESRs: H3091D05-5
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://igsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3091 row: D column: 05
Seq primer: -21M13 Forward
High quality sequence stop: 563
POLYA=yes.
Location/Qualifiers
source 1..563
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="H3091D05"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
libraries"
/lab_host="DH10B"
/Note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5 embryos
, and E12.5 female mesonephros/gonad) and one newborn
ovary cDNA library. Average insert size 1.5 kb. All
source libraries are cloned unidirectionally with Oligo(dt
)-Not primers. References include: (1) Genome-wide
expression profiling of mid-gestation placenta and embryo
using a 15,000 mouse developmental cDNA microarray, 2000,
Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex
and under-representation on the X chromosome, 1998, Hum
Mol Genet 7: 1967-1978."
Mol Genet 7: 1967-1978."

BASE COUNT 150 a 175 c 131 g 107 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 173; Length 563;
Best Local Similarity 90.5%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaacgttccagatga 22
  ||||| ||||| ||||| |||||
Db 437 GGCTGTGAATGTTCCAGATGA 417

RESULT 12
AZ699837 572 bp DNA GSS 24-JAN-2001
LOCUS RPCI-23-235F18.TJ RPCI-23 Mus musculus genomic clone RPCI-23-235F18
DEFINITION , DNA sequence.
ACCESSION AZ699837
VERSION AZ699837.1 GI:12420668
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:49 ; Search time 515.84 Seconds  
(without alignments)  
26.779 Million cell updates/sec

Title: US-09-713-136-4  
Perfect score: 22  
Sequence: 1 tgaactgtgaacgttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues  
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0601.\*  
1: /SIDSB/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SIDSB/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SIDSB/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SIDSB/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SIDSB/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
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11: /SIDSB/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
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21: /SIDSB/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SIDSB/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AAV80099	Immunomodulatory o
2	22	100.0	22	AAV80101	Immunomodulatory o
3	22	100.0	22	AA96254	Sequence of a stab
4	22	100.0	22	AA38088	Immunostimulatory
5	22	100.0	22	AAA38070	Immunostimulatory
6	22	100.0	22	AA77043	Immunostimulatory
7	21.2	96.4	22	AA77045	Immunostimulatory
8	21	95.5	22	AA255877	Immunomodulatory o
9	20.4	92.7	22	AAV32079	Nucleotide sequenc
10	20.4	92.7	22	AA36624	ISS-ODN DY1018 nuc
11	20.4	92.7	22	AAV80097	Immunomodulatory o

12	20.4	92.7	22	20	AAV80102	Immunomodulatory o
13	20.4	92.7	22	20	AAV80103	Immunomodulatory o
14	20.4	92.7	22	21	AA64051	Immunostimulatory
15	20.4	92.7	22	21	AA96253	Sequence of a stab
16	20.4	92.7	22	21	AA90458	CpG adjuvant oligo
17	20.4	92.7	22	21	AA14467	Immunostimulatory
18	20.4	92.7	22	21	AA38065	Immunostimulatory
19	20.4	92.7	22	21	AA38071	Immunostimulatory
20	20.4	92.7	22	21	AA38072	Immunostimulatory
21	20.4	92.7	22	21	AA255876	Immunomodulatory o
22	20.4	92.7	22	22	AA77040	Immunomodulatory D
23	20.4	92.7	22	22	AA729800	Cholera toxin immu
24	20.4	92.7	22	22	AA82107	Oligonucleotide OD
25	20.4	92.7	22	22	AA92377	CG motif and CFA c
26	19.6	89.1	22	22	AA77046	Immunostimulatory
27	19.4	88.2	22	21	AA255880	Immunomodulatory o
28	18.8	85.5	22	20	AAV80105	Oligo used in expe
29	18.8	85.5	22	20	AAV80096	Immunomodulatory o
30	18.8	85.5	22	21	AA96260	Sequence of a stab
31	18.8	85.5	22	21	AA38066	Immunostimulatory
32	18.8	85.5	22	22	AA77041	Immunostimulatory
33	18.8	85.5	22	22	AA77047	Immunostimulatory
34	18.4	83.6	22	21	AA255881	Immunomodulatory o
35	17.2	78.2	22	19	AAV32080	Nucleotide sequenc
36	17.2	78.2	22	20	AA36625	ISS-ODN mutant DY1
37	17.2	78.2	22	20	AAV5790	Immunostimulatory
38	17.2	78.2	22	20	AAV5797	Immunostimulatory
39	17.2	78.2	22	20	AAV5788	Immunostimulatory
40	17.2	78.2	22	20	AAV80106	Oligo used in expe
41	17.2	78.2	22	20	AAV80104	Oligo used in expe
42	17.2	78.2	22	21	AA64052	Non-CpG control ph
43	17.2	78.2	22	21	AA96252	Sequence of a stab
44	17.2	78.2	22	21	AA90459	CpG adjuvant oligo
45	17.2	78.2	22	22	AA92378	CG motif and CFA c

ALIGNMENTS

RESULT 1

AAV80099  
ID AAV80099 standard; DNA; 22 BP.  
XX AAV80099;  
AC AAV80099;  
XX 12-MAR-1999 (first entry)  
DT 12-MAR-1999 (first entry)  
XX Immunomodulatory oligo comprising an ISS sequence.  
DE Immunomodulatory oligo comprising an ISS sequence.  
XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
XX Synthetic.  
OS Synthetic.  
XX WO9855495-A2.  
PN WO9855495-A2.  
XX 10-DEC-1998.  
PD 10-DEC-1998.  
XX 05-JUN-1998; 98WO-US11578.  
PF 05-JUN-1998; 98WO-US11578.  
XX 06-JUN-1997; 97US-0048793.  
PR 06-JUN-1997; 97US-0048793.  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX Dina D, Roman M, Schwartz D;  
PI Dina D, Roman M, Schwartz D;  
XX WPI; 1999-059898/05.  
XX Immunostimulatory oligonucleotides regulate the immune system - and  
PT contain an immune-stimulating octanucleotide sequence; for treating  
PT cancer, allergic and infectious diseases

XX  
PS  
XX  
XX  
Claim 8; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
CC patients needing immune regulation, such as those suffering from cancer,  
CC an allergic disease and asthma. They are also used to prevent infectious  
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
CC Schistosoma. The immunomodulatory sequences are used to screen for human  
CC immunostimulatory activity by incubating macrophage cells and the  
CC oligonucleotide; and determining the relative amount of Th1-biased  
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
CC specific claimed examples of such immunomodulatory oligonucleotides.

XX  
XX  
SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttccagatga 22  
DB 1 tgactgtgaacgttccagatga 22  
|||||

RESULT 2  
AAV80101  
ID AAV80101 standard; DNA: 22 BP.  
XX  
XX AAV80101;  
XX  
XX 13-MAR-1999 (first entry)  
XX  
XX Immunomodulatory oligo comprising an ISS sequence.

XX  
XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.  
XX  
XX Synthetic.

XX  
XX Key Location/Qualifiers  
FT modified\_base 11  
FT /\*tag= a  
FT /note= "5-bromocytosine"

XX  
XX WO9855495-A2.  
XX  
XX 10-DEC-1998.  
XX  
XX 05-JUN-1998; 98WO-US11578.  
XX  
XX 06-JUN-1997; 97US-0048793.  
XX  
XX (DYNA-) DYNAX TECHNOLOGIES CORP.  
XX  
XX Dina D, Roman M, Schwartz D;  
XX  
XX WPI; 1999-059898/05.  
XX  
XX Immunostimulatory oligonucleotides regulate the immune system - and  
PT contain an immune-stimulating octanucleotide sequence; for treating  
PT cancer, allergic and infectious diseases

XX  
XX Claim 22; Page 30; 63pp; English.

XX  
XX The invention relates to immunomodulatory oligonucleotides that comprise

CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
CC patients needing immune regulation, such as those suffering from cancer,  
CC an allergic disease and asthma. They are also used to prevent infectious  
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
CC Schistosoma. The immunomodulatory sequences are used to screen for human  
CC immunostimulatory activity by incubating macrophage cells and the  
CC oligonucleotide; and determining the relative amount of Th1-biased  
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
CC specific claimed examples of such immunomodulatory oligonucleotides.

XX  
XX  
SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttccagatga 22  
DB 1 tgactgtgaacgttccagatga 22  
|||||

RESULT 3  
AAV96254  
ID AAA96254 standard; DNA: 22 BP.  
XX  
XX AAA96254;  
XX  
XX 08-FEB-2001 (first entry)  
XX  
XX Sequence of a stabilised oligonucleotide with antitumour activity.

XX  
XX Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;  
KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.  
XX  
XX Synthetic.

XX  
XX WO200056342-A2.  
XX  
XX 28-SEP-2000.  
XX  
XX 17-MAR-2000; 2000WO-FR00676.  
XX  
XX 19-MAR-1999; 99FR-0003433.  
XX  
XX (ASST-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
XX (INRM) INST NAT SANTE & RECH MEDICALE.  
XX  
XX Carpentier A;  
XX  
XX WPI; 2000-602192/57.  
XX  
XX Use of stabilized oligonucleotides as antitumor agents, particularly  
PT against nervous system tumors, have optimal activity and are not toxic

XX  
XX  
XX Example 13; Page 46; 57pp; French.

XX The present sequence represents a stabilised oligonucleotide which has  
CC antitumour activity. The oligonucleotide comprises an octamer motif  
CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where  
CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are  
CC immunostimulatory, and are not toxic. They may be adapted for use in  
CC animals or humans. The stabilised oligonucleotides are used for  
CC treating tumours, of any type and any degree of anaplasia, particularly  
CC human tumours, in the peripheral or central nervous systems, specifically  
CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.

XX  
XX  
SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgtccagatga 22  
 |||||  
 Db 1 tgactgtgaacgtccagatga 22

RESULT 4  
 AAA38068  
 ID AAA38068 standard; DNA; 22 BP.  
 AC AAA38068;  
 XX  
 XX 24-AUG-2000 (first entry)  
 DT  
 XX  
 DE Immunostimulatory sequence (ISS) #4.

XX Immunostimulatory sequence; ISS; Immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; Immune response; infection;  
 KW development; ss.  
 XX  
 XX Synthetic.

OS  
 XX WO200021556-A1.  
 PN  
 XX  
 XX 20-APR-2000.  
 PD  
 XX  
 XX 08-OCT-1999; 99WO-US23677.  
 PF  
 XX  
 XX 09-OCT-1998; 98US-0103733.  
 PR  
 PR 07-OCT-1999; 99US-0415186.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PA Tighe H, Raz E, Schwartz D, Takabayashi K;  
 XX WPI; 2000-317846/27.  
 XX  
 XX Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual -  
 PT  
 XX Disclosure; Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory polynucleotide, or is proximately  
 CC conjugated to an immunomodulatory polynucleotide, is used for modulating or  
 CC associated to it and not conjugated, is used for modulating or  
 CC stimulating a specific immune response against gp120 in an individual by  
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
 CC is also used for suppressing or delaying development of HIV infection in  
 CC an individual infected with HIV or an individual at risk of infection  
 CC with HIV, respectively. It is also used for treating an individual  
 CC infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgtccagatga 22  
 |||||  
 Db 1 tgactgtgaacgtccagatga 22

RESULT 5  
 AAA38070  
 ID AAA38070 standard; DNA; 22 BP.  
 XX  
 AC AAA38070;  
 XX  
 XX 24-AUG-2000 (first entry)  
 DT  
 XX  
 DE Immunostimulatory sequence (ISS) #6.

XX Immunostimulatory sequence; ISS; Immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; Immune response; infection;  
 KW development; ss.  
 XX  
 XX Synthetic.

OS  
 XX Key Location/Qualifiers  
 FH modified\_base 11  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "5-Bromocytosine"

PN WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PA Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual -

XX Disclosure; Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory polynucleotide, or is proximately  
 CC conjugated to an immunomodulatory polynucleotide, is used for modulating or  
 CC associated to it and not conjugated, is used for modulating or  
 CC stimulating a specific immune response against gp120 in an individual by  
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
 CC is also used for suppressing or delaying development of HIV infection in  
 CC an individual infected with HIV or an individual at risk of infection  
 CC with HIV, respectively. It is also used for treating an individual  
 CC infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgtccagatga 22  
 |||||  
 Db 1 tgactgtgaacgtccagatga 22

RESULT 6  
 AAF77043  
 ID AAF77043 standard; DNA; 22 BP.



XX AAF77043;  
 AC  
 XX  
 DT 15-MAY-2001 (first entry)  
 DE XX  
 DE Immunostimulatory DNA #3.  
 XX  
 KW Modulate; Immune; antigen; immunostimulatory; ds.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200112223-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-US22835.  
 XX  
 PR 19-AUG-1999; 99US-0149768.  
 XX  
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX  
 PI Van Nest-G;  
 XX  
 DR WPI; 2001-211136/21.  
 XX  
 XX Modulating immune response to a second antigen in humans involves  
 PT administering an immunostimulatory polynucleotide comprising an  
 PT immunostimulatory sequence and a first antigen  
 XX  
 PS Disclosure; Page 15; 63pp; English.  
 XX  
 CC The present invention relates to modulating an immune response to  
 CC a second antigen in an individual, involving  
 CC administering to the individual an immunomodulatory polynucleotide  
 CC comprising an immunostimulatory sequence (ISS) and a first antigen.  
 XX  
 SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 22; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcacagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcacagatga 22

RESULT 7  
 AAF77045  
 ID AAF77045 standard; DNA; 22 BP.  
 AC  
 XX  
 AC AAF77045;  
 XX  
 DT 15-MAY-2001 (first entry)  
 DE XX  
 DE Immunostimulatory DNA #5.  
 XX  
 KW Modulate; Immune; antigen; immunostimulatory; ds.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200112223-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-US22835.  
 XX  
 PR 19-AUG-1999; 99US-0149768.  
 XX  
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX  
 PI Van Nest G;

XX WPI; 2001-211136/21.  
 DR  
 XX  
 PT Modulating immune response to a second antigen in humans involves  
 PT administering an immunostimulatory polynucleotide comprising an  
 PT immunostimulatory sequence and a first antigen  
 XX  
 XX  
 XX Disclosure; Page 15; 63pp; English.  
 XX  
 CC The present invention relates to modulating an immune response to  
 CC a second antigen in an individual, involving  
 CC administering to the individual an immunomodulatory polynucleotide  
 CC comprising an immunostimulatory sequence (ISS) and a first antigen.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 6 G; 6 T; 1 other;

Query Match 96.4%; Score 21.2; DB 22; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.095;  
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcacagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcacagatga 22

RESULT 8  
 AAZ55877  
 ID AAZ55877 standard; DNA; 22 BP.  
 XX  
 AC AAZ55877;  
 XX  
 DT 10-APR-2000 (first entry)  
 XX  
 DE Immunomodulatory oligonucleotide SEQ ID NO: 2.  
 XX  
 KW Immunomodulation; immunostimulatory sequence; adjuvant;  
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
 KW asthma; immunocontraception; 5-bromocytosine; ss.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..22  
 FT /\*tag= a  
 FT /note= "Phosphorothioate linkages"  
 FT misc\_feature 9..16  
 FT /\*tag= b  
 FT /note= "Immunostimulatory sequence (ISS)"  
 FT modified\_base 11  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "5-bromocytosine"  
 FT  
 FT  
 PN WO9962923-A2.  
 XX  
 XX 09-DEC-1999.  
 PD  
 XX  
 XX 04-JUN-1999; 99WO-US12538.  
 PF  
 XX  
 XX 05-JUN-1998; 98US-0088310.  
 PR  
 PR 01-JUN-1999; 99US-0324191.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX  
 XX Schwartz D;  
 PI WPI; 2000-105687/09.  
 XX  
 DR Novel immunomodulatory oligonucleotide used to induce a Th1-type immune  
 XX response, e.g. to tumor antigens  
 XX  
 XX

PS Claim 29; Page 35; 54pp; English.

XX Sequences AA25876-25877 and AA25880-25886 represent immunomodulatory  
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,  
 CC AACGTC, AACGTT, AGCGTC, AGCGTT, GACGTC, GACGTT, GCGGTT,  
 CC AACGTTCC and GACGTTCC). The invention relates to oligonucleotides  
 CC comprising one or more ISSs, where the ISS comprises at least  
 CC one modified cytosine with an electron-withdrawing moiety at  
 CC position C-5 or C-6 of the base. Sequences AA25877 and AA25886  
 CC contain ISSs comprising at least one bromocytosine, whereas sequence  
 CC AA25876 contains an unmodified ISS. The immunomodulatory  
 CC oligonucleotides have an adjuvant-like effect; when formulated with an  
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,  
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),  
 CC while simultaneously downregulating the Th2-type response. The Th1  
 CC response is particularly effective for control of viruses and  
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
 CC particularly when formulated with an antigen or a facilitator, for  
 CC modulating immune responses. Such compositions may be used in tumour  
 CC therapy, in treatment of allergy (including asthma), for inducing a  
 CC vigorous cellular response (against a virus, bacterium, fungus or  
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.  
 XX Sequence 22 BP; 6 A; 3 C; 6 G; 6 T; 1 other;

Query Match 95.5%; Score 21; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.12;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaacggtccagatga 22  
 Db 1 tgactgtgaacggtccagatga 22

RESULT 9

AAV32079

ID AAV32079 standard; DNA; 22 BP.

XX AAV32079;

XX 09-SEP-1998 (first entry)

XX Nucleotide sequence of DY1018.

XX DY1018; beta-gal; ISS-PN/IMM; antigen; Immune response; antibody;  
 KW immunisation; anaphylaxis; IgE; retinopathies; ss.

XX synthetic.

XX Key Location/Qualifiers

XX modified\_base 1..22

XX /tag= a

XX /note= "phosphothioate backbone"

XX WO9816247-A1.

XX 23-APR-1998.

XX 09-OCT-1997; 97WO-US19004.

XX 11-OCT-1996; 96US-0028118.

XX (REGC ) UNIV CALIFORNIA.

XX Carson DA, Raz E, Roman M;

XX WPI; 1998-261028/23.

XX New immunomodulatory compositions - comprising an antigen conjugated  
 PT to a polynucleotide that contains an immunostimulatory sequence

XX Example 1; Page 36; 69pp; English.

XX This is the nucleotide sequence of DY1018, which is conjugated to  
 CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule  
 CC (IMM), which comprises an antigen conjugated to a polynucleotide  
 CC (PN) that contains at least one immunostimulatory nucleotide sequence  
 CC (ISS). The conjugate synergistically boost the magnitude of the host  
 CC immune response against an antigen to a level greater than the host  
 CC immune response to either the IMM, antigen or ISS-PN alone. These  
 CC responses to ISS-PN/IMM conjugates are particularly acute during  
 CC the important early phase of the host immune response to an antigen.  
 CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular  
 CC (Th1 type) immune responses of the host. Thus, use of the method to  
 CC boost the immune responsiveness of a host to subsequent challenge by a  
 CC sensitising antigen without immunisation avoids the risk of  
 CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE  
 CC production in response to the antigen challenge. The conjugates can  
 CC also be used to combat pathogenic infection and to stimulate  
 CC therapeutic angiogenesis to treat conditions in which localised blood  
 CC flow plays a significant etiological role, e.g. retinopathies.  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 19; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.24;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaacggtccagatga 22

Db 1 tgactgtgaacggtccagatga 22

RESULT 10

AAX36624

ID AAX36624 standard; DNA; 22 BP.

XX AAX36624;

XX 09-JUL-1999 (first entry)

XX ISS-ODN DY1018 nucleotide sequence.

XX Antigen-stimulated inflammation; immunostimulatory oligonucleotide;  
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;  
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;  
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;  
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;  
 KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.

XX WO9911275-A2.

XX 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18382.

XX 05-SEP-1997; 97US-0927120.

XX (REGC ) UNIV CALIFORNIA.

XX Ray E;

XX WPI; 1999-312404/26.

XX Reducing antigen-stimulated granulocyte-mediated inflammation

XX Example 2; Page 30; 69pp; English.

XX This is the ISS-ODN DY1018 nucleotide sequence.

XX The invention relates to a method for preventing or reducing  
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:

CC (a) reduction in, or the absence of, a Th2 type immune response is  
 CC measured; or (b) there is a reduction or absence of other clinical signs  
 CC of inflammation in the host after antigen challenge. The method is used  
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
 CC and to modulate the host's immune responsiveness to an antigen,  
 CC particularly where the subject suffers from asthma, nasal polyposis,  
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
 CC antigen immunisation, the method is an antigen-independent method,  
 CC and avoids host production of both interleukin-4 (IL-4), which carries  
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
 CC adhesion to endothelia.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 Other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.24;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcagatga 22

RESULT 11  
 AAV80097  
 ID AAV80097 standard; DNA: 22 BP.  
 AC AAV80097;  
 XX  
 DT 12-MAR-1999 (first entry)  
 XX  
 DE Immunomodulatory oligo comprising an ISS sequence.  
 XX  
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9855495-A2.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 05-JUN-1998; 98WO-US11578.  
 XX  
 PR 06-JUN-1997; 97US-0048793.  
 XX  
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX  
 PI Dina D, Roman M, Schwartz D;  
 XX  
 DR WPI: 1999-059898/05.  
 XX

PT Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases  
 XX  
 PS Claim 5; Page 29; 63pp; English.

CC The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 Other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.24;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcagatga 22

RESULT 12  
 AAV80102  
 ID AAV80102 standard; DNA: 22 BP.  
 AC AAV80102;  
 XX  
 DT 12-MAR-1999 (first entry)  
 XX  
 DE Immunomodulatory oligo comprising an ISS sequence.  
 XX  
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.  
 XX  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 modified\_base 11  
 FT FT  
 FT /\*tag= a  
 XX /note= "5-bromocytosine"  
 PN WO9855495-A2.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 05-JUN-1998; 98WO-US11578.  
 XX  
 PR 06-JUN-1997; 97US-0048793.  
 XX

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX  
 PI Dina D, Roman M, Schwartz D;  
 XX  
 DR WPI: 1999-059898/05.  
 XX

PT Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases  
 XX  
 PS Claim 23; Page 30; 63pp; English.

CC The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX	Query Match	92.7%;	Score 20.4;	DB 20;	Length 22;
SQ	Best Local Similarity	95.5%;	Pred. No. 0.24;		
	Matches 21; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
	Query Match	92.7%;	Score 20.4;	DB 20;	Length 22;
	Best Local Similarity	95.5%;	Pred. No. 0.24;		
	Matches 21; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
QY	1 tgactgtgaacgttcagatga 22				
DB	1 tgactgtgaacgttcagatga 22				
RESULT 13					
AAV80103					
ID	AAV80103 standard; DNA; 22 BP.				
XX					
AC	AAV80103;				
XX					
DT	12-MAR-1999 (first entry)				
XX					
DE	Immunomodulatory oligo comprising an ISS sequence.				
XX					
KW	Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;				
KW	ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;				
KW	human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;				
KW	B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.				
XX					
OS	Synthetic.				
XX					
Key	Location/Qualifiers				
FT	modified_base 11				
FT	/*tag= a				
FT	/note= "5-bromocytosine"				
XX					
PN	WO9855495-A2.				
XX					
PD	10-DEC-1998.				
XX					
XX	05-JUN-1998; 98WO-US11578.				
XX					
PR	06-JUN-1997; 97US-0048793.				
XX					
PA	(DYNA-) DYNAVAX TECHNOLOGIES CORP.				
XX					
PI	Dina D, Roman M, Schwartz D;				
XX					
XX	WPI; 1999-059898/05.				
XX					
PT	Immunostimulatory oligonucleotides regulate the immune system - and				
PT	contain an immune-stimulating octanucleotide sequence; for treating				
PT	cancer, allergic and infectious diseases				
XX					
PS	Claim 24; Page 30; 63pp; English.				
XX					
CC	The invention relates to immunomodulatory oligonucleotides that comprise				
CC	at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS				
CC	sequences are selected from the group consisting of AACGTTC, AACGTTCG,				
CC	GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat				
CC	patients needing immune regulation, such as those suffering from cancer,				
CC	an allergic disease and asthma. They are also used to prevent infectious				
CC	diseases such as influenza, herpes, hepatitis B, human immunodeficiency				
CC	and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and				
CC	Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and				
CC	Schistosoma. The immunomodulatory sequences are used to screen for human				
CC	immunostimulatory activity by incubating macrophage cells and the				
CC	oligonucleotide; and determining the relative amount of Th1-biased				
CC	cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent				
CC	specific claimed examples of such immunomodulatory oligonucleotides.				
XX					
SQ	Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;				

Query Match	92.7%;	Score 20.4;	DB 21;	Length 22;
Best Local Similarity	95.5%;	Pred. No. 0.24;		
Matches 21; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
QY	1 tgactgtgaacgttcagatga 22			
DB	1 tgactgtgaacgttcagatga 22			
RESULT 14				
AAC64051				
ID	AAC64051 standard; DNA; 22 BP.			
XX				
AC	AAC64051;			
XX				
DT	15-FEB-2001 (first entry)			
XX				
DE	Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.			
XX				
KW	CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;			
KW	enhanced antigen presentation; antigen-presenting cell; APC;			
KW	T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;			
KW	vaccine; ss.			
XX				
OS	Synthetic.			
XX				
PN	WO200062787-A1.			
XX				
PD	26-OCT-2000.			
XX				
XX	11-APR-2000; 2000WO-US09664.			
XX				
PR	15-APR-1999; 99US-0292278.			
XX				
PA	(REGC ) UNIV CALIFORNIA.			
XX				
PI	Raz E, Martin-Orozco E;			
XX				
XX	WPI; 2000-679548/66.			
XX				
PT	Enhancing antigen-presentation capabilities of T-cells for cancer			
PT	immunotherapy, by contacting cells with an immunostimulatory			
PT	oligonucleotide			
XX				
PS	Example 1; Page 18; 42pp; English.			
XX				
CC	The invention relates to a method of inducing activation of T-cells			
CC	to respond to an antigen, comprising contacting antigen-presenting cells			
CC	(APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs			
CC	thus treated have enhanced antigen presenting capabilities compared to			
CC	antigen-activated APCs. APCs with enhanced antigen-presentation			
CC	capabilities then present the antigen to T-cells. The method is useful			
CC	for cancer immunotherapy. The ISS-ODN is used to enhance the tumour			
CC	antigen presenting capacity of tumour cells, thereby inducing T-cell			
CC	activation, and is therefore useful for treating tumours. Additionally,			
CC	tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.			
CC	ISS-ODN treated APCs are induced to take up antigen through upregulation			
CC	of Fc-receptor expression, to present antigen through upregulation of			
CC	major histocompatibility complex (MHC) Class I and II expression and			
CC	CD1d expression, to produce co-stimulatory factors (B7 and CD40), to			
CC	provide cell-to-cell adhesion through upregulation of intercellular			
CC	adhesion molecule (ICAM) expression, and to increase Th1 stimulatory			
CC	cytokine production, all at levels greater than that achieved through			
CC	contact of APC with antigen alone. The present sequence represents			
CC	a phosphorothioate CpG ISS-ODN used in the exemplifications of the			
XX				
XX				
SQ	Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;			

Query Match	92.7%;	Score 20.4;	DB 21;	Length 22;
Best Local Similarity	95.5%;	Pred. No. 0.24;		
Matches 21; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
QY	1 tgactgtgaacgttcagatga 22			
DB	1 tgactgtgaacgttcagatga 22			
RESULT 13				
AAV80103				
ID	AAV80103 standard; DNA; 22 BP.			
XX				
AC	AAV80103;			
XX				
DT	12-MAR-1999 (first entry)			
XX				
DE	Immunomodulatory oligo comprising an ISS sequence.			
XX				
KW	Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;			
KW	ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;			
KW	human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;			
KW	B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.			
XX				
OS	Synthetic.			
XX				
Key	Location/Qualifiers			
FT	modified_base 11			
FT	/*tag= a			
FT	/note= "5-bromocytosine"			
XX				
PN	WO9855495-A2.			
XX				
PD	10-DEC-1998.			
XX				
XX	05-JUN-1998; 98WO-US11578.			
XX				
PR	06-JUN-1997; 97US-0048793.			
XX				
PA	(DYNA-) DYNAVAX TECHNOLOGIES CORP.			
XX				
PI	Dina D, Roman M, Schwartz D;			
XX				
XX	WPI; 1999-059898/05.			
XX				
PT	Immunostimulatory oligonucleotides regulate the immune system - and			
PT	contain an immune-stimulating octanucleotide sequence; for treating			
PT	cancer, allergic and infectious diseases			
XX				
PS	Claim 24; Page 30; 63pp; English.			
XX				
CC	The invention relates to immunomodulatory oligonucleotides that comprise			
CC	at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS			
CC	sequences are selected from the group consisting of AACGTTC, AACGTTCG,			
CC	GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat			
CC	patients needing immune regulation, such as those suffering from cancer,			
CC	an allergic disease and asthma. They are also used to prevent infectious			
CC	diseases such as influenza, herpes, hepatitis B, human immunodeficiency			
CC	and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and			
CC	Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and			
CC	Schistosoma. The immunomodulatory sequences are used to screen for human			
CC	immunostimulatory activity by incubating macrophage cells and the			
CC	oligonucleotide; and determining the relative amount of Th1-biased			
CC	cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent			
CC	specific claimed examples of such immunomodulatory oligonucleotides.			
XX				
SQ	Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;			

```

Oy 1 tgactgtgaacgttcagatga 22
    |||||
Db 1 tgactgtgaacgttcagatga 22

RESULT 15
AAA96253
ID AAA96253 standard; DNA; 22 BP.
XX
XX AC AAA96253;
XX
XX 08-FEB-2001 (first entry)
XX
XX Sequence of a stabilised oligonucleotide with antitumour activity.
XX
XX Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.
XX
XX Synthetic.
XX
XX WO200056342-A2.
XX
XX 28-SEP-2000.
XX
XX 17-MAR-2000; 2000WO-FR00676.
XX
XX 19-MAR-1999; 99FR-0003433.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
XX Carpentier A;
PI
XX
XX WPI; 2000-602192/57.
XX
XX Use of stabilised oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic
PT
XX
XX Example 2; Page 16; 57pp; French.
XX
XX The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octamer motif
CC of the type 5'-purine-pyrimidine-pyrimidine-X-X-3', where
CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
CC immunostimulatory, and are not toxic. They may be adapted for use in
CC animals or humans. The stabilised oligonucleotides are used for
CC treating tumours, of any type and any degree of anaplasia, particularly
CC human tumours in the peripheral or central nervous systems, specifically
CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ

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Query Match 92.7%; Score 20.4; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.24;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 tgactgtgaacgttcagatga 22
    |||||
Db 1 tgactgtgaacgttcagatga 22

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Search completed: October 9, 2001, 16:26:49  
 Job time: 2979 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:37 ; Search time 10334.3 Seconds  
(without alignments)  
31.457 Million cell updates/sec

Title: US-09-713-136-4  
Perfect score: 22  
Sequence: 1 tgaactgtgaacgttcagatga 22  
Scoring table:  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues  
Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*  
28: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq.\*  
29: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq.\*  
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55: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	16	US-09-296-477-6
2	22	100.0	22	18	US-09-415-186-4
3	22	100.0	22	25	US-09-642-492-4
4	22	100.0	22	28	US-09-713-136-4
5	21.2	96.4	22	18	US-09-415-186-6
6	21	95.5	22	16	US-09-296-477-12
7	21	95.5	22	17	US-09-324-191A-2
8	21	95.5	22	25	US-09-642-492-6
9	21	95.5	22	28	US-09-713-136-6
10	20.4	92.7	22	1	PCT-US00-18229-32
11	20.4	92.7	22	1	PCT-US00-35064-1
12	20.4	92.7	22	1	PCT-US01-03039-1
13	20.4	92.7	22	1	PCT-US01-06034-1
14	20.4	92.7	22	1	PCT-US01-10118-1
15	20.4	92.7	22	1	PCT-US01-10118-3
16	20.4	92.7	22	1	PCT-US01-11290-1
17	20.4	92.7	22	1	PCT-US01-14508-1
18	20.4	92.7	22	1	PCT-US99-21203-19
19	20.4	92.7	22	13	US-09-927-120-19
20	20.4	92.7	22	15	US-09-167-039-19
21	20.4	92.7	22	16	US-09-235-742-19
22	20.4	92.7	22	16	US-09-296-477-2
23	20.4	92.7	22	17	US-09-308-036A-1
24	20.4	92.7	22	17	US-09-324-191A-1
25	20.4	92.7	22	17	US-09-347-343-32
26	20.4	92.7	22	17	US-09-397-198-1
27	20.4	92.7	22	18	US-09-415-186-1
28	20.4	92.7	22	18	US-09-470-382-69
29	20.4	92.7	22	22	US-09-565-908-2
30	20.4	92.7	22	22	US-09-570-325-19
31	20.4	92.7	22	25	US-09-642-492-1
32	20.4	92.7	22	28	US-09-700-354-1
33	20.4	92.7	22	28	US-09-713-136-1
34	20.4	92.7	22	29	US-09-746-130-1
35	20.4	92.7	22	30	US-09-774-403-1
36	20.4	92.7	22	30	US-09-791-500-1
37	20.4	92.7	22	31	US-09-820-484-1
38	20.4	92.7	22	31	US-09-820-484-3
39	20.4	92.7	22	31	US-09-828-505-1
40	19.6	89.1	22	18	US-09-415-186-7
41	19.4	88.2	22	16	US-09-296-477-15
42	19.4	88.2	22	17	US-09-324-191A-5
43	19.4	88.2	22	25	US-09-642-492-7
44	19.4	88.2	22	28	US-09-713-136-7
45	18.8	85.5	22	31	US-09-828-505-2

## ALIGNMENTS

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RESULT 1
US-09-296-477-6
; Sequence 6, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-6

Query Match      100.0%; Score 22; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
Db 1 tgactgtgaacgttccagatga 22

RESULT 2
US-09-415-186-4
; Sequence 4, Application US/09415186
; GENERAL INFORMATION:
; APPLICANT: Tighe, Helen
; APPLICANT: Raz, Eyal
; APPLICANT: Schwartz, David
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of
; FILE REFERENCE: 377882000700
; CURRENT APPLICATION NUMBER: US/09/415,186
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: 60/103,733
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-415-186-4

Query Match      100.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22

RESULT 3
US-09-642-492-4
; Sequence 4, Application US/09642492
; GENERAL INFORMATION:
; APPLICANT: Van Nest, G.
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE
; FILE REFERENCE: 377882000800
; CURRENT APPLICATION NUMBER: US/09/642,492
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,768
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-642-492-4

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Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
Db 1 tgactgtgaacgttccagatga 22

RESULT 4
US-09-713-136-4
; Sequence 4, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713,136
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-4

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Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-415-186-6
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; Sequence 6, Application US/09415186
; GENERAL INFORMATION:
; APPLICANT: Tighe, Helen
; APPLICANT: Raz, Eyal
; APPLICANT: Schwartz, David
; APPLICANT: Takebayashi, Kenji
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of
; FILE REFERENCE: 37788200700
; CURRENT APPLICATION NUMBER: US/09/415,186
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: 60/103,733
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-415-186-6

```

```

Query Match          96.4%; Score 21.2; DB 18; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 tgactgtgaacgttccagatga 22
    |||||
DB 1 tgactgtgaabgttccagatga 22

```

```

RESULT 6
US-09-296-477-12
; Sequence 12, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINIA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
US-09-296-477-12

```

```

Query Match          95.5%; Score 21; DB 16; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 tgactgtgaacgttccagatga 22
    |||||
DB 1 tgactgtgaabgttccagatga 22

```

```

RESULT 7
US-09-324-191A-2
; Sequence 2, Application US/09324191A
; GENERAL INFORMATION:
; APPLICANT: Schwartz, David
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH
; MODIFIED BASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 377882000200
; CURRENT APPLICATION NUMBER: US/09/324,191A
; CURRENT FILING DATE: 1999-06-01
; EARLIER APPLICATION NUMBER: 60/088,310
; EARLIER FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
US-09-324-191A-2

```

```

Query Match          95.5%; Score 21; DB 17; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 tgactgtgaacgttccagatga 22
    |||||
DB 1 tgactgtgaangttccagatga 22

```

```

RESULT 8
US-09-642-492-6
; Sequence 6, Application US/09642492
; GENERAL INFORMATION:
; APPLICANT: Van Nest, G.
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE
; USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE
; THEREIN
; FILE REFERENCE: 377882000800
; CURRENT APPLICATION NUMBER: US/09/642,492
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,768
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: N = 5-bromocytosine
; OTHER INFORMATION: Synthetic construct
US-09-642-492-6

```

```

Query Match          95.5%; Score 21; DB 25; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 tgactgtgaacgttccagatga 22
    |||||
DB 1 tgactgtgaangttccagatga 22

```



```
RESULT 9
US-09-713-136-6
; Sequence 6, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 37782001500
; CURRENT APPLICATION NUMBER: US/09/713,136
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: modified_base
; LOCATION: (11)...(0)
; OTHER INFORMATION: N = 5-bromocytosine
US-09-713-136-6
```

```
Query Match 95.5%; Score 21; DB 28; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 tgactgtgaacgttcagatga 22
|||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 10
PCT-US00-18229-32
; Sequence 32, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Kobayashi, Hiroko
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 6510-189W01
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-32
```

```
Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 tgactgtgaacgttcagatga 22
|||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 11
PCT-US00-35064-1
; Sequence 1, Application PC/TUS0035064
; GENERAL INFORMATION:
```

```
; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: 06510/201W01
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/171,830
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule
PCT-US00-35064-1
```

```
Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 tgactgtgaacgttcagatga 22
|||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 12
PCT-US01-03029-1
; Sequence 1, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides In
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
PCT-US01-03029-1
```

```
Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 tgactgtgaacgttcagatga 22
|||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 13
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
```

```

; FILE REFERENCE: 6510-202MO
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; OTHER INFORMATION: oligonucleotide primer
; PCT-US01-06034-1

Query Match          92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgactgtgaacggtccagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacggtccagatga 22

RESULT 14
PCT-US01-10118-1
; Sequence 1, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response In vivo.
; FILE REFERENCE: 06510-188WO1
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
; PCT-US01-10118-1

Query Match          92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgactgtgaacggtccagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacggtccagatga 22

RESULT 15
PCT-US01-10118-3
; Sequence 3, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
```

GenCore version 4.5  
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OW nucleic - nucleic search, using .sw model

Run on: October 9, 2001, 21:36:13 ; Search time 1391.6 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-09-713-136-4  
Perfect score: 22  
Sequence: 1 tgactgtgaacgttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues  
Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	7 US-09-802-518-4	Sequence 4, Appli
2	22	100.0	22	7 US-09-802-359-4	Sequence 4, Appli
3	22	100.0	22	7 US-09-802-376-4	Sequence 4, Appli
4	21	95.5	22	7 US-09-802-518-6	Sequence 6, Appli
5	21	95.5	22	7 US-09-802-359-6	Sequence 6, Appli
6	21	95.5	22	7 US-09-802-376-6	Sequence 6, Appli
7	20.4	92.7	22	7 US-09-802-518-1	Sequence 1, Appli
8	20.4	92.7	22	7 US-09-802-359-1	Sequence 1, Appli
9	20.4	92.7	22	7 US-09-802-376-1	Sequence 1, Appli
10	19.4	88.2	22	7 US-09-802-359-7	Sequence 7, Appli
11	19.4	88.2	22	7 US-09-802-376-7	Sequence 7, Appli
12	19.4	88.2	22	7 US-09-770-943-2	Sequence 2, Appli
13	18.8	85.5	22	7 US-09-802-518-2	Sequence 2, Appli
14	18.8	85.5	22	7 US-09-802-359-2	Sequence 2, Appli
15	18.8	85.5	22	7 US-09-802-376-2	Sequence 2, Appli
16	18.8	85.5	252	5 US-09-825-790-331	Sequence 331, App
17	18.8	85.5	22	7 US-09-802-518-8	Sequence 8, Appli
18	18.4	83.6	22	7 US-09-802-359-8	Sequence 8, Appli
19	18.4	83.6	22	7 US-09-802-376-8	Sequence 8, Appli
20	18.4	83.6	22	7 US-09-802-359-2	Sequence 2, Appli
21	17.8	80.9	427	6 US-09-909-629-21114	Sequence 21114, A
22	17.8	80.9	445	6 US-09-906-555-9048	Sequence 9048, Ap
23	17.4	79.1	24853	7 US-09-764-874-10235	Sequence 10235, A
24	17.4	79.1	32212	7 US-09-764-874-10236	Sequence 10236, A
25	17.2	78.2	22	6 US-09-770-943-1	Sequence 1, Appli

Sequence 3, Appli  
Sequence 10, Appli  
Sequence 10, Appli  
Sequence 11, Appli  
Sequence 9, Appli  
Sequence 10, Appli  
Sequence 10, Appli  
Sequence 1362, Ap  
Sequence 4959, Ap  
Sequence 1286, Ap  
Sequence 10462, Ap  
Sequence 1982, Ap  
Sequence 570, App  
Sequence 14227, A  
Sequence 10373, A  
Sequence 2667, Ap  
Sequence 39362, A  
Sequence 7434, Ap  
Sequence 25567, A

26 17.2 78.2 22 6 US-09-770-943-3  
27 17.2 78.2 22 6 US-09-770-943-10  
28 17.2 78.2 22 7 US-09-802-518-10  
29 17.2 78.2 22 7 US-09-802-518-11  
30 17.2 78.2 22 7 US-09-802-359-9  
31 17.2 78.2 22 7 US-09-802-359-10  
32 17.2 78.2 22 7 US-09-802-376-9  
33 17.2 78.2 22 7 US-09-802-376-10  
34 17.2 78.2 103785 6 US-09-803-736-1362  
35 16.8 76.4 280 5 US-09-534-858-4959  
36 16.8 76.4 649 7 US-09-902-540-1286  
37 16.4 74.5 303 7 US-09-850-147-10462  
38 16.4 74.5 307 5 US-09-534-852-1982  
39 16.4 74.5 448 7 US-09-864-761-570  
40 16.4 74.5 448 7 US-09-864-761-14227  
41 16.2 73.6 132 7 US-09-724-750-10373  
42 16.2 73.6 171 7 US-09-764-874-2667  
43 16.2 73.6 207 8 US-60-253-457-39362  
44 16.2 73.6 268 8 US-60-253-456-7434  
45 16.2 73.6 308 8 US-60-253-456-25567

ALIGNMENTS

RESULT 1  
US-09-802-518-4  
; Sequence 4, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-4

Query Match 100.0%; Score 22; DB 7; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.073; Indels 0; Caps 0;  
Matches 22; Conservative 0; Mismatches 0

QY 1 tgactgtgaacgttccagatga 22  
Db 1 tgactgtgaacgttccagatga 22  
|||||

RESULT 2  
US-09-802-359-4  
; Sequence 4, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4

```
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-4

Query Match          100.08; Score 22; DB 7; Length 22;
Best Local Similarity 100.08; Pred. No. 0.073;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   |||||
Db 1 tgactgtgaacgttcacagatga 22

RESULT 3
US-09-802-376-4
; Sequence 6, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802.376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-4

Query Match          100.08; Score 22; DB 7; Length 22;
Best Local Similarity 100.08; Pred. No. 0.073;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   |||||
Db 1 tgactgtgaacgttcacagatga 22

US-09-802-518-6
; Sequence 6, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 37788201100
; CURRENT APPLICATION NUMBER: US/09/802.518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-6

Query Match          100.08; Score 22; DB 7; Length 22;
Best Local Similarity 100.08; Pred. No. 0.073;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   |||||
Db 1 tgactgtgaacgttcacagatga 22

US-09-802-376-6
; Sequence 6, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802.376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-6

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   |||||
Db 1 tgactgtgaacgttcacagatga 22

US-09-802-359-6
; Sequence 6, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802.359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-6

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   |||||
Db 1 tgactgtgaacgttcacagatga 22

US-09-802-376-6
; Sequence 6, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802.376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-6
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Query Match 95.5%; Score 21; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.24; 1; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

QY 1 tgactgtgaacgttcacgatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaangttccacgatga 22

RESULT 7  
US-09-802-518-1  
; Sequence 1, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 37788201100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-1

Query Match 92.7%; Score 20.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcacgatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgttcacgatga 22

RESULT 8  
US-09-802-359-1  
; Sequence 1, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-359-1

Query Match 92.7%; Score 20.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcacgatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgttcacgatga 22

RESULT 9  
US-09-802-376-1  
; Sequence 1, Application US/09802376  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201700  
; CURRENT APPLICATION NUMBER: US/09/802,376  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,557  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-376-1

Query Match 92.7%; Score 20.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcacgatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaacgttcacgatga 22

RESULT 10  
US-09-802-518-7  
; Sequence 7, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-518-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 1.7;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcacgatga 22  
||||| ||||| ||||| ||||| |||||  
Db 1 tgactgtgaangttccacgatga 22

RESULT 11  
US-09-802-359-7  
; Sequence 7, Application US/09802359  
; GENERAL INFORMATION:

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; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 12
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 13
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
```

```
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match      85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 14
US-09-802-518-2
; Sequence 2, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-2

Query Match      85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgacgtgtgaacgttcgagatga 22

RESULT 15
US-09-802-359-2
; Sequence 2, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
```

; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-359-2

Query Match 85.5%; Score 18.8; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 3.4;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcagatga 22  
||| ||||| |||||  
Db 1 tgaccgtgaacgttcagatga 22

Search completed: October 9, 2001, 21:36:14  
Job time: 21234 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:02 ; Search time 217.64 Seconds  
(without alignments)  
19.136 Million cell updates/sec

Title: US-09-713-136-4  
Perfect score: 22  
Sequence: 1 tgactgtgaacgttcacagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	18.8	85.5	22	4	US-09-092-314-2
2	17.2	78.2	22	4	US-09-092-314-1
3	17.2	78.2	22	4	US-09-092-314-3
4	17.2	78.2	22	4	US-09-092-314-10
5	16.2	73.6	913	2	US-08-975-316-61
6	15.8	71.8	1166	1	US-08-121-063-7
7	15.6	70.9	22	4	US-09-092-314-4
8	15.2	69.1	588	3	US-08-965-904B-1
9	15.2	69.1	773	3	US-08-934-131-2
10	15.2	69.1	5408	1	US-08-471-058-20
11	15.2	69.1	5408	3	US-08-471-057-20
12	14.8	67.3	1743	3	US-09-032-365A-18
13	14.8	67.3	1876	3	US-08-714-918-33
14	14.8	67.3	1876	4	US-09-265-315-33
15	14.8	67.3	1876	4	US-09-265-315-33
16	14.8	67.3	1876	4	US-09-266-417-33
17	14.8	67.3	4975	2	US-08-249-687C-1
18	14.8	67.3	4989	2	US-08-666-392A-3
19	14.8	67.3	4989	2	US-08-625-819-1
20	14.8	67.3	4989	3	US-08-755-558-4
21	14.8	67.3	4989	3	US-08-746-559A-1
22	14.8	67.3	4993	3	US-08-746-559A-3
23	14.8	67.3	10207	1	US-08-920-812-2
24	14.8	67.3	10207	1	US-08-920-827-2
25	14.8	67.3	10207	1	US-08-921-177-2
26	14.8	67.3	10207	1	US-08-362-577C-2
27	14.8	67.3	10207	2	US-08-920-828-2

C	28	14.6	66.4	718	4	US-08-998-416-682	Sequence 682, App
	29	14.6	66.4	1532	3	US-09-118-324-1	Sequence 1, Appl
C	30	14.6	66.4	1994	3	US-08-600-982-22	Sequence 22, Appl
C	31	14.6	66.4	1994	5	PCT-US94-10261A-22	Sequence 22, Appl
	32	14.6	66.4	2694	3	US-08-975-703-5	Sequence 5, Appl
	33	14.6	66.4	2694	4	US-09-515-884-5	Sequence 5, Appl
C	34	14.6	66.4	4344	2	US-08-532-547-4	Sequence 4, Appl
C	35	14.6	66.4	4344	2	US-08-379-6568-4	Sequence 4, Appl
C	36	14.6	66.4	4344	4	US-08-455-838-4	Sequence 4, Appl
C	37	14.6	66.4	4344	3	US-09-019-809-4	Sequence 23, Appl
C	38	14.6	66.4	5496	3	US-08-600-982-23	Sequence 23, Appl
C	39	14.6	66.4	5496	5	PCT-US94-10261A-23	Sequence 23, Appl
C	40	14.6	66.4	176373	3	US-09-128-155-17	Sequence 17, Appl
C	41	14.4	65.5	1460	1	US-08-133-038A-1	Sequence 1, Appl
C	42	14.4	65.5	1460	1	US-08-161-988A-1	Sequence 1, Appl
	43	14.2	64.5	27	2	US-08-308-952-18	Sequence 18, Appl
	44	14.2	64.5	27	4	US-09-124-141-27	Sequence 27, Appl
	45	14.2	64.5	536	6	5208218-2	Patent No. 5208218

ALIGNMENTS

RESULT 1  
US-09-092-314-2  
; Sequence 2, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-2

Query Match 85.5%; Score 18.8; DB 4; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.26;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22  
|||||  
Db 1 tgactgtgaacgttagagatga 22

RESULT 2  
US-09-092-314-1  
; Sequence 1, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06



; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-1

Query Match 78.2%; Score 17.2; DB 4; Length 22;  
Best Local Similarity 86.4%; Pred. No. 1.8;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22  
||||| ||| ||| ||| |||  
DB 1 tgactgtgaaggtagagatga 22

## RESULT 3

US-09-092-314-3  
; Sequence 3, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048.794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-3

Query Match 78.2%; Score 17.2; DB 4; Length 22;  
Best Local Similarity 86.4%; Pred. No. 1.8;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22  
||||| ||| ||| ||| |||  
DB 1 tgactgtgaaccttagagatga 22

## RESULT 4

US-09-092-314-10  
; Sequence 10, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048.794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10

; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-10

Query Match 78.2%; Score 17.2; DB 4; Length 22;  
Best Local Similarity 86.4%; Pred. No. 1.8;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22  
||||| ||| ||| ||| |||  
DB 1 tgactgtgaatgttagagatga 22

## RESULT 5

US-08-975-316-61  
; Sequence 61, Application US/08975316  
; Patent No. 5952486  
; GENERAL INFORMATION:  
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka  
; APPLICANT: and GRIERSON, Alastair W.  
; TITLE OF INVENTION: MATERIALS AND METHODS FOR  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/975.316  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/713,000  
; FILING DATE: September 11, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SLEATH, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000/1003c1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 913 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-975-316-61

Query Match 73.6%; Score 16.2; DB 2; Length 913;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gactgtgaacgttccagatga 22  
||||| ||| ||| ||| |||  
DB 513 GACTGTGAATTTACACATCA 533

## RESULT 6

US-08-121-063-7  
; Sequence 7, Application US/08121063  
; Patent No. 5446143  
; GENERAL INFORMATION:  
; APPLICANT: Simpson, Evan R.  
; APPLICANT: Mahendroo, Mala  
; APPLICANT: Mendelson, Carole R.  
; TITLE OF INVENTION: Adipose-Specific Promoter Regions of  
; TITLE OF INVENTION: Human Aromatase Cytochrome P450 gene  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121.063  
; FILING DATE: 14-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: UTSD:351  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-320-7200  
; TELEFAX: 512-474-7577  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1166 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-121-063-7

Query Match 71.8%; Score 15.8; DB 1; Length 1166;  
Best Local Similarity 89.5%; Pred. No. 20;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ctgtgaacgttccagatga 22  
||||| |||||||  
Db 525 CTGTGAAGTTCACAGA 543

RESULT 7  
US-09-092-314-4  
; Sequence 4, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-1730U1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-4

Query Match 70.9%; Score 15.6; DB 4; Length 22;  
Best Local Similarity 81.8%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttccagatga 22  
||||| |||||||  
Db 1 tgactgtgaacgttccagatga 22

RESULT 8  
US-08-965-904B-1  
; Sequence 1, Application US/08965904B  
; Patent No. 6030811  
; GENERAL INFORMATION:  
; APPLICANT: CHABOT-FLETCHER, MARIE  
; APPLICANT: ANDERSON, KAREN M.  
; TITLE OF INVENTION: A HUMAN MYOTROPHIN CLONE,  
; TITLE OF INVENTION: HSABH01  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/965.904B  
; FILING DATE: 07-NOV-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030.677  
; FILING DATE: 13-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Prestia, Paul F.  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: ATG-50026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0700  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 588 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-965-904B-1

Query Match 69.1%; Score 15.2; DB 3; Length 588;  
Best Local Similarity 85.0%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaacgttccagatg 21  
||||| |||||||  
Db 341 GACTGTGAAGGCCAGATG 360

RESULT 9  
US-08-934-131-2  
; Sequence 2, Application US/08934131

Patent No. 6153423  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer  
APPLICANT: Corley, Neil  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: HUMAN MYOTROPHIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,131  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0387 US  
TELEPHONE: 650-855-05  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 773 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT22  
CLONE: 2591910  
US-08-934-131-2

Query Match 69.1%; Score 15.2; DB 3; Length 773;  
Best Local Similarity 85.0%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Caps 0;  
QY 2 gactgtgaacgttcacagatg 21  
||||||| | |||||  
DB 544 GACTGTGAAGGCCACATG 563  
RESULT 10  
US-08-471-058-20/c  
Sequence 20, Application US/08471058  
Patent No. 5770443  
GENERAL INFORMATION:  
APPLICANT: Kiefer, Michael C.  
APPLICANT: Barr, Philip J.  
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING  
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,058  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/320,157  
FILING DATE: 07-OCT-1994  
APPLICATION NUMBER: 08/160,067  
FILING DATE: 30-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20007.12  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5408 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1665...1928  
OTHER INFORMATION:  
US-08-471-058-20  
Query Match 69.1%; Score 15.2; DB 1; Length 5408;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Caps 0;  
QY 3 actgtgaacgttcacagatga 22  
||||| | ||||| |||||  
DB 3226 ACTTAGAACCTTCACATGA 3207  
RESULT 11  
US-08-471-057-20/c  
Sequence 20, Application US/08471057  
Patent No. 6015687  
GENERAL INFORMATION:  
APPLICANT: KIEFER, MICHAEL C.  
APPLICANT: BARR, PHILIP J.  
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,057  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/320,157  
FILING DATE: 07-OCT-1994  
ATTORNEY/AGENT INFORMATION:

NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20007.20  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5408 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1665..1928  
US-08-471-057-20

Query Match 69.1%; Score 15.2; DB 3; Length 5408;  
Best Local Similarity 85.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 actgtgaacgttcacgatga 22  
||| |||| ||||| |||||  
DB 3226 ACTGAGACCTCCAGATGA 3207

RESULT 12  
US-09-032-365A-18  
; Sequence 18, Application US/09032365A  
; Patent No. 6114502  
; GENERAL INFORMATION:  
; APPLICANT: No. 6114502th, Michael  
; APPLICANT: Nishina, Patsy  
; APPLICANT: Naggart, Juergen  
; APPLICANT: No. 6114502en-Trauth, Konrad  
; TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bozicevic & Reed, LLP  
; STREET: 285 Hamilton Avenue, Suite 200  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,365A  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sherwood, Pamela J  
; REGISTRATION NUMBER: 36,677  
; REFERENCE/DOCKET NUMBER: SEQ-2CIP2  
; TELEPHONE: 650-327-3400  
; TELEFAX: 650 327-3231  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1743 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

MOLECULE TYPE: cDNA  
US-09-032-365A-18

Query Match 67.3%; Score 14.8; DB 3; Length 1743;  
Best Local Similarity 88.9%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcacg 18  
||||||| |||||  
DB 1327 TGACTGTGATCTCCAG 1344

RESULT 13  
US-08-714-918-33/c  
; Sequence 33, Application US/08714918  
; Patent No. 6037123  
; GENERAL INFORMATION:  
; APPLICANT: Benton, Bret  
; APPLICANT: Lee, Ving  
; APPLICANT: Malouin, Francois  
; APPLICANT: Martin, Patrick K.  
; APPLICANT: Schmid, Molly B.  
; APPLICANT: Sun, Dongxu  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL  
; TITLE OF INVENTION: TARGET GENES  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/714,918  
; FILING DATE: September 13, 1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/009,102  
; FILING DATE: December 22, 1995  
; APPLICATION NUMBER: 60/003,798  
; FILING DATE: September 15, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 222/005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1876 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-714-918-33

Query Match 67.3%; Score 14.8; DB 3; Length 1876;  
Best Local Similarity 88.9%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaacgttcacga 19  
||||||| |||||

Db 844 GACTGTAATGTTCCAGA 827

## RESULT 14

US-09-265-315-33/c  
; Sequence 33, Application US/09265315  
; Patent No. 6187541

## GENERAL INFORMATION:

APPLICANT: Benton, Bret  
APPLICANT: Lee, Ving J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/265,315  
FILING DATE: March 9, 1999

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/714,918  
FILING DATE: September 13, 1996  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 240/247  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1876 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-265-315-33

Query Match 67.3%; Score 14.8; DB 4; Length 1876;  
Best Local Similarity 88.9%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttcaga 19

||||| |||||||

Db 844 GACTGTAATGTTCCAGA 827

## RESULT 15

US-09-265-315-33/c  
; Sequence 33, Application US/09265315  
; Patent No. 6187541

GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Ving J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
TITLE OF INVENTION: TARGET GENES  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996

APPLICATION NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 240/247

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 1876 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-265-315-33

Query Match 67.3%; Score 14.8; DB 4; Length 1876;  
Best Local Similarity 88.9%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttcaga 19

||||| |||||||

Db 844 GACTGTAATGTTCCAGA 827

Search completed: October 9, 2001, 15:42:03  
Job time: 293 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:19:04 ; Search time 2150.93 Seconds  
(without alignments)  
186.971 Million cell updates/sec

Title: US-09-713-136-5  
Perfect score: 26  
Sequence: 1 tccataacgttcgcctaacgttgc 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- GenEmbl:\*
- 1: gb\_ba1:\*
  - 2: gb\_ba2:\*
  - 3: gb\_ba3:\*
  - 4: gb\_in1:\*
  - 5: gb\_in2:\*
  - 6: gb\_in3:\*
  - 7: gb\_om:\*
  - 8: gb\_ov:\*
  - 9: gb\_pat1:\*
  - 10: gb\_pat2:\*
  - 11: gb\_ph:\*
  - 12: gb\_p11:\*
  - 13: gb\_p12:\*
  - 14: gb\_p13:\*
  - 15: gb\_p14:\*
  - 16: em\_ba1:\*
  - 17: em\_ba2:\*
  - 18: em\_fun:\*
  - 19: em\_htgo\_hum:\*
  - 20: em\_htgo\_inv:\*
  - 21: em\_htgo\_rod:\*
  - 22: em\_htg\_hum1:\*
  - 23: em\_htg\_hum2:\*
  - 24: em\_htg\_hum3:\*
  - 25: em\_htg\_hum4:\*
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  - 27: em\_htg\_hum6:\*
  - 28: em\_htg\_hum7:\*
  - 29: em\_htg\_hum8:\*
  - 30: em\_htg\_inv1:\*
  - 31: em\_htg\_inv2:\*
  - 32: em\_htg\_rod:\*
  - 33: em\_hum1:\*
  - 34: em\_hum2:\*
  - 35: em\_hum3:\*
  - 36: em\_hum4:\*
  - 37: em\_hum5:\*
  - 38: em\_hum6:\*
  - 39: em\_hum7:\*
  - 40: em\_in:\*
  - 41: em\_om:\*
  - 42: em\_or:\*
  - 43: em\_or:\*

- 44: em\_ov:\*
- 45: em\_pat:\*
- 46: em\_ph:\*
- 47: em\_p1:\*
- 48: em\_ro:\*
- 49: em\_sts:\*
- 50: em\_sv:\*
- 51: em\_un:\*
- 52: em\_v1:\*
- 53: gb\_sts1:\*
- 54: gb\_sts2:\*
- 55: gb\_sts3:\*
- 56: gb\_sv:\*
- 57: gb\_un:\*
- 58: gb\_v1:\*
- 59: gb\_v12:\*
- 60: gb\_htg1:\*
- 61: gb\_htg2:\*
- 62: gb\_htg3:\*
- 63: gb\_htg4:\*
- 64: gb\_htg5:\*
- 65: gb\_htg6:\*
- 66: gb\_htg7:\*
- 67: gb\_htg8:\*
- 68: gb\_htg9:\*
- 69: gb\_htg10:\*
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- 72: gb\_htg13:\*
- 73: gb\_htg14:\*
- 74: gb\_htg15:\*
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- 77: gb\_htg18:\*
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- 82: gb\_htg23:\*
- 83: gb\_htg24:\*
- 84: gb\_htg25:\*
- 85: gb\_pr1:\*
- 86: gb\_pr2:\*
- 87: gb\_pr3:\*
- 88: gb\_pr4:\*
- 89: gb\_pr5:\*
- 90: gb\_pr6:\*
- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_rol:\*
- 95: gb\_rod:\*
- 96: gb\_in4:\*
- 97: gb\_pr10:\*
- 98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
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2	18.2	70.0	40400	63	AC012915	AC012915 Drosophila
c 3	18.2	70.0	42141	6	CEY54G9A	AL032648 Caenorhab
4	18.2	70.0	158322	62	AC011759	AC011759 Drosophila
5	18.2	70.0	274388	4	AE003574	AE003574 Drosophila
c 6	18.2	70.0	300197	83	CEY54G9	298869 Caenorhabdi
7	18	69.2	1900	89	AK024330	AK024330 Homo sapi
8	18	69.2	80677	13	ATM3E9	AL022223 Arabidops

```

c 9 18 69.2 81975 60 AC005415
c 10 18 69.2 92837 60 AC005716
c 11 18 69.2 110525 85 AB020878
c 12 18 69.2 175007 4 AC008342
c 13 18 69.2 190429 79 ALJ353141
c 14 18 69.2 198320 13 ATCHRIV65
c 15 18 69.2 211784 65 AC017903
c 16 18 69.2 259445 5 AE003811
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## ALIGNMENTS

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LOCUS Sequence 5 from Patent WO0112223.
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VERSION AX083679.1 GI:13185411
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 26)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
Dynamax Technologies Corporation (US)
Patent: WO 011223-A 5 22-FEB-2001.
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ORIGIN
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS pieces.
AC012915
AC012915.1 GI:6223407
VERSION HTG: HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 40400)
ACCESSION AC012915
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10211446 by the submitter.
For further information on this sequence you may e-mail to
fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Best Local Similarity 87.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 cataacgttcgcctaacgttcgtc 25
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ACCESSION AL032648 298869
VERSION AL032648.1 GI:3810715
KEYWORDS HTG.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 42141)
REFERENCE 1 (bases 1 to 42141)
AUTHORS none.
TITLE Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
JOURNAL Science 282 (5396), 2012-2018 (1998)
MEDLINE 99069613
REMARK The C. elegans Sequencing Consortium.
REFERENCE 2 (bases 1 to 42141)
AUTHORS Smeyers, R.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1998) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jesse@sanger.ac.uk or twenematode.wustl.edu
COMMENT Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.

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\* 157670 158322: contig of 653 bp in length.  
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Best Local Similarity 87.0%; Pred. No. 2.5e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 cataacgttcgcctaacgttcgt 25  
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LOCUS Drosophila melanogaster genomic scaffold 142000013386033 section 1  
DEFINITION of 2, complete sequence.  
ACCESSION AE003574 AE002629  
VERSION AE003574.3 GI:10803726  
KEYWORDS HTG.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE  
1 (bases 1 to 274388)  
Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,  
Amanatides,P.G., Scherer,S.E., Li,P.M., Hoskins,R.A., Galle,R.F.,  
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\* 156876 156955: gap of unknown length  
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Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T.,  
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 Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,  
 Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.  
 The genome sequence of *Drosophila melanogaster*  
 Science 287 (5461), 2185-2195 (2000)  
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 2 (bases 1 to 274388)  
 Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.  
 Direct Submission  
 Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,  
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 On Oct 16, 2000 this sequence version replaced gi:10726352.  
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 LOCUS  
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 PROGRESS \*\*\*, in unordered pieces.

ACCESSION 298869.1 GI:3191951

VERSION HTG; HTGS\_PHASE1.

KEYWORDS Caenorhabditis elegans.

SOURCE Caenorhabditis elegans.

ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

REFERENCE Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 300197)

FEATURES

source

Location/Qualifiers

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ORIGIN

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Best Local Similarity 87.0%; Pred. No. 2.5e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 7

AK024330

LOCUS

DEFINITION Homo sapiens cDNA FLJ14268 fls, clone PLACE1003383.

29-SEP-2000

PRI

AK024330

LOCUS

DEFINITION Homo sapiens cDNA FLJ14268 fls, clone PLACE1003383.

29-SEP-2000

PRI

AK024330

LOCUS

DEFINITION Homo sapiens cDNA FLJ14268 fls, clone PLACE1003383.

29-SEP-2000

PRI

AK024330

LOCUS

DEFINITION Homo sapiens cDNA FLJ14268 fls, clone PLACE1003383.

29-SEP-2000

PRI

AK024330

LOCUS

DEFINITION Homo sapiens cDNA FLJ14268 fls, clone PLACE1003383.

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PRI

AK024330

LOCUS

DEFINITION Homo sapiens cDNA FLJ14268 fls, clone PLACE1003383.

ACCESSION

AK024330

VERSION

GI:10436689

KEYWORDS

oligo capping; fls (full insert sequence).

SOURCE

Homo sapiens

clone: PLACE1003383.

ORGANISM

Homo sapiens

Eukaryota; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (sites)

Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,

Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,

Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,K., Takeuchi,K.,

Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamanoto,J.,

Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuho,Y. and Oshima,A.

NEDO human cDNA sequencing project

Unpublished (2000)

2 (bases 1 to 1900)

Isogai,T. and Otsuki,T.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao

Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana,

Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp,

Tel:81-438-52-3951, Fax:81-438-52-3952)

NEDO human cDNA sequencing project supported by Ministry of

International Trade and Industry of Japan; cDNA full insert

sequencing; Research Association for Biotechnology; cDNA library

construction, 5'- & 3'-end one pass sequencing and clone selection;

Helix Research Institute (supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science,

University of Tokyo.

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="PLACE1003383"

/clone\_lib="PLACE1"

/tissue\_type="placenta"

/note="Cloning vector: pME185FL3"

BASE COUNT 460 a 420 c 454 g 566 t

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Best Local Similarity 80.8%; Pred. No. 3.7e+02;

Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgttcgc 26

Db 916 TCCCTAAGGTTCTCTAACTTCTTC 941

RESULT 8

ATM3E9

LOCUS

80677 bp DNA PLN 05-AUG-1999

DEFINITION Arabidopsis thaliana DNA chromosome 4, P1 clone M3E9 (ESSA

project).

ACCESSION AL022223

VERSION AL022223.3 GI:5708090

KEYWORDS

SOURCE

thale cress.

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 80677)

Bevan,M., Vandenbol,M., Jallet,C., Portetelle,D., Hohensei,J.,

Mewes,H.W., Mayer,K.F.X., Lemcke,K. and Schueller,C.

Unpublished

2 (bases 1 to 80677)

EU Arabidopsis sequencing project.

Direct Submission

TITLE

JOURNAL

REFERENCE

Submitted (05-AUG-1999) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitze 18a, D-82152 Martinsried, FRG, E-mail:

schuellemips.biochem.mpg.de,mayeremips.biochem.mpg.de Project  
 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge  
 Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,  
 E-mail: michael.bevan@bbsrc.ac.uk  
 On Aug 6, 1999 this sequence version replaced gi:4468103.  
 Information on performance of analysis and a more detailed  
 annotation of this entry and other sequences of chromosomes 3, 4  
 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

## COMMENT

## FEATURES

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exon  
 gene  
 CDS



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Query Match 69.2%; Score 18; DB 60; Length 81975;  
 Best Local Similarity 80.8%; Pred. NO. 3.2e+02;  
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 56750 TCCAGTACGTCGCTGCTCGAC 56725

# RESULT 10

AC005716/c

LOCUS

DEFINITION

AC005716 92837 bp DNA HTG 23-NOV-1999

Drosophila melanogaster chromosome 2 clone DS00150 (D438) map

51E9-51F2 strain Y; cn bw sp, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 13

unordered pieces.

AC005716

AC005716.8 GI:6466502

HTG: HTGS\_PHASE1.

SOURCE

ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 92837)

REFERENCE

AUTHORS

Celniker, S.E., Agbayani, A., Arcalona, T.T., Baxter, E., Blazej, R.G.,

Agbayani, A., Arcalona, T.T., Baxter, E., Blazej, R.G., Chavez, C.,

Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A.,

Hummas, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B.,

Lomtan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R.,

Moshrefi, M., Nixon, K., Paclet, J.M., Park, S., Pfeiffer, B.,

Snir, E., Twomey, B., Wan, K.H., Webster, D.,

Woolley, P., Yang, S., Yee, M., Yu, C., and Rubin, G.M.

Sequencing of Drosophila melanogaster

Unpublished

2 (bases 1 to 92837)

Celniker, S.E., Agbayani, A., Arcalona, T.T., Baxter, E., Blazej, R.G.,

Agbayani, A., Arcalona, T.T., Baxter, E., Blazej, R.G., Chavez, C.,

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Moshrefi, M., Nixon, K., Paclet, J.M., Park, S., Pfeiffer, B.,

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Celniker, S.E., Agbayani, A., Arcalona, T.T., Baxter, E., Blazej, R.G.,

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Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A.,

Hummas, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B.,

Lomtan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R.,

Moshrefi, M., Nixon, K., Paclet, J.M., Park, S., Pfeiffer, B.,

Snir, E., Twomey, B., Wan, K.H., Webster, D.,

Woolley, P., Yang, S., Yee, M., Yu, C., and Rubin, G.M.

Sequencing of Drosophila melanogaster

Unpublished

2 (bases 1 to 92837)

Celniker, S.E., Agbayani, A., Arcalona, T.T., Baxter, E., Blazej, R.G.,

Agbayani, A., Arcalona, T.T., Baxter, E., Blazej, R.G., Chavez, C.,

Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A.,

Hummas, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B.,

Lomtan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R.,

Moshrefi, M., Nixon, K., Paclet, J.M., Park, S., Pfeiffer, B.,

Snir, E., Twomey, B., Wan, K.H., Webster, D.,

Woolley, P., Yang, S., Yee, M., Yu, C., and Rubin, G.M.

Sequencing of Drosophila melanogaster

Unpublished





Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.

1 (bases 1 to 175007)

REFERENCE  
AUTHORS  
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Cocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banton, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champs, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ingwam, C., Jalali, M., Kruse, D., Li, P., Matteli, B., Moshrefi, A., Mcintosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleib, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
Sequencing of Drosophila chromosome 2R, region 51F-51F

2 (bases 1 to 175007)

Unpublished

CELNIKER, S.E., ADAMS, M.D., KRONMILLER, B., TYLER, D., WAN, K.H., BUTENHOFF, C., CHAMPE, M., CHAVEZ, C., CHEW, M., CIESIOLOKA, L., DOYLE, C.M., FARFAN, D.E., GALLE, R., GEORGE, R.A., HARRIS, N.L., HOSKINS, R.A., HOUSTON, K.A., HUMMASTI, S.R., KARRA, K., KEARNEY, L., KIM, E., LEE, B., LEWIS, S., LI, P., LOMOTAN, M.A., MAZDA, P., MOSHREFI, A.R., MOSHREFI, M., NIXON, K., PACLEIB, J.M., PARK, S., PFEIFFER, B., POON, L., SEQUEIRA, A., SETHI, H., SNIR, E., SVIRSKAS, R.R., WAN, K.H., WEINBURG, T., ZHANG, R., ZIERAN, L.L. and RUBIN, G.M.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
Direct Submission

Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Mar 22, 2001 this sequence version replaced gi:7118739.

Sequence submitted by:  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory, MS 64-121  
Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (<http://www.fruitfly.org/sequence/>) or send email to [bdgpf@fruitfly.berkeley.edu](mailto:bdgpf@fruitfly.berkeley.edu).

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/strain="v: cn bw sp"  
/db\_xref="taxon:7227"  
/chromosome="2R"  
/map="51F-51F"  
/clone="BACR33K06 (D930)"  
/clone\_lib="RPCI-98 (Roswell Park Cancer Institute  
Drosophila melanogaster BAC library, partial EcoRI in  
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BASE COUNT 51366 a 37358 c 37136 g 48947 t  
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Query Match 69.2%; Score 18; DB 4; Length 175007;  
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Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgtc 26  
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Db 87729 TCCAGTACGTCGCTGCTCGAC 87704

RESULT 13  
LOCUS AL353141/c  
DEFINITION Homo sapiens chromosome 9 clone RP11-58C3, \*\*\* SEQUENCING IN  
PROGRESS \*\*\*, 10 unordered pieces.  
ACCESSION AL353141  
VERSION AL353141.8 GI:13016504  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE  
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human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 190429)  
Plumb, B.  
Direct Submission  
Submitted (18-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
On Feb 20, 2001 this sequence version replaced gi:12964411.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
----- Project information  
Center project name: BA58C3  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: M13; M77815; 0% of reads  
Sequencing vector: plasmid; L08752; 99% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 184146 bases at least Q40  
Consensus quality: 186729 bases at least Q30  
Consensus quality: 188260 bases at least Q20  
Insert size: 189529; sum-of-contigs  
Insert size: 217333; agarose-fp  
Quality coverage: 5.94x in Q20 bases; sum-of-contigs Quality  
coverage: 5.52x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 10 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 72909: contig of 72909 bp in length  
\* 72910 73009: gap of 100 bp  
\* 73010 85724: contig of 12715 bp in length  
\* 85725 85824: gap of 100 bp  
\* 85825 89598: contig of 3774 bp in length  
\* 89599 89698: gap of 100 bp  
\* 89699 94785: contig of 5087 bp in length  
\* 94786 94885: gap of 100 bp  
\* 94886 98698: contig of 3813 bp in length  
\* 98699 98798: gap of 100 bp  
\* 98799 151407: contig of 52609 bp in length  
\* 151408 151507: gap of 100 bp  
\* 151508 155590: contig of 4083 bp in length  
\* 155591 155690: gap of 100 bp  
\* 155691 184932: contig of 29242 bp in length  
\* 184933 185032: gap of 100 bp  
\* 185033 187234: contig of 2202 bp in length  
\* 187235 187334: gap of 100 bp  
\* 187335 190429: contig of 3095 bp in length.  
\* 187335 190429: contig of 3095 bp in length.  
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/note="assembly\_fragment:02762  
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85825..89598  
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85825..89598

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98799..151407  
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151508..155590  
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/note="assembly\_fragment:02112"  
185033..187234  
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187335..190429  
/note="assembly\_fragment:02735"  
BASE COUNT 56376 a 39536 c 38540 g 56071 t 906 others  
ORIGIN

Query Match 69.2% Score 18; DB 79; Length 190429;  
Best Local Similarity 80.8%; Pred. No. 3.2e+02;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaagcttcgc 26  
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Db 129081 TCCCTAAGGTTCTCCTAACTTCTTC 129056

## RESULT 14

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LOCUS ATCHRIV65 198320 bp DNA PLN 16-MAR-2000  
DEFINITION Arabidopsis thaliana DNA chromosome 4., contig fragment No. 65.  
ACCESSION AL161565  
VERSION AL161565.2 GI:7269481  
KEYWORDS thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 25731 to 106407)  
AUTHORS Vandenbol,M., Jallet,C., Portetelle,D., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  
JOURNAL Unpublished  
REFERENCE 2 (bases 68133 to 160789)  
AUTHORS Zimmermann,W., Grueneisen,A., Wambutt,R., Kalicki,J., Wohldmann,P., Smith,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  
JOURNAL Unpublished  
REFERENCE 3 (bases 92775 to 93172)  
AUTHORS Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  
JOURNAL Unpublished  
REFERENCE 4 (bases 149164 to 198320)  
AUTHORS Lecharny,A., Cheddor,F., Krivitzky,M., Kreis,M., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  
JOURNAL Unpublished  
REFERENCE 5 (bases 1 to 42972)  
AUTHORS Rose,M., Hempel,S., Entian,K.-D., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  
JOURNAL Unpublished  
REFERENCE 6 (bases 1 to 198320)  
AUTHORS EU Arabidopsis sequencing,project.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemckemips.biochem.mpg.de,mayer@mips.biochem.mpg.de  
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@ebc.ac.uk  
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>  
this fragment has an overlap with ATCHRIV64 at the 5' end and an overlap with ATCHRIV66 at the 3' end.

FEATURES  
source

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complement(join(5578..5688,5802..5900,5995..6063,6449..6538,6620..6689,6872..6941,7047..7233,7337..7421,7592..7770,7871..7975,8089..8172,8302..8382,8490..8705,8795..8896,8975..9050,9148..9287,9374..9448,10198..10287))  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:19 ; Search time 6788.49 Seconds  
(without alignments)  
36.205 Million cell updates/sec

Title: US-09-713-136-5

Perfect score: 26

Sequence: 1 tccataacgttcgcctaacttcgtc 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_est4:\*
- 5: gb\_est5:\*
- 6: gb\_est6:\*
- 7: gb\_est7:\*
- 8: gb\_est8:\*
- 9: gb\_est9:\*
- 10: gb\_est10:\*
- 11: gb\_est11:\*
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249: gb_est180:*
250: gb_est181:*
251: gb_est182:*
252: gb_est183:*
253: gb_est184:*
254: gb_est185:*
255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	18.6	71.5	788	137	BE547778	601073614
C 2	18.6	71.5	820	168	BF679824	602154407
C 3	18.2	70.0	241	104	AJ285626	4A3B-RAV-
C 4	17.6	67.7	694	23	AI657535	AEMTBD55
C 5	17.4	66.9	639	32	AV679043	AV679043
C 6	17.2	66.2	511	238	A2139831	SP_0002_B
C 7	17.2	66.2	666	11	AA736360	SMOVL3CAN
C 8	17.2	66.2	970	219	CNS0184T	AL108887
C 9	17.2	66.2	318	121	AW883193	Drosophila
C 10	17.2	65.4	392	225	AO182480	HS_3077_A
C 11	17.2	65.4	461	12	AA787178	AO182480
C 12	17.2	65.4	544	154	BC486179	dad23h02
C 13	17.2	65.4	635	142	BE976680	bs4e12.y
C 14	17.2	65.4	673	142	BE975036	bs37h07.y
C 15	17.2	65.4	894	136	BE542042	601066950
C 16	16.8	64.6	242	161	BE576549	BB576549
C 17	16.8	64.6	360	156	C13137	C13137
C 18	16.8	64.6	376	156	C68546	C68546
C 19	16.8	64.6	388	1	AA002481	mq42c12.r
C 20	16.8	64.6	439	151	BF648336	NF044H02E
C 21	16.8	64.6	535	151	BF643349	NF003E11E
C 22	16.8	64.6	576	175	BC269530	LO-3615T3
C 23	16.8	64.6	581	137	BE576991	LO-1602T3
C 24	16.8	64.6	656	151	BF646041	NF065A11E
C 25	16.8	64.6	735	162	BE034900	ML05H05.M
C 26	16.8	64.6	862	162	BE035137	MM03G09.M
C 27	16.6	63.8	329	157	D64542	CELK054B9R
C 28	16.6	63.8	460	31	AV639729	AV639729
C 29	16.6	63.8	470	20	AI466838	mz48e08.y
C 30	16.6	63.8	504	164	BE195754	HVSMEH009
C 31	16.6	63.8	574	16	AI113909	GH10417.5
C 32	16.6	63.8	598	231	AQ657044	Sheared.D
C 33	16.6	63.8	608	232	AQ676154	HS_2133_B
C 34	16.6	63.8	750	239	A2183794	SP_1002_A
C 35	16.6	63.8	843	172	BF975514	602245859
C 36	16.6	63.8	902	136	BE541188	601064049
C 37	16.6	63.8	1098	220	CNS037VI	Tetraodon
C 38	16.4	63.1	179	120	AW799829	PML-UM005
C 39	16.4	63.1	211	121	AW838879	CMO-LT005
C 40	16.4	63.1	216	170	BF820251	CMO-RT001
C 41	16.4	63.1	290	120	AW728832	GA-Ea002
C 42	16.4	63.1	345	19	AI359428	gy31g02.x
C 43	16.4	63.1	352	110	AW023566	df56h03.y
C 44	16.4	63.1	360	26	AV190522	AV190522
C 45	16.4	63.1	360	156	C40605	C40605

ALIGNMENTS

RESULT	BE547778/c	1
LOCUS	601073614F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3459602 5', mRNA sequence.	788 bp EST 09-AUG-2000
DEFINITION	BE547778	
ACCESSION	BE547778	
VERSION	BE547778.1	GI:9776423
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	1 (bases 1 to 788)	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D.	

Email: cgapbs-remail.nih.gov	
Tissue Procurement: ATCC	
CDNA Library Arrayed by: Incyte Genomics, Inc.	
CDNA Sequencing by: Incyte Genomics, Inc.	
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	
http://image.llnl.gov	
High quality sequence stop: 372.	
Location/Qualifiers	
1. 788	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:3459602"	
/clone_lib="NIH_MGC_12"	
/issue_type="cervical carcinoma cell line"	
/lab_host="DH10B"	
/note="Organ: Cervix; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies."	
BASE COUNT	168 a 247 c 197 g 176 t
ORIGIN	
Query Match 71.5%; Score 18.6; DB 137; Length 788;	
Best Local Similarity 84.0%; Pred. No. 30;	
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY 2 ccataacgttcgcctaacgttcgc 26	
Db 412 CCAGAAAGTTCGCTCAGTTCCTC 388	
RESULT 2	
LOCUS	BF679824/c
DEFINITION	BF679824 820 bp mRNA EST 21-DEC-2000
ACCESSION	602154407F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295593 5', mRNA sequence.
VERSION	BF679824
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 820)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov	
Tissue Procurement: CLONETECH Laboratories, Inc.	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
CDNA Sequencing by: Incyte Genomics, Inc.	
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	
http://image.llnl.gov	
High quality sequence stop: 599.	
Location/Qualifiers	
1. 820	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:4295593"	
/clone_lib="NIH_MGC_83"	
/lab_host="DH10B (T1 phage-resistant)"	
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggcgcgtcgcc); Site: 2: SfiI (ggcattatggcc ); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTTATGGCC-3' and 3' adaptor	

sequence: 5'-ATTCTAGAGCGGCGGCGGACATG-dt(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

BASE COUNT 284 a 180 c 201 g 175 t  
ORIGIN

Query Match 71.5%; Score 18.6; DB 168; Length 820;  
Best Local Similarity 84.0%; Pred. No. 31;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgt 25  
||||| ||||| ||||| ||||| |||||

Db 593 TCCATCAGTCGCGCTAACTTTGT 569

## RESULT 3

LOCUS AJ285626 241 bp mRNA EST 30-JUN-2000  
DEFINITION 4A3B-AAV-D-11-R Anopheles gambiae immune competent 4A3B Anopheles  
gambiae cDNA clone 4A3B-AAV-D-11, mRNA sequence.

ACCESSION AJ285626

VERSION AJ285626.1 GI:6933507

KEYWORDS EST.

SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae  
; Anopheles.

REFERENCE 1 (bases 1 to 241)

AUTHORS Dimopoulos G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,  
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B.  
and Kafatos, F.C.

TITLE Anopheles gambiae pilot gene discovery project: identification of  
mosquito innate immunity genes from expressed sequence tags  
generated from immune-competent cell lines

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

MEDLINE 20300950

COMMENT Contact: Dimopoulos G  
Fotis C. Kafatos laboratory  
European Molecular Biology Laboratory  
Meyerhofstrasse 1, 69117 Heidelberg, Germany.  
Location/Qualifiers

## FEATURES

source  
1..241  
/organism="Anopheles gambiae"  
/strain="4A r/r"  
/db\_xref="taxon:7165"  
/clone="4A3B-AAV-D-11"  
/clone\_lib="Anopheles gambiae immune competent 4A3B"  
/cell\_line="immune competent 4A3B"  
/lab\_host="E. coli DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from  
the forward priming site that reads from the 3' end of  
cDNA. The 4A3B is a directionally cloned and normalized  
cDNA library that was constructed from the 4A3B cell line  
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares  
(1996): Normalization and Subtraction: Two Approaches To  
Facilitate Gene Discovery, Genome Research 6, 791-806."

BASE COUNT 40 a 43 c 40 g 118 t

## ORIGIN

Query Match 70.0%; Score 18.2; DB 104; Length 241;  
Best Local Similarity 87.0%; Pred. No. 43;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ccataacgttcgcctaacgttcg 24  
||||| ||||| ||||| ||||| |||||

Db 189 CCATTAACGTTCCCTAACGCTCG 211

## RESULT 4

LOCUS AI657535/c 594 bp mRNA EST 05-MAY-1999  
DEFINITION AEMTBD55 Aedes aegypti MT pSPORT Library Aedes aegypti cDNA clone  
BD55 5', mRNA sequence.

ACCESSION AI657535

VERSION AI657535.1 GI:4753625

KEYWORDS EST.

SOURCE yellow fever mosquito.

ORGANISM Aedes aegypti

REFERENCE 1 (bases 1 to 694)  
Gill, S.S., Ross, L.S. and Wadiak, H.  
Expressed sequence tags of cDNA clones from an enriched Malpighian  
tubule and gut library from Aedes aegypti  
Unpublished (1999)

JOURNAL

COMMENT Contact: Gill SS  
Environmental Toxicology  
University of California, Riverside  
5419 Boyce Hall, Riverside, CA 92521, USA  
Tel: 909 787 3547  
Fax: 909 787 3087  
Email: sarjeet.gill@ucr.edu  
Seq primer: CCAAGCTCTAATACGACTCACTAT  
High quality sequence stop: 694.  
Location/Qualifiers

FEATURES source

1..694  
/organism="Aedes aegypti"  
/db\_xref="taxon:7159"  
/clone="BD55"  
/clone\_lib="Aedes aegypti MT pSPORT Library"  
/sex="female"  
/tissue\_type="malpighian tubules and gut"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; The  
cDNA was cloned into the SalI/NotI sites of pSPORT1."  
BASE COUNT 195 a 150 c 154 g 195 t  
ORIGIN

Query Match 67.7%; Score 17.6; DB 23; Length 694;  
Best Local Similarity 83.3%; Pred. No. 98;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 cataacgttcgcctaacgttcgct 26  
||| ||||| ||||| ||||| |||||

Db 422 CACATCGTTCTCCTAACGTTGTC 399

## RESULT 5

LOCUS AV679043 639 bp mRNA EST 05-OCT-2000  
DEFINITION AV679043 Nori Satoh unpublished cDNA library Ciona intestinalis  
cDNA clone rcitb14j20 3', mRNA sequence.

ACCESSION AV679043

VERSION AV679043.1 GI:10117042

KEYWORDS EST.

SOURCE Ciona intestinalis.

ORGANISM Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
Phlebobranchia; Cionidae; Ciona.

REFERENCE 1 (bases 1 to 639)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.

TITLE Expressed genes in Ciona intestinalis

JOURNAL Unpublished (2000)

COMMENT Contact: Nori Satoh  
Department of Zoology  
Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: sato@ascidian.zool.kyoto-u.ac.jp.

# FEATURES

Location/Qualifiers  
1. 639

/organism="Clona intestinalis"  
/db\_xref="taxon:7719"  
/clone="rcitb14j20"  
/clone\_lib="Nori Sato unpublished cDNA library"  
/tissue\_type="whole animal"  
/dev\_stage="tailbud"

169 a 142 c 141 g 187 t

BASE COUNT  
ORIGIN

Query Match 66.9%; Score 17.4; DB 32; Length 639;  
Best Local Similarity 94.7%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 catacgttcgcctaact 21  
|||||

DB 464 CATCAGTTCGCCTACGT 482

# RESULT 6

AZ139831 511 bp DNA GSS 28-AUG-2000  
SP\_0002.B2.F04.T7 Strongylocentrotus purpuratus, purple sea urchin,  
sperm genomic BAC library Strongylocentrotus purpuratus genomic  
clone Plate-2 Col-8 Row-L, DNA sequence.

ACCESSION AZ139831  
VERSION AZ139831.1 GI:8291734

KEYWORDS Strongylocentrotus purpuratus  
SOURCE GSS.

ORGANISM Strongylocentrotus purpuratus  
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
Echinoidea; Euechinoidea; Echinacea; Echinoida;  
Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 511)  
AUTHORS Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,  
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray  
G.A., Etensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and  
Hood,L.

TITLE A sea urchin genome project: Sequence scan, virtual map, and  
additional resources  
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)

MEDLINE 20402565

COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L  
Division of Biology 156-29  
California Institute of Technology  
Pasadena California 91125, USA  
Tel: (626) 395-8421  
Fax: (626) 793-3047  
Email: acameron@caltech.edu

Plate: 2 row: L column: 8  
Seq primer: T7

Class: BAC ends  
High quality sequence stop: 511.

Location/Qualifiers  
1. 511

/organism="Strongylocentrotus purpuratus"  
/db\_xref="taxon:7668"

/clone="plate-2 Col-8 Row-L"  
/clone\_lib="Strongylocentrotus purpuratus, purple sea  
urchin, sperm genomic BAC library."  
/note="Organ: Sperm; Vector: BAC3.6; BAC Clones in E-Coli  
DH10B"

127 a 125 c 106 g 153 t

BASE COUNT  
ORIGIN

Query Match 66.2%; Score 17.2; DB 238; Length 511;

Best Local Similarity 86.4%; Pred. NO. 1.5e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ataacgttcgcctaactcgt 25  
|||||

DB 381 ATCAGTTCGCCTAATGTAGT 402

# RESULT 7

AZ736360/c 666 bp mRNA EST 12-JAN-1998  
LOCUS SMOVL3CAN06F1L3K Onchocerca volvulus infective larva cDNA  
DEFINITION (SAW94WL-OVL3) Onchocerca volvulus cDNA clone SMOVL3CAN06F1L 5',  
mRNA sequence.

ACCESSION AZ736360  
VERSION AZ736360.1 GI:2767117

KEYWORDS EST.

SOURCE Onchocerca volvulus.

ORGANISM Onchocerca volvulus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Onchocerca.

REFERENCE 1 (bases 1 to 666)  
AUTHORS Williams,S.A., Lu,W., Lizotte-Waniewski,M. and Laney,S.J.  
TITLE Genes expressed in infective third stage larvae of Onchocerca  
volvulus  
JOURNAL Unpublished (1995)

COMMENT Contact: Steven A. Williams

Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: genomesmith.edu

Seq primer: pluescript SK.  
Location/Qualifiers  
1. 666

/organism="Onchocerca volvulus"  
/strain="Sierra Leone"  
/db\_xref="taxon:6282"

/clone="SMOVL3CAN06F1L"  
/clone\_lib="Onchocerca volvulus infective larva cDNA  
(SAW94WL-OVL3)"  
/lab\_host="X11-Blue MRF"

/note="Vector: lambda UniZap XR; Site\_1: Ecor I; Site\_2:  
Xho I; Cutaneous filarial nematode parasite of humans.  
mRNA was prepared from third stage infective larvae of  
Onchocerca volvulus isolated from mosquitoes 10 days after  
infection and converted to double stranded cDNA using  
reverse transcriptase and oligo(dT) followed by RNase H  
and DNAPol I. The library had 1.8 x 10E5 independent  
recombinants and average insert size was 900 base pairs.  
The library was constructed by Wenhong Lu. The library is  
available from Dr. S.A. Williams, email genomesmith.edu."

BASE COUNT 232 a 101 c 129 g 179 t 25 others  
ORIGIN

Query Match 66.2%; Score 17.2; DB 11; Length 666;  
Best Local Similarity 86.4%; Pred. No. 1.6e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaactt.22  
|||||

DB 492 TCCATAACGTTTCATCTAATCTT 471

# RESULT 8

CNS0184T 970 bp DNA GSS 26-JUL-1999  
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
DEFINITION BACN01B10 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.



```

ACCESSION AL108887
VERSION AL108887.1 GI:5629191
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Plasmid Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
          Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 970)
          Genoscope.
          TITLE Direct Submission
          JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
          COMMENT Determination of this BAC-end sequence was carried out as part of a
          collaboration with the European Drosophila Genome Project (EDGP) -
          http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
          library (Dros BAC) was made by Alain Billaud at CEPH (Centre
          d'Etude du Polymorphisme Humain) with funding provided by a MRC
          project grant. The DNA was prepared from embryos by Alain Bucheton
          and Genevieve Payan. It has been constructed in the vector
          pBelobAC11.
FEATURES             Location/Qualifiers
     source           1..970
                     /organism="Drosophila melanogaster"
                     /plasmid="pBelobAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN01B10"
                     /note="end : T7"
BASE COUNT  414 a 107 c 114 g 188 t 147 others
ORIGIN
Query Match      66.2%; Score 17.2; DB 219; Length 970;
Best Local Similarity 86.4%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tccataacgttcgctaacgtt 22
    | ||||| ||||| || |||
Db 521 TTCATAACGTTCCGCCAATGTT 500

RESULT 9
AW883193
LOCUS AW883193 318 bp mRNA EST 23-MAY-2000
DEFINITION QV2-OT00062-010500-177-f09 OT0062 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW883193
VERSION AW883193.1 GI:8045205
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 318)
          Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
          Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
          Goldman, G. H., Carvalho, A. F., Matsukuma, A. A., Baia, G. S., Simpson, D. H.,
          Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare
          , M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
          Simpson, A. J.
          TITLE Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
          JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000).
          MEDLINE 20202663
          COMMENT Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-QV2-OT0062-010
500-177-f09&tl=2000-05-01&tl=1)
Seq primer: puc 18 forward
High quality sequence start: 86
High quality sequence stop: 165.
FEATURES             Location/Qualifiers
     source           1..318
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="OT0062"
                     /dev_stage="Adult"
                     /note="Organ: ovary; Vector: puc18; Site: 1; SmaI; Site: 2;
                     SmaI; A mini-library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 - Ludwig Institute for Cancer Research) profiles
                     into the puc 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT  70 a 87 c 81 g
ORIGIN
Query Match      65.4%; Score 17; DB 121; Length 318;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ccataacgttcgctaacgttcgtc 26
    | ||||| ||||| || |||
Db 21 CCATGAAGTTCGCTCACTTTCCTC 45

RESULT 10
AQ182480/c
LOCUS AQ182480 392 bp DNA GSS 28-OCT-1998
DEFINITION HS.3077-AL.E11.MR.CIT Approved Human Genomic Sperm Library D Homo
          sapiens genomic clone Plate=3077 Col=21 Row=I, DNA sequence.
ACCESSION AQ182480
VERSION AQ182480.1 GI:3579847
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 392)
          Mahairas, G. G., Wallace, J. C., Smith, K., Swartzell, S., Holzman, T.,
          Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M. D. and
          Hood, L.
          TITLE Sequence-tagged connectors: A sequence approach to mapping and
          scanning the human genome
          JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
          MEDLINE 99380589
          COMMENT Contact: Mahairas GG, Wallace JC, Hood L
          High Throughput Sequencing Center
          University of Washington
          401 Queen Anne Avenue North, Seattle, WA 98109, USA
          Tel: (206) 616-3618
          Fax: (206) 616-3887
          Email: jwallace@u.washington.edu
          Sequence Tagged Connector
          Plate: 3077 row: I column: 21
          Class: BAC ends
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                     /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
                     E-Coli DH10B"

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Tissue isolation and library construction performed at the National Institute of Diabetes and Digestive and Kidney Diseases, NIH (see <http://www.niddk.nih.gov/intramur/people/bojiliver.htm>). DNA sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC; see <http://www.nisc.nih.gov>).

Page: 54 row: e column: 12  
Seq primer: M13RP1 reverse primer (ABI).

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/lab_host="DH10B"
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ORIGIN

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Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Search completed: October 9, 2001, 18:20:22
Job time: 9792 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:49 ; Search time 515.84 Seconds  
(without alignments)  
31.648 Million cell updates/sec

Title: US-09-713-136-5

Perfect score: 26  
Sequence: 1 tccataacgttcgctaactgcgtc 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SID58/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	26	100.0	26	AAV80100	Immunomodulatory o
2	26	100.0	26	AAAF38069	Immunostimulatory
3	26	100.0	26	AAF77044	Immunostimulatory
4	24	92.3	24	AAV80115	Oligo used in expe
5	24	92.3	24	AAV80116	Oligo used in expe
6	23	88.5	24	AAZ55885	Immunomodulatory o
7	22	84.6	24	AAZ55886	Immunomodulatory o
8	16.4	63.1	1034	AAC74251	Human secreted pro
c 9	16.4	63.1	1317	AAH13867	Enterococcus faeca
c 10	16.4	63.1	1413	AA42901	Arabidopsis thalia
11	16.4	63.1	1830	AAAC84343	Wheat Nph2-2 prote

c 12	16.4	63.1	2120	22	AAAC84345	Wheat Nph2-2 cDNA
c 13	16.4	63.1	3096	22	AAF75864	Histidine protein k
c 14	16.4	63.1	3708	22	AAF75866	Histidine protein k
c 15	16.4	63.1	4679	22	AAF75865	Histidine protein k
c 16	16.4	63.1	5245	21	AACT75103	Human ORFX ORF658
c 17	16.4	63.1	6184	22	AAAC86935	Nucleotide sequenc
c 18	16.4	63.1	7669	21	AAA52956	Xenorhabdus lumine
c 19	16	61.5	646	21	AAAC38576	Arabidopsis thalia
c 20	16	61.5	4453	20	AAAC38519	Human kidney amino
c 21	15.6	60.0	801	20	AAAC32664	Cassava Cu2n super
c 22	15.6	60.0	1005	21	AAAC49769	Human ARF-Related
c 23	15.6	60.0	119950	20	AAAC90201	Human yes1 gene.
c 24	15.4	59.2	46	21	AAAC99364	Human serum albumi
c 25	15.4	59.2	46	21	AAAC99511	Human serum albumi
c 26	15.4	59.2	51	21	AAAC99371	Human serum albumi
c 27	15.4	59.2	51	21	AAAC99518	Human serum albumi
c 28	15.4	59.2	542	18	AAH84047	DNA encoding a Sta
c 29	15.4	59.2	555	20	AAV89091	EST clone CD107.
c 30	15.4	59.2	553	21	AAA30907	Breast cancer DDPC
c 31	15.4	59.2	624	21	AAAF10147	Fusarium venenatum
c 32	15.4	59.2	648	21	AAAC00981	Human secreted pro
c 33	15.4	59.2	1029	17	AAAT30113	1-aminocyclopropan
c 34	15.4	59.2	1029	19	AAV09720	P. chloroaphis iso
c 35	15.4	59.2	1064	21	AAAC76897	Human ORFX ORF2452
c 36	15.4	59.2	1411	22	AAAF32659	Human cDNA encodin
c 37	15.4	59.2	1440	18	AAV74847	Staphylococcus aur
c 38	15.4	59.2	1758	13	AAO27462	Human ORFX ORF2452
c 39	15.4	59.2	1761	10	AAAC90997	Human serum albumi
c 40	15.4	59.2	1778	21	AAAC99311	Artificial gene co
c 41	15.4	59.2	1778	21	AAAC99458	Human serum albumi
c 42	15.4	59.2	1801	21	AAAC99310	Human serum albumi
c 43	15.4	59.2	1801	21	AAAC99457	Human serum albumi
c 44	15.4	59.2	1849	21	AAAC99308	Recombinant human
c 45	15.4	59.2	1849	21	AAAC99455	Recombinant human

ALIGNMENTS

RESULT 1	
AAV80100	
ID AAV80100 standard; DNA; 26 BP.	
XX AAV80100;	
AC AAV80100;	
XX 12-MAR-1999 (first entry)	
DT Immunomodulatory oligo comprising an ISS sequence.	
DE Immunomodulatory; Immunostimulatory; octanucleotide; immune regulation;	
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;	
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;	
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.	
XX Synthetic.	
OS OS	
XX WO9855495-A2.	
PN 10-DEC-1998.	
XX 05-JUN-1998; 98WO-US11578.	
XX 06-JUN-1997; 97US-0048793.	
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.	
XX Dina D, Roman M, Schwartz D;	
PI WPI; 1999-059898/05.	
XX Immunostimulatory oligonucleotides regulate the immune system - and	
PT contain an immune-stimulating octanucleotide sequence; for treating	
PT cancer, allergic and infectious diseases	

XX Claim 9; Page 29; 63pp; English.

PS The invention relates to immunomodulatory oligonucleotides that comprise

XX at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,

CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat

CC patients needing immune regulation, such as those suffering from cancer,

CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the

CC oligonucleotide; and determining the relative amount of Th1-biased

CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent

XX specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 26 BP; 5 A; 9 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 26; DB 20; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.00058;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgttcgc 26  
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 DB 1 tccataacgttcgcctaacgttcgc 26

RESULT 2

AAA38069

ID AAA38069 standard; DNA; 26 BP.

XX AC AAA38069;

XX 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #5:

XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;

KW gp120; human immunodeficiency virus; HIV; immune response; infection;

KW development; ss.

XX Synthetic.

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and

PT HIV glycoprotein gp120 useful for modulating, stimulating an immune

PT response against HIV in an HIV infected individual.

XX Disclosure; Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition

CC comprising a human immunodeficiency virus (HIV) antigen, and an

CC immunomodulatory polynucleotide comprising an immunostimulatory sequence

CC (ISS). This sequence represents an ISS that can be used in the

CC composition. An immunostimulatory composition which comprises a gp120

CC conjugated to an immunomodulatory polynucleotide, or is proximately

CC associated to it and not conjugated, is used for modulating or

CC stimulating a specific immune response against gp120 in an individual by

CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It

CC is also used for suppressing or delaying development of HIV infection in

CC an individual infected with HIV or an individual at risk of infection

CC with HIV, respectively. It is also used for treating an individual

XX infected with HIV in need of immune modulation.

XX Sequence 26 BP; 5 A; 9 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.00058;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgttcgc 26  
 |||||  
 DB 1 tccataacgttcgcctaacgttcgc 26

RESULT 3

AAF77044

ID AAF77044 standard; DNA; 26 BP.

XX AC AAF77044;

XX 15-MAY-2001 (first entry)

XX Immunostimulatory DNA #4.

XX Modulate; immune; antigen; immunostimulatory; ds.

XX Synthetic.

XX WO200112223-A2.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US22835.

XX 19-AUG-1999; 99US-0149768.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Van Nest G;

XX WPI; 2001-211136/21.

XX Modulating immune response to a second antigen in humans involves

PT administering an immunostimulatory polynucleotide comprising an

PT immunostimulatory sequence and a first antigen.

XX Disclosure; Page 15; 63pp; English.

XX The present invention relates to modulating an immune response to

CC a second antigen in an individual, involving

CC administering to the individual an immunomodulatory polynucleotide

CC comprising an immunostimulatory sequence (ISS) and a first antigen.

XX Sequence 26 BP; 5 A; 9 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 26; DB 22; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.00058;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgttcgc 26  
 |||||  
 DB 1 tccataacgttcgcctaacgttcgc 26

RESULT 4

AAV80115

```

ID  AAV80115 standard; DNA; 24 BP.
XX  AAV80115;
XX  12-MAR-1999 (first entry)
XX  Oligo used in experiments for stimulation of cytokine production.
XX  Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
XX  ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
XX  human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss:
XX  B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX  Synthetic.
XX  Key      Location/Qualifiers
FH  modified_base      8      /*tag= a
FT  /*tag= a
FT  /note= "5-bromocytosine"
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FT  /note= "5-bromocytosine"
XX  W09855495-A2.
XX  10-DEC-1998.
XX  05-JUN-1998; 98WO-US11578.
XX  06-JUN-1997; 97US-0048793.
XX  (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX  Dina D, Roman M, Schwartz D;
XX  WPI; 1999-059898/05.
XX  Immunostimulatory oligonucleotides regulate the immune system - and
XX  contain an immune-stimulating octanucleotide sequence; for treating
XX  cancer, allergic and infectious diseases
XX  Example 2; Page 30; 63pp; English.
XX  The invention relates to immunomodulatory oligonucleotides that comprise
XX  at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX  sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
XX  GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
XX  patients needing immune regulation, such as those suffering from cancer,
XX  an allergic disease and asthma. They are also used to prevent infectious
XX  diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX  and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX  Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
XX  Schistosoma. The immunomodulatory sequences are used to screen for human
XX  immunostimulatory activity by incubating macrophage cells and the
XX  oligonucleotide; and determining the relative amount of Th1-biased
XX  cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
XX  oligonucleotides that were tested for immunostimulatory activity. These
XX  were used in experiments for the stimulation of cytokine production and
XX  were found to lack immunostimulatory activity. The invention provides
XX  specific claimed examples (AAV80096-103) of immunomodulatory sequences.
XX  Sequence 24 BP; 5 A; 8 C; 4 G; 7 T; 0 other;
XX  Query Match      92.3%; Score 24; DB 20; Length 24;
XX  Best Local Similarity 100.0%; Pred. No. 0.0056;
XX  Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 1 tccataacgcttcgctaacttcg 24
XX  Db 1 tccataacgcttcgctaacttcg 24
XX  RESULT 5
XX  AAV80116
XX  ID AAV80116 standard; DNA; 24 BP.

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XX  AAV80116;
XX  12-MAR-1999 (first entry)
XX  Oligo used in experiments for stimulation of cytokine production.
XX  Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
XX  ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
XX  human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss:
XX  B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX  Synthetic.
XX  Key      Location/Qualifiers
FH  modified_base      8      /*tag= a
FT  /*tag= a
FT  /note= "5-bromocytosine"
FT  19
FT  modified_base
FT  /*tag= b
FT  /note= "5-bromocytosine"
XX  W09855495-A2.
XX  10-DEC-1998.
XX  05-JUN-1998; 98WO-US11578.
XX  06-JUN-1997; 97US-0048793.
XX  (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX  Dina D, Roman M, Schwartz D;
XX  WPI; 1999-059898/05.
XX  Immunostimulatory oligonucleotides regulate the immune system - and
XX  contain an immune-stimulating octanucleotide sequence; for treating
XX  cancer, allergic and infectious diseases
XX  Example 2; Page 30; 63pp; English.
XX  The invention relates to immunomodulatory oligonucleotides that comprise
XX  at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX  sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
XX  GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
XX  patients needing immune regulation, such as those suffering from cancer,
XX  an allergic disease and asthma. They are also used to prevent infectious
XX  diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX  and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX  Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
XX  Schistosoma. The immunomodulatory sequences are used to screen for human
XX  immunostimulatory activity by incubating macrophage cells and the
XX  oligonucleotide; and determining the relative amount of Th1-biased
XX  cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
XX  oligonucleotides that were tested for immunostimulatory activity. These
XX  were used in experiments for the stimulation of cytokine production and
XX  were found to lack immunostimulatory activity. The invention provides
XX  specific claimed examples (AAV80096-103) of immunomodulatory sequences.
XX  Sequence 24 BP; 5 A; 8 C; 4 G; 7 T; 0 other;
XX  Query Match      92.3%; Score 24; DB 20; Length 24;
XX  Best Local Similarity 100.0%; Pred. No. 0.0056;
XX  Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 1 tccataacgcttcgctaacttcg 24
XX  Db 1 tccataacgcttcgctaacttcg 24
XX  RESULT 6
XX  AAV80116
XX  ID AAV80116 standard; DNA; 24 BP.

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AAZ55885  
 ID AAZ55885 standard; DNA; 24 BP.  
 AC AAZ55885;  
 DT 10-APR-2000 (first entry)  
 XX Immunomodulatory oligonucleotide SEQ ID NO: 10.  
 DE  
 XX Immunomodulation; immunostimulatory sequence; adjuvant;  
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
 KW asthma; immunocontraception; 5-bromocytosine; ss.  
 XX Mus musculus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..24  
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 FT /\*note= "Phosphorothioate linkages"  
 FT 6..13  
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 FT /\*note= "Immunostimulatory sequence (ISS) 1"  
 FT modified\_base 8  
 FT /\*tag= c  
 FT /\*mod\_base= OTHER  
 FT /\*note= "5-bromocytosine"  
 FT 17..24  
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 FT /\*note= "Immunostimulatory sequence (ISS) 2"  
 FT  
 XX WO9962923-A2.  
 PN  
 XX  
 PD 09-DEC-1999.  
 XX  
 XX 04-JUN-1999; 99WO-US12538.  
 PF  
 XX 05-JUN-1998; 98US-0088310.  
 PR  
 XX 01-JUN-1999; 99US-0324191.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX Schwartz D;  
 PI  
 XX WPI; 2000-105687/09.  
 DR Novel immunomodulatory oligonucleotide used to induce a Th1-type immune  
 XX response, e.g. to tumor antigens  
 XX  
 XX Example 1; Page 35; 54pp; English.  
 CC Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory  
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,  
 CC AACGTC, AACGTT, AGCGTC, AGCGT, AGCGT, GACGTC, GACGTT, GCGGTT,  
 CC AACGTTCC and GACGTTCC). The invention relates to oligonucleotides  
 CC comprising one or more ISSs, where the ISS comprises at least  
 CC one modified cytosine with an electron-withdrawing moiety at  
 CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886  
 CC contain ISSs comprising at least one bromocytosine, whereas sequence  
 CC AAZ55876 contains an unmodified ISS. The immunomodulatory  
 CC oligonucleotides have an adjuvant-like effect; when formulated with an  
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,  
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),  
 CC while simultaneously downregulating the Th2-type response. The Th1  
 CC response is particularly effective for control of viruses and  
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
 CC particularly when formulated with an antigen or a facilitator, for  
 CC modulating immune responses. Such compositions may be used in tumour  
 CC therapy, in treatment of allergy (including asthma), for inducing a  
 CC vigorous cellular response (against a virus, bacterium, fungus or  
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.  
 XX Sequence 24 BP; 5 A; 7 C; 4 G; 7 T; 1 other;

Query Match 88.5%; Score 23; DB 21; Length 24;  
 Best Local Similarity 95.8%; Pred. No. 0.018;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 ||||| ||||| ||||| ||||| |||||  
 Db 1 tccataangttcgcctaaacgttcg 24  
 RESULT 7  
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 ID AAZ55886 standard; DNA; 24 BP.  
 XX  
 AC AAZ55886;  
 DT 10-APR-2000 (first entry)  
 XX Immunomodulatory oligonucleotide SEQ ID NO: 11.  
 DE  
 XX Immunomodulation; immunostimulatory sequence; adjuvant;  
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
 KW asthma; immunocontraception; 5-bromocytosine; ss.  
 XX Mus musculus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..24  
 FT /\*tag= a  
 FT /\*note= "Phosphorothioate linkages"  
 FT 6..13  
 FT /\*tag= b  
 FT /\*note= "Immunostimulatory sequence (ISS) 1"  
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 FT  
 XX WO9962923-A2.  
 PN  
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 PD 09-DEC-1999.  
 XX  
 XX 04-JUN-1999; 99WO-US12538.  
 PF  
 XX 05-JUN-1998; 98US-0088310.  
 PR  
 XX 01-JUN-1999; 99US-0324191.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX Schwartz D;  
 PI  
 XX WPI; 2000-105687/09.  
 DR Novel immunomodulatory oligonucleotide used to induce a Th1-type immune  
 XX response, e.g. to tumor antigens  
 XX  
 XX Example 1; Page 35; 54pp; English.  
 CC Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory  
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,  
 CC AACGTC, AACGTT, AGCGTC, AGCGT, AGCGT, GACGTC, GACGTT, GCGGTT,  
 CC AACGTTCC and GACGTTCC). The invention relates to oligonucleotides  
 CC comprising one or more ISSs, where the ISS comprises at least  
 CC one modified cytosine with an electron-withdrawing moiety at  
 CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886  
 CC contain ISSs comprising at least one bromocytosine, whereas sequence  
 CC AAZ55876 contains an unmodified ISS. The immunomodulatory  
 CC oligonucleotides have an adjuvant-like effect; when formulated with an  
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,  
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),  
 CC while simultaneously downregulating the Th2-type response. The Th1  
 CC response is particularly effective for control of viruses and  
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
 CC particularly when formulated with an antigen or a facilitator, for  
 CC modulating immune responses. Such compositions may be used in tumour  
 CC therapy, in treatment of allergy (including asthma), for inducing a  
 CC vigorous cellular response (against a virus, bacterium, fungus or  
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.  
 XX Sequence 24 BP; 5 A; 7 C; 4 G; 7 T; 1 other;



CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886  
 CC contain ISSs comprising at least one bromocytosine, whereas sequence  
 CC AAZ55876 contains an unmodified ISS. The immunomodulatory  
 CC oligonucleotides have an adjuvant-like effect: when formulated with an  
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,  
 CC and induce a Th1-type immune response (activation of cytotoxic T cells).  
 CC while simultaneously downregulating the Th2-type response. The Th1  
 CC response is particularly effective for control of viruses and  
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
 CC particularly when formulated with an antigen or a facilitator, for  
 CC modulating immune responses. Such compositions may be used in tumour  
 CC therapy, in treatment of allergy (including asthma), for inducing a  
 CC vigorous cellular response (against a virus, bacterium, fungus or  
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.  
 XX Sequence 24 BP: 5 A; 6 C; 4 G; 7 T; 2 other;  
 SQ

Query Match 84.6%; Score 22; DB 21; Length 24;  
 Best Local Similarity 91.7%; Pred. No. 0.055;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgttcg 24  
 ||||| ||||| ||||| |||||  
 Db 1 tccataangttcgcctaaagtctg 24

RESULT 8  
 AAC74251  
 ID AAC74251 standard; cDNA; 1034 BP.  
 XX AAC74251;  
 AC  
 XX  
 DT 02-FEB-2001 (first entry)  
 XX  
 DE Human secreted protein gene 29 SEQ ID NO:39.  
 XX  
 KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
 KW neuroprotective; antibacterial; virucide; fungicide; neoplasm;  
 KW ophthalmological; autoimmune disease; rheumatoid arthritis; angiogenesis;  
 KW hyperproliferative disorder; cardiovascular disorder; infection;  
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
 KW wound healing; chemotaxis; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200056754-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 16-MAR-2000; 2000WO-US06792.  
 XX  
 PR 19-MAR-1999; 99US-0125362.  
 XX  
 PR 10-DEC-1999; 99US-0169980.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen GA, Ruben SM, Komatsoulis G;  
 XX  
 DR WPI; 2000-579483/54.  
 DR P-PSDB; AAB39207.  
 XX  
 XX Isolated nucleic acid molecule encoding a human secreted protein is  
 PT used in preventing, treating or ameliorating a medical condition -  
 XX  
 XX Claim 1: Page 356-357; 434pp; English.  
 PS  
 CC The polynucleotide sequences given in AAC74223-C74279 encode the human  
 CC secreted proteins represented in AAB39179-B39226. Sequences  
 CC AAB39227-B39308 are alternative proteins encoded by the genes, and also  
 CC protein sequences with which they share homology. The proteins have  
 CC activities based on the tissues and cells in which they are expressed.

CC Examples of activities include: immunosuppressive; antiarthritic;  
 CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
 CC cerebroprotective; neuroprotective; antibacterial; virucide;  
 CC fungicide; and ophthalmological. The human secreted proteins,  
 CC polynucleotides, antagonists and agonists of the invention may be useful  
 CC in the treatment, prevention, and/or diagnosis of various disease,  
 CC disorders and conditions such as autoimmune diseases e.g. rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders  
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
 CC fungi and ocular disorders e.g. corneal infection. The polypeptides can  
 CC also be used to aid wound healing and epithelial cell proliferation, to  
 CC regenerate tissues, maintain organs before transplantation, in  
 CC chemotaxis and as a food additive or preservative e.g. to increase  
 CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used  
 CC during the isolation and characterisation of the genes of the invention.  
 XX  
 SQ Sequence 1034 BP: 325 A; 146 C; 171 G; 391 T; 1 other;

Query Match 63.1%; Score 16.4; DB 21; Length 1034;  
 Best Local Similarity 76.9%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgttcgc 26  
 ||||| ||||| ||||| |||||  
 Db 636 tccattaagtttcgcaaacattgtc 661

RESULT 9  
 AAX13867/C  
 ID AAX13867 standard; DNA; 1317 BP.  
 XX  
 AC AAX13867;  
 XX  
 DT 19-MAR-1999 (first entry)  
 XX  
 DE Enterococcus faecalis genome contig SEQ ID NO:930.  
 XX  
 KW Enterococcus faecalis; contig; detection; Enterococcal infection;  
 KW vaccine; attenuation; computer readable medium; ds.  
 XX  
 OS Enterococcus faecalis.  
 XX  
 PN WO9850555-A2.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 04-MAY-1998; 98WO-US08985.  
 XX  
 PR 14-NOV-1997; 97US-0066009.  
 XX  
 PR 06-MAY-1997; 97US-0044031.  
 XX  
 PR 16-MAY-1997; 97US-0046655.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Barash SC, Dillon PJ, Kunsch CA;  
 XX  
 DR WPI; 1999-045171/04.  
 XX  
 XX New isolated Enterococcus faecalis polynucleotides and polypeptides  
 PT - used to develop products for the detection of Enterococcus and for  
 PT use in vaccines for prevention or attenuation of Enterococcus  
 PT infection.  
 XX  
 XX Claim 1: Page 2052-2053; 2084pp; English.  
 PS  
 CC A computer readable medium has been developed which has recorded on it  
 CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.  
 CC AAX12938 to AAX13919 represent these nucleotide sequences which are  
 CC primary nucleotide sequences, also known as contigs. The computer-based  
 CC system can identify fragments of the Enterococcus faecalis genome with

CC commercial importance. The products can be used to detect the presence  
 CC of Enterococcus faecalis in samples. They can also be used for  
 CC diagnosing Enterococcal infection in an animal and monitoring  
 CC progression of disease, and for identifying agents which can be used to  
 CC modulate the growth or pathogenicity of Enterococcus faecalis, or  
 CC another related organism, in vivo or in vitro. In particular the  
 CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences  
 CC can be used in vaccines to prevent or attenuate an Enterococcal  
 CC infection.

XX Sequence 1317 BP; 357 A; 314 C; 223 G; 422 T; 1 other;

Query Match 63.1%; Score 16.4; DB 20; Length 1317;

Best Local Similarity 76.9%; Pred. No. 46;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaactcgtcgc 26

DB 623 TGCAGAACGTTGCTTAACCTACCTC 598

# RESULT 10

AAC42901/c

ID AAC42901 standard; DNA; 1413 BP.

XX

AC AAC42901;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37283.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; terminator; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR

PR 05-MAR-1999; 99US-0123180.

PR

PR 09-MAR-1999; 99US-0123548.

PR

PR 23-MAR-1999; 99US-0125788.

PR

PR 25-MAR-1999; 99US-0126264.

PR

PR 29-MAR-1999; 99US-0126785.

PR

PR 01-APR-1999; 99US-0127462.

PR

PR 06-APR-1999; 99US-0128234.

PR

PR 08-APR-1999; 99US-0128714.

PR

PR 16-APR-1999; 99US-0129845.

PR

PR 19-APR-1999; 99US-0130077.

PR

PR 21-APR-1999; 99US-0130449.

PR

PR 23-APR-1999; 99US-0130510.

PR

PR 28-APR-1999; 99US-0130891.

PR

PR 28-APR-1999; 99US-0131449.

PR

PR 30-APR-1999; 99US-0132048.

PR

PR 30-APR-1999; 99US-0132407.

PR

PR 04-MAY-1999; 99US-0132484.

PR

PR 05-MAY-1999; 99US-0132485.

PR

PR 06-MAY-1999; 99US-0132486.

PR

PR 07-MAY-1999; 99US-0132487.

PR

PR 11-MAY-1999; 99US-0132863.

PR

PR 14-MAY-1999; 99US-0134256.

PR

PR 14-MAY-1999; 99US-0134218.

PR

PR 14-MAY-1999; 99US-0134219.

PR

PR 14-MAY-1999; 99US-0134221.

PR

PR 14-MAY-1999; 99US-0134370.

PR

PR 18-MAY-1999; 99US-0134768.

PR

PR 19-MAY-1999; 99US-0134941.

PR

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139452.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.



Best Local Similarity 76.9%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaaacgttcgctc 26  
||||| ||||||| |||||  
Db 16 tccataacgttcgcctcctcgtcgtc 41

## RESULT 12

AAC84345  
ID AAC84345 standard; cDNA; 2120 BP.

XX AC  
AAC84345;

XX 19-MAR-2001 (first entry)

XX Wheat Nph2-2 cDNA sequence.

XX Acquired resistance gene; Nph1; Nph2; rice; Nph2-1; Nph2-2; wheat;  
KW plant pathogen; transgenic; disease resistance; ss.

XX OS Triticum aestivum.

XX FH Key Location/Qualifiers  
FT CDS 157..1986  
FT /\*tag= a  
FT /note= "the coding sequence (AAC84343) is specifically  
FT. claimed for in claim 4"

XX WO200070069-A1.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13307.

XX 13-MAY-1999; 99US-0133965.

XX (MONS ) MONSANTO CO.

XX Bougr1 OV, Rommens CMT, Srivastava N, Swords KM;

XX WPI; 2001-016244/02.

XX P-PSDB; AAB48088.

XX New acquired resistance genes Nph1 from rice, Oryza sativa, and Nph2-1  
PT and Nph2-2 from wheat, Triticum aestivum, useful for producing  
PT transgenic plants with increased disease resistance

XX Claim 17; Page 83; 101pp; English.

XX The invention relates to acquired resistance genes Nph1 from rice, and  
CC Nph2-1 and Nph2-2 from wheat. The Nph1 and Nph2 polypeptides can be  
CC expressed by standard recombinant methodology. The Nph1 and Nph2  
CC polynucleotides or polypeptides can be used to enhance acquired  
CC resistance in plants (e.g. wheat or rice) to control plant pathogens e.g.  
CC the genes can be introduced to make transgenic plants with increased  
CC disease resistance. The polynucleotides are also useful to produce probes  
CC and primers useful to detect the polynucleotides (to identify transgenic  
CC plants containing an acquired resistance gene) and to isolate similar  
CC sequences e.g. from other species. The polypeptides can be used to make  
CC antibodies useful to monitor protein production e.g. in transgenic  
CC plants. The present sequence represents the cDNA sequence of the wheat  
CC Nph2-2 gene.

XX Sequence 2120 BP; 497 A; 559 C; 606 G; 458 T; 0 other;

## Query Match

Best Local Similarity 63.1%; Score 16.4; DB 22; Length 2120;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaaacgttcgctc 26  
||||| ||||||| |||||

Db 172 tccataacgttcgcctcctcgtcgtc 197

## RESULT 13

AAF75864/c

ID AAF75864 standard; cDNA; 3096 BP.

XX AC  
AAF75864;

XX 18-MAY-2001 (first entry)

XX Histidine protein kinase coding sequence #1.

XX Histidine protein kinase; signal transduction; cytokinin; plant breeding;  
KW plant flowering; plant aging prevention; side root elongation; ss.

XX Arabidopsis thaliana.

XX WO200116332-A1.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-JP05772.

XX 26-AUG-1999; 99JP-0240433.

XX (SUNR ) SUNTORY LTD.

XX PA (SAOK ) NIPPON PAPER IND CO LTD.

XX PI Kakimoto T;

XX WPI; 2001-235110/24.

XX P-PSDB; AAB73274.

XX New Arabidopsis thaliana gene encoding a protein participating in  
PT signal transduction of cytokinin, for use in plant breeding with  
PT regulation of regeneration, differentiation and growth

XX Claim 3; Page 34-41; 78pp; Japanese.

XX The present sequence is a coding sequence for histidine protein kinase  
CC from Arabidopsis thaliana. Histidine protein kinase participates in the  
CC signal transduction of cytokinin. Histidine protein kinase is useful in  
CC plant breeding, in regulating growth of a plant or plant cell and  
CC regulating the flowering period of a plant or plant cell. Using histidine  
CC protein kinase, it is possible to provide the regulation of regeneration,  
CC differentiation and growth, thereby controlling physiological functions  
CC like elongation of side roots, prevention of aging, flowering period,  
CC promoting increase of fruit size and prevention of fruit dropping.

XX Sequence 3096 BP; 1001 A; 522 C; 760 G; 813 T; 0 other;

## Query Match

Best Local Similarity 63.1%; Score 16.4; DB 22; Length 3096;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaaacgttcgctc 26  
||||| || ||| ||||| |||||

Db 2888 TCCATACCATTTTCATACATTCTTC 2863

## RESULT 14

AAF75866/c

ID AAF75866 standard; DNA; 3708 BP.

XX AC  
AAF75866;

XX 18-MAY-2001 (first entry)

XX Histidine protein kinase coding sequence #3.

XX Histidine protein kinase; signal transduction; cytokinin; plant breeding;

```

KW plant flowering: plant aging prevention; side root elongation; ds.
XX Arabidopsis thaliana.
XX WO200116332-A1.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-JP05772.
XX 26-AUG-1999; 99JP-0240433.
XX (SUNR ) SUNTORY LTD.
XX (SAOK ) NIPPON PAPER IND CO LTD.
XX Kakimoto T;
XX WPI: 2001-235110/24.
XX P-PSDB; AAB73276.
XX New Arabidopsis thaliana gene encoding a protein participating in
PT signal transduction of cytokinin, for use in plant breeding with
PT regulation of regeneration, differentiation and growth
XX Example 2; Page 60-68; 78pp; Japanese.
XX The present sequence is a coding sequence for histidine protein kinase
CC from Arabidopsis thaliana. Histidine protein kinase participates in the
CC signal transduction of cytokinin. Histidine protein kinase is useful in
CC plant breeding, in regulating growth of a plant or plant cell and
CC regulating the flowering period of a plant or plant cell. Using histidine
CC protein kinase, it is possible to provide the regulation of regeneration,
CC differentiation and growth, thereby controlling physiological functions
CC like elongation of side roots, prevention of aging, flowering period,
CC promoting increase of fruit size and prevention of fruit dropping.
XX Sequence 3708 BP; 1170 A; 612 C; 854 G; 1072 T; 0 other;
SQ
Query Match 63.1%; Score 16.4; DB 22; Length 3708;
Best Local Similarity 76.9%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 tccataacggttcgcctaacggttcgtc 26
Db 3641 TCCATACCATTGGCATAACATTCTTC 3616
RESULT 15
AAF75865/c
ID AAF75865 standard; DNA; 4679 BP.
XX AAF75865;
XX 18-MAY-2001 (first entry)
XX Histidine protein kinase coding sequence #2.
XX Histidine protein kinase; signal transduction; cytokinin; plant breeding;
KW plant flowering; plant aging prevention; side root elongation; ds.
XX Arabidopsis thaliana.
XX WO200116332-A1.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-JP05772.
XX 26-AUG-1999; 99JP-0240433.
XX (SUNR ) SUNTORY LTD.
XX (SAOK ) NIPPON PAPER IND CO LTD.
PA
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XX Kakimoto T;
XX WPI: 2001-235110/24.
XX P-PSDB; AAB73275.
XX New Arabidopsis thaliana gene encoding a protein participating in
PT signal transduction of cytokinin, for use in plant breeding with
PT regulation of regeneration, differentiation and growth
XX Example 2; Page 46-54; 78pp; Japanese.
XX The present sequence is a coding sequence for histidine protein kinase
CC from Arabidopsis thaliana. Histidine protein kinase participates in the
CC signal transduction of cytokinin. Histidine protein kinase is useful in
CC plant breeding, in regulating growth of a plant or plant cell and
CC regulating the flowering period of a plant or plant cell. Using histidine
CC protein kinase, it is possible to provide the regulation of regeneration,
CC differentiation and growth, thereby controlling physiological functions
CC like elongation of side roots, prevention of aging, flowering period,
CC promoting increase of fruit size and prevention of fruit dropping.
XX Sequence 4679 BP; 1416 A; 811 C; 999 G; 1453 T; 0 other;
SQ
Query Match 63.1%; Score 16.4; DB 22; Length 4679;
Best Local Similarity 76.9%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 tccataacggttcgcctaacggttcgtc 26
Db 4612 TCCATACCATTGGCATAACATTCTTC 4587
Search completed: October 9, 2001, 16:26:51
Job time: 2981 sec
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: October 9, 2001, 21:12:37 : Search time 10334.3 Seconds  
(without alignments)  
37.177 Million cell updates/sec

Title: US-09-713-136-5  
Perfect score: 26  
Sequence: . 1 tccataacgttcgcttaacgttcgctc 26  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues  
Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*
  - 4: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq.\*
  - 5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*
  - 6: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*
  - 7: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq.\*
  - 8: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq.\*
  - 9: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq.\*
  - 10: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq.\*
  - 11: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq.\*
  - 12: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq.\*
  - 13: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq.\*
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  - 20: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq.\*
  - 21: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*
  - 22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*
  - 23: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*
  - 24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*
  - 25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*
  - 26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*
  - 27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*
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  - 30: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq.\*
  - 31: /cgn2\_6/ptodata/1/pna/US098\_COMB.seq.\*
  - 32: /cgn2\_6/ptodata/1/pna/US099\_COMB.seq.\*
  - 33: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq.\*
  - 34: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq.\*
  - 35: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq.\*
  - 36: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq.\*
  - 37: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq.\*
  - 38: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq.\*
  - 39: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq.\*
  - 40: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq.\*
  - 41: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq.\*
  - 42: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq.\*
  - 43: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq.\*
  - 44: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq.\*
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44:	/cgn2_6/ptodata/1/pna/US6012_COMB.seq.*
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54:	/cgn2_6/ptodata/1/pna/US6022_COMB.seq.*
55:	/cgn2_6/ptodata/1/pna/US6023_COMB.seq.*
56:	/cgn2_6/ptodata/1/pna/US6024_COMB.seq.*
57:	/cgn2_6/ptodata/1/pna/US6025_COMB.seq.*
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59:	/cgn2_6/ptodata/1/pna/US6027_COMB.seq.*
60:	/cgn2_6/ptodata/1/pna/US6028_COMB.seq.*

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	100.0	26	16	US-09-296-477-7 Sequence 7, Appli
2	26	100.0	26	18	US-09-415-186-5 Sequence 5, Appli
3	26	100.0	26	25	US-09-642-492-5 Sequence 5, Appli
4	26	100.0	26	28	US-09-713-136-5 Sequence 5, Appli
5	23	88.5	24	16	US-09-296-477-20 Sequence 20, Appl
6	23	88.5	24	16	US-09-296-477-21 Sequence 21, Appl
7	23	88.5	24	17	US-09-324-191A-10 Sequence 10, Appl
8	22	84.6	24	17	US-09-324-191A-11 Sequence 11, Appl
9	18.8	72.3	324	18	US-09-417-507-21974 Sequence 21974, A
10	18.6	71.5	25	55	US-60-234-049-69495 Sequence 69495, A
11	18.2	70.0	40400	48	US-60-161-932-126 Sequence 126, App
12	18.2	70.0	267904	19	US-09-528-237A-818 Sequence 818, App
13	18	69.2	366	25	US-09-654-617-168972 Sequence 168972,
14	18	69.2	366	27	US-09-684-016-168972 Sequence 168972,
15	18	69.2	383	25	US-09-654-617-168112 Sequence 168112,
16	18	69.2	383	27	US-09-684-016-168112 Sequence 168112,
17	18	69.2	385	25	US-09-654-617-130014 Sequence 130014,
18	18	69.2	385	27	US-09-684-016-130014 Sequence 130014,
19	18	69.2	624	18	US-09-489-039A-3800 Sequence 3800, Ap
20	18	69.2	7803	48	US-60-167-217-15844 Sequence 15844, A
21	18	69.2	29553	49	US-60-173-464-20558 Sequence 20558, A
22	18	69.2	29555	51	US-60-191-637-25011 Sequence 25011, A
23	18	69.2	29555	51	US-60-191-681-19701 Sequence 19701, A
24	18	69.2	80677	20	US-09-534-859-631 Sequence 631, App
25	18	69.2	219666	19	US-09-528-237A-1269 Sequence 1269, Ap
26	17.2	66.2	298	19	US-09-521-640-36319 Sequence 36319, A
27	17.2	66.2	318	19	US-09-521-640-99316 Sequence 99316, A
28	17.2	66.2	333	19	US-09-521-640-226531 Sequence 226531,
29	17.2	66.2	344	19	US-09-521-640-139795 Sequence 139795,
30	17.2	66.2	379	19	US-09-521-640-172477 Sequence 172477,
31	17.2	66.2	382	19	US-09-521-640-159397 Sequence 159397,
32	17.2	66.2	382	46	US-60-140-769-3782 Sequence 3782, Ap
33	17.2	66.2	401	19	US-09-521-640-125779 Sequence 125779,
34	17.2	66.2	405	19	US-09-521-640-99173 Sequence 99173, A
35	17.2	66.2	434	19	US-09-521-640-218971 Sequence 218971,
36	17.2	66.2	441	19	US-09-521-640-154536 Sequence 154536,
37	17.2	66.2	452	19	US-09-521-640-264041 Sequence 264041,
38	17.2	66.2	453	19	US-09-521-640-49827 Sequence 49827, A
39	17.2	66.2	453	46	US-60-140-769-49827 Sequence 49827, A
40	17.2	66.2	469	19	US-09-521-640-171560 Sequence 171560,
41	17.2	66.2	469	46	US-60-140-769-7866 Sequence 7866, Ap
42	17.2	66.2	472	19	US-09-521-640-5539 Sequence 5539, Ap
43	17.2	66.2	474	16	US-09-270-849B-152076 Sequence 152076,
44	17.2	66.2	583	19	US-09-521-640-24842 Sequence 24842, A
45	17.2	66.2	1473	16	US-09-252-991A-4812 Sequence 4812, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query Match 100.0%; Score 26; DB 16; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.006;  
Matches 26; Conservative 0; Mismatches 0; Indels

Query Match 100.0%; Score 26; DB 18; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.006;  
Matches 26; Conservative 0; Mismatches 0; Indels

Qy 1 tccataacggttcgcctaacggttcgtc 26

Db 1 tccataacggttcgcctaacggttcgtc 26

**RESULT 3**

```

US-09-642-492-5
; Sequence 5, Application US/09642492
; GENERAL INFORMATION:
; APPLICANT: Van Nest, G.
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: 377882008600
; CURRENT APPLICATION NUMBER: US/09/642,492
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,768
; PRIOR FILING DATE: 1999-08-19.
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-09-642-492-5

```

Query Match	100.0%	Score 26:	DB 25:
Best Local Similarity	100.0%	Pred. No.	0.006;
Matches 26:	Conservative	0;	Mismatches
		0;	Indels
		0;	Gaps
		0;	

Qy 1 tccataacgttcgcctaacgttcgctc 26  
|||||  
Db 1 tccataacgttcgcctaacgttcgctc 26

## RESULT 4

```

US-09-713-136-5
; Sequence 5, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713,136
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-5

```

Query Match	100.0%	Score 26;	DB 28;
Best Local Similarity	100.0%;	Pred. NO. 0.006;	Length 26;
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			

Qy 1 tccataacgttcgcctaacgttcgtc 26  
|||||  
Db 1 tccataacgttcgcctaacgttcgtc 26

**RESULT** 5

US-09-296-477-20

; Sequence 20, Application US/09296477A  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, E.  
; APPLICANT: SCHWARTZ, D.  
; APPLICANT: ROMAN, M.  
; APPLICANT: DINA, D.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,  
; COMPOSITIONS THEREOF AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 377882000420  
; CURRENT APPLICATION NUMBER: US/09/296,477A  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: 09/092,329  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 60/048,793  
; EARLIER FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8)...(8)  
; OTHER INFORMATION: 5-bromocytosine  
US-09-296-477-20

Query Match 88.5%; Score 23; DB 16; Length 24;  
Best Local Similarity 95.8%; Pred. No. 0.2;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcataacgttcgcctaacgttcg 24  
||||| |||||||||  
DB 1 tcataaangttgcctaacgttcg 24

RESULT 6  
US-09-296-477-21  
; Sequence 21, Application US/09296477A  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, E.  
; APPLICANT: SCHWARTZ, D.  
; APPLICANT: ROMAN, M.  
; APPLICANT: DINA, D.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,  
; COMPOSITIONS THEREOF AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 377882000420  
; CURRENT APPLICATION NUMBER: US/09/296,477A  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: 09/092,329  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 60/048,793  
; EARLIER FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8)...(8)  
; OTHER INFORMATION: 5-bromocytosine  
US-09-296-477-21

Query Match 88.5%; Score 23; DB 16; Length 24;  
Best Local Similarity 95.8%; Pred. No. 0.2;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcataacgttcgcctaacgttcg 24  
||||| |||||||||  
DB 1 tcataaangttgcctaacgttcg 24

RESULT 7  
US-09-324-191A-10  
; Sequence 10, Application US/09324191A  
; GENERAL INFORMATION:  
; APPLICANT: Schwartz, David  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH  
; MODIFIED BASES AND METHODS OF USE THEREOF  
; FILE REFERENCE: 377882000200  
; CURRENT APPLICATION NUMBER: US/09/324,191A  
; CURRENT FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: 60/088,310  
; PRIOR FILING DATE: 1998-06-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note-synthetic construct  
; NAME/KEY: modified\_base  
; LOCATION: (8)...(8)  
; OTHER INFORMATION: 5-bromocytosine  
US-09-324-191A-10

Query Match 88.5%; Score 23; DB 17; Length 24;  
Best Local Similarity 95.8%; Pred. No. 0.2;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcataacgttcgcctaacgttcg 24  
||||| |||||||||  
DB 1 tcataaangttgcctaacgttcg 24

RESULT 8  
US-09-324-191A-11  
; Sequence 11, Application US/09324191A  
; GENERAL INFORMATION:  
; APPLICANT: Schwartz, David  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH  
; MODIFIED BASES AND METHODS OF USE THEREOF  
; FILE REFERENCE: 377882000200  
; CURRENT APPLICATION NUMBER: US/09/324,191A  
; CURRENT FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: 60/088,310  
; PRIOR FILING DATE: 1998-06-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note-synthetic construct  
; NAME/KEY: modified\_base  
; LOCATION: (8)...(8)  
; OTHER INFORMATION: 5-bromocytosine  
; NAME/KEY: modified\_base  
; LOCATION: (19)...(19)  
; OTHER INFORMATION: 5-bromocytosine  
US-09-324-191A-11



```
Query Match      84.6%; Score 22; DB 17; Length 24;
Best Local Similarity 91.7%; Pred. No. 0.65;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcg 24
    ||||| ||||| ||||| |||||
Db 1 tccataaangttcgctaangttcg 24

RESULT 9
US-09-417-507-21974/c
; Sequence 21974, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417.507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 21974
; LENGTH: 324
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-21974

Query Match      72.3%; Score 18.8; DB 18; Length 324;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ataacgttcgcctaacgttcgt 25
    ||||| ||||| ||||| |||||
Db 116 ATAACGTTCCGCTGACGTTCT 95

RESULT 10
US-60-234-049-69495
; Sequence 69495, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234.049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69495
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-69495

Query Match      71.5%; Score 18.6; DB 55; Length 25;
Best Local Similarity 84.0%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgt 25
    ||||| ||||| ||||| |||||
Db 1 tccataacgttcgcctaacgttcgt 25

RESULT 11
US-60-161-932-126
; Sequence 126, Application US/60161932
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
```

```
Acid Sequences, Systems Containin the Nucleic Acid Sequences
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: CL000122
; CURRENT APPLICATION NUMBER: US/60/161.932
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 2626
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 40400
; TYPE: DNA
; ORGANISM: Drosophila
US-60-161-932-126

Query Match      70.0%; Score 18.2; DB 48; Length 40400;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 cataacgttcgcctaacgttcgt 25
    ||||| ||||| ||||| |||||
Db 36169 catacgttcgcgcgaagtctgt 36191

RESULT 12
US-09-528-237A-818/c
; Sequence 818, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528.237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 818
; LENGTH: 267904
; TYPE: DNA
; ORGANISM: Drosophila
US-09-528-237A-818

Query Match      70.0%; Score 18.2; DB 19; Length 267904;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 cataacgttcgcctaacgttcgt 25
    ||||| ||||| ||||| |||||
Db 231735 CATACGTTCCGCGAAGTTCGT 231713

RESULT 13
US-09-654-617-168972/c
; Sequence 168972, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654.617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 168972
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana nossen
US-09-654-617-168972

Query Match      69.2%; Score 18; DB 25; Length 366;
Best Local Similarity 80.8%; Pred. No. 91;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

QY 1 tccataacgcttcgcctaacgcttcgctc 26  
||| ||| ||| ||| ||| ||| ||| |||  
Db 172 TCAAAACTTTCTCCTAACGTTCTC 147

RESULT 14  
US-09-684-016-168972/c  
; Sequence 168972, Application US/09684016  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong Annotated Plant Genes  
; TITLE OF INVENTION: 38-21(15097)D  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/684,016  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 168972  
; LENGTH: 366  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana nossen  
US-09-684-016-168972

Query Match 69.2%; Score 18; DB 27; Length 366;  
Best Local Similarity 80.8%; Pred. No. 91;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tccataacgcttcgcctaacgcttcgctc 26  
||| ||| ||| ||| ||| ||| ||| |||  
Db 172 TCAAAACTTTCTCCTAACGTTCTC 147

RESULT 15  
US-09-654-617-168112/c  
; Sequence 168112, Application US/09654617  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong Annotated Plant Genes  
; TITLE OF INVENTION: 38-21(15097)D  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/654,617  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 168112  
; LENGTH: 383  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana nossen  
US-09-654-617-168112

Query Match 69.2%; Score 18; DB 25; Length 383;  
Best Local Similarity 80.8%; Pred. No. 91;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tccataacgcttcgcctaacgcttcgctc 26  
||| ||| ||| ||| ||| ||| ||| |||  
Db 171 TCAAAACTTTCTCCTAACGTTCTC 146

Search completed: October 9, 2001, 21:12:47  
Job time: 20072 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:14 ; Search time 1391.6 seconds  
(without alignments)  
42.642 Million cell updates/sec

Title: US-09-713-136-5

Perfect score: 26

Sequence: 1 tccataacgttcgcctaacgttcgtc 26

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 204985 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2.6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2.6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2.6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2.6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2.6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2.6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 7: /cgn2.6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 8: /cgn2.6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	7 US-09-802-518-5	Sequence 5, Appli
2	26	100.0	26	7 US-09-802-359-5	Sequence 5, Appli
3	26	100.0	26	7 US-09-802-376-5	Sequence 5, Appli
4	18	69.2	80677	6 US-09-803-736-631	Sequence 631, App
5	16.6	63.8	424	7 US-09-692-257A-3964	Sequence 3964, App
6	16.6	63.8	42459	6 US-09-803-736-361	Sequence 361, App
7	16.6	63.8	96066	6 US-09-803-736-360	Sequence 360, App
8	16.4	63.1	194	1 PCT-US01-08631-4195	Sequence 4195, App
9	16.4	63.1	424	6 US-09-804-703-5632	Sequence 5632, App
10	16.4	63.1	424	7 US-09-840-145-6383	Sequence 6383, App
11	16.4	63.1	462	6 US-09-804-730-13181	Sequence 13181, A
12	16.4	63.1	541	7 US-09-823-327-2465	Sequence 2465, App
13	16.4	63.1	669	7 US-09-764-905-6468	Sequence 6468, App
14	16.4	63.1	1290	1 PCT-US01-08631-5184	Sequence 5184, App
15	16.4	63.1	1290	1 PCT-US01-08631-25681	Sequence 25681, A
16	16.4	63.1	1953	1 PCT-US01-08631-28832	Sequence 28832, A
17	16.4	63.1	2659	1 PCT-US01-08631-28643	Sequence 28643, A
18	16.4	63.1	3421	6 US-09-836-472-1284	Sequence 1284, App
19	16.4	63.1	5274	8 US-60-278-232-7126	Sequence 7126, App
20	16.4	63.1	14212	7 US-09-764-905-34504	Sequence 34504, A
21	16.4	63.1	14212	7 US-09-764-905-34836	Sequence 34836, A
22	16.4	63.1	14212	7 US-09-764-905-40733	Sequence 40733, A
23	16.4	63.1	42694	6 US-09-803-736-1418	Sequence 1418, App
24	16.4	63.1	86424	6 US-09-803-736-1	Sequence 1, Appli
25	16.4	63.1	99123	6 US-09-803-736-740	Sequence 740, App

```

c 26 16.4 63.1 104386 6 US-09-803-736-1385 Sequence 1385, Ap
c 27 16.4 63.1 118718 6 US-09-803-736-579 Sequence 579, App
c 28 16.2 62.3 1206 6 US-09-738-626-1966 Sequence 1966, Ap
c 29 16.2 62.3 91825 6 US-09-803-736-1142 Sequence 1142, Ap
c 30 16 61.5 244 7 US-09-440-305A-7 Sequence 7, Appli
c 31 16 61.5 368 7 US-09-783-590-740 Sequence 740, App
c 32 16 61.5 1899 7 US-09-902-540-4427 Sequence 4427, Ap
c 33 16 61.5 2865 1 PCT-US01-08631-15928 Sequence 15928, A
c 34 16 61.5 2865 1 PCT-US01-08631-15941 Sequence 15941, A
c 35 16 61.5 2865 1 PCT-US01-08631-28923 Sequence 28923, A
c 36 16 61.5 2865 1 PCT-US01-08631-30323 Sequence 30323, A
c 37 16 61.5 3672 1 PCT-US01-08631-25889 Sequence 25889, A
c 38 16 61.5 22761 7 US-09-902-540-1219 Sequence 1219, Ap
c 39 16 61.5 93695 6 US-09-803-736-640 Sequence 640, App
c 40 16 61.5 205065 6 US-09-803-736-584 Sequence 584, App
c 41 16 61.5 206420 6 US-09-803-736-678 Sequence 678, App
c 42 15.8 60.8 75475 6 US-09-803-736-692 Sequence 692, App
c 43 15.8 60.8 96936 6 US-09-803-736-1402 Sequence 1402, Ap
c 44 15.6 60.0 126 6 US-09-504-576A-1871 Sequence 1871, Ap
c 45 15.6 60.0 445 7 US-09-813-155-10330 Sequence 10330, A

```

#### ALIGNMENTS

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RESULT 1
US-09-802-518-5
; Sequence 5, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-5

```

```

Query Match 100.0%; Score 26; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 tccataacgttcgcctaacgttcgtc 26
    |||
Db 1 tccataacgttcgcctaacgttcgtc 26

```

```

RESULT 2
US-09-802-359-5
; Sequence 5, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

```

```
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-5

Query Match      100.0%; Score 26; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgc 26
   ||||| ||||| ||||| ||||| |||||
Db 1 tccataacgttcgcctaacgttcgc 26

RESULT 3
US-09-802-376-5
; Sequence 5, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802.376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-5

Query Match      100.0%; Score 26; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgc 26
   ||||| ||||| ||||| ||||| |||||
Db 1 tccataacgttcgcctaacgttcgc 26

RESULT 4
US-09-803-736-631
; Sequence 631, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803.736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 631
; LENGTH: 80677
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-631
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```
Query Match      69.2%; Score 18; DB 6; Length 80677;
Best Local Similarity 80.8%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgc 26
   || | ||| ||| ||| ||| ||| |||
Db 56083 tcaaaactttctcctaacgttcgc 56108

RESULT 5
US-09-692-257A-3964/c
; Sequence 3964, Application US/09692257A
; GENERAL INFORMATION:
; APPLICANT: Miller, Phillip W.
; APPLICANT: Peng, Ming
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15771)B
; CURRENT APPLICATION NUMBER: US/09/692.257A
; CURRENT FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US 60/162,747
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 14882
; SEQ ID NO 3964
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-001-Pl-K1-A4
US-09-692-257A-3964

Query Match      63.8%; Score 16.6; DB 7; Length 424;
Best Local Similarity 82.6%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ccataacgttcgcctaacgttcgc 24
   . |||| | ||| ||||| |||
Db 51 CCATCTCGATCGCCTACGATCG 29

RESULT 6
US-09-803-736-361
; Sequence 361, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803.736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 361
; LENGTH: 42499
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-361

Query Match      63.8%; Score 16.6; DB 6; Length 42499;
Best Local Similarity 82.6%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttc 23
   ||||| ||| ||| |||||
```



Query Match 63.1%; Score 16.4; DB 7; Length 424;  
Best Local Similarity 76.9%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 tccataacgttcgcctaactgctc 26  
||||| ||| ||| ||| ||| |||  
Db 74 tccattaagtgttgcacaaattgtc 99

## RESULT 11

US-09-804-730-13181/C  
; Sequence 13181, Application US/09804730  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Hammond-Kosack, Kim  
; APPLICANT: Masucci, James D.  
; APPLICANT: Urban, Martin  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51838)B  
; CURRENT APPLICATION NUMBER: US/09/804,730  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: US 60/189,657  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 22828  
; SEQ ID NO 13181  
; LENGTH: 462  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(462)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3399-002-PI-K1-C8  
US-09-804-730-13181

Query Match 63.1%; Score 16.4; DB 6; Length 462;  
Best Local Similarity 76.9%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 tccataacgttcgcctaactgctc 26  
||||| ||| ||| ||| ||| |||  
Db 172 TTCATAACCTTCTCCAACTGTCGTC 147

## RESULT 12

US-09-823-327-2465  
; Sequence 2465, Application US/09823327  
; GENERAL INFORMATION:  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: MacBeth, Kyle J.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.2083-001  
; CURRENT APPLICATION NUMBER: US/09/823,327  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,433  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 9746  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2465  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(541)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-823-327-2465

Query Match 63.1%; Score 16.4; DB 7; Length 541;  
Best Local Similarity 76.9%; Pred. No. 56;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 tccataacgttcgcctaactgctc 26  
||||| ||| ||| ||| ||| |||  
Db 330 tccattaagtgttgcacaaattgtc 355

## RESULT 13

US-09-764-905-6468  
; Sequence 6468, Application US/09764905  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC004  
; CURRENT APPLICATION NUMBER: US/09/764,905  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
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; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
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; PRIOR APPLICATION NUMBER: 60/251,869  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/224,518  
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; PRIOR APPLICATION NUMBER: 60/236,369  
; PRIOR FILING DATE: 2000-09-29  
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; PRIOR APPLICATION NUMBER: 60/241,809  
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; PRIOR APPLICATION NUMBER: 60/249,299  
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;; PRIOR APPLICATION NUMBER: 60/241,785  
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;; PRIOR FILING DATE: 2000-11-01  
;; PRIOR APPLICATION NUMBER: 60/225,268  
;; PRIOR FILING DATE: 2000-08-14  
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;; PRIOR APPLICATION NUMBER: 60/229,345  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,287  
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;; PRIOR APPLICATION NUMBER: 60/231,413  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/229,509  
;; PRIOR FILING DATE: 2000-09-05  
;; PRIOR APPLICATION NUMBER: 60/236,367  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/237,039  
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;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/236,370  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/236,802  
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;; PRIOR APPLICATION NUMBER: 60/237,037  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,040  
;; PRIOR FILING DATE: 2000-10-02  
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;; PRIOR APPLICATION NUMBER: 60/226,681  
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;; PRIOR APPLICATION NUMBER: 60/225,213  
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;; PRIOR APPLICATION NUMBER: 60/235,836  
;; PRIOR FILING DATE: 2000-09-27  
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;; PRIOR APPLICATION NUMBER: 60/241,786  
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;; PRIOR APPLICATION NUMBER: 60/241,221  
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;; PRIOR APPLICATION NUMBER: 60/246,475  
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;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,065  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,398

Query Match 63.1%; Score 16.4; DB 7; Length 669;  
Best Local Similarity 76.9%; Pred. No. 58;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Caps 0;  
QY 1 tccataacgttcgcctaacttcgtc 26  
||||||| | ||||| ||| ||

Search completed: October 9, 2001, 21:36:22  
Job time: 21242 sec

Db 206 tccataacataactcctaatttcctc 231

## RESULT 14

PCT-US01-08631-5184/C  
; Sequence 5184, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 5184  
; LENGTH: 1290  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (817)..(1287)  
; OTHER INFORMATION: 96% homologous to Escherichia coli No definition line  
; OTHER INFORMATION: found,accession number U00039,Smith-Waterman Score=805.  
PCT-US01-08631-5184

Query Match 63.1%; Score 16.4; DB 1; Length 1290;  
Best Local Similarity 76.9%; Pred. No. 63;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 tccataacgttcgcctaactcgttcgc 26  
|| ||| | ||| ||||| |||||  
Db 740 TCGTTAAAGCGCGCCCAACGTCGTC 715

## RESULT 15

PCT-US01-08631-25681  
; Sequence 25681, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 25681  
; LENGTH: 1290  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (474)..(4)  
; OTHER INFORMATION: 96% homologous to Escherichia coli No definition line  
; OTHER INFORMATION: found,accession number U00039,Smith-Waterman Score=805.  
PCT-US01-08631-25681

Query Match 63.1%; Score 16.4; DB 1; Length 1290;  
Best Local Similarity 76.9%; Pred. No. 63;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 tccataacgttcgcctaactcgttcgc 26  
|| ||| | ||| ||||| |||||  
Db 551 tcgtfaagcgcgcccaacgttcgc 576



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:03 ; Search time 217.64 seconds  
(without alignments)  
22.616 Million cell updates/sec

Title: US-09-713-136-5  
Perfect score: 26  
Sequence: 1 tcataacgttcgctaagcttcgctc 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.6	60.0	801	US-09-291-562-1	Sequence 1, Appli
C 2	15.6	60.0	1005	US-09-103-359-4	Sequence 4, Appli
C 3	15.4	59.2	1029	US-07-809-457A-15	Sequence 15, Appl
C 4	15.4	59.2	1029	US-08-553-943-15	Sequence 15, Appl
C 5	15.4	59.2	1029	PCT-US91-09437-15	Sequence 15, Appl
C 6	15.4	59.2	1758	PCT-US92-01015-1	Sequence 1, Appli
C 7	15	57.7	3027	US-09-132-619-9	Sequence 9, Appli
C 8	15	57.7	3027	US-09-282-803B-9	Sequence 9, Appli
C 9	15	57.7	26700	US-08-472-217-1	Sequence 1, Appli
C 10	15	57.7	26700	US-08-488-199-5	Sequence 5, Appli
C 11	15	57.7	26700	US-08-760-534A-1	Sequence 1, Appli
C 12	14.8	56.9	1587	US-08-680-506-6	Sequence 6, Appli
C 13	14.8	56.9	2210	US-07-710-361-2	Sequence 2, Appli
C 14	14.8	56.9	2400	US-08-967-513-1	Sequence 1, Appli
C 15	14.8	56.9	2400	US-08-687-645B-1	Sequence 1, Appli
C 16	14.8	56.9	4781	US-09-001-273-1	Sequence 1, Appli
C 17	14.8	56.9	4781	US-08-843-459A-1	Sequence 1, Appli
C 18	14.8	56.9	4847	US-09-061-400-1	Sequence 1, Appli
C 19	14.6	56.2	538	US-08-998-416-649	Sequence 649, App
C 20	14.6	56.2	1040	US-08-682-643-2	Sequence 2, Appli
C 21	14.6	56.2	1934	US-07-941-651-1	Sequence 1, Appli
C 22	14.6	56.2	1934	US-08-279-996-1	Sequence 1, Appli
C 23	14.6	56.2	3635	US-08-252-626A-1	Sequence 1, Appli
C 24	14.4	55.4	1020	US-09-146-675-1	Sequence 1, Appli
C 25	14.4	55.4	1149	US-08-844-305-1	Sequence 1, Appli
C 26	14.4	55.4	1650	US-09-001-826-24	Sequence 24, Appli
C 27	14.4	55.4	2468	US-07-779-049-2	Sequence 2, Appli

C 28	14.4	55.4	2468	1	US-08-080-240-2	Sequence 2, Appli
C 29	14.4	55.4	2809	3	US-08-448-194-5	Sequence 5, Appli
C 30	14.4	55.4	3536	3	US-09-418-640-3	Sequence 3, Appli
C 31	14.4	55.4	3720	1	US-08-074-967-1	Sequence 1, Appli
C 32	14.4	55.4	3720	2	US-08-553-541B-1	Sequence 1, Appli
C 33	14.4	55.4	3720	4	US-09-268-202-1	Sequence 1, Appli
C 34	14.4	55.4	3720	5	PCT-US94-06669-1	Sequence 1, Appli
C 35	14.4	55.4	21126	1	US-08-008-216-19	Sequence 19, Appli
C 36	14.4	55.4	21126	1	US-08-459-569-19	Sequence 19, Appli
C 37	14.4	55.4	21126	1	US-08-458-831-19	Sequence 19, Appli
C 38	14.2	54.6	648	4	US-08-998-416-1064	Sequence 1064, Ap
C 39	14.2	54.6	807	1	US-07-706-691G-53	Sequence 53, Appl
C 40	14.2	54.6	807	1	US-07-706-691G-54	Sequence 54, Appl
C 41	14.2	54.6	807	1	US-07-706-691G-55	Sequence 55, Appl
C 42	14.2	54.6	807	1	US-07-706-691G-56	Sequence 56, Appl
C 43	14.2	54.6	807	1	US-07-706-691G-57	Sequence 57, Appl
C 44	14.2	54.6	807	1	US-07-706-691G-58	Sequence 58, Appl
C 45	14.2	54.6	807	1	US-07-706-691G-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1  
US-09-291-562-1/c  
; Sequence 1, Application US/09291562  
; Patent No. 6084152  
; GENERAL INFORMATION:  
; APPLICANT: Sang Soo Kwak  
; APPLICANT: Jae-Whune Kim  
; APPLICANT: Haeng-Soon Lee  
; APPLICANT: Suk Yoon Kwon  
; TITLE OF INVENTION: METHOD FOR PRODUCING TRANSGENIC CUCUMBER  
; FILE REFERENCE: 118.1-US-01  
; CURRENT APPLICATION NUMBER: US/09/291.562  
; CURRENT FILING DATE: 1999-04-14  
; EARLIER APPLICATION NUMBER: KS 98 13205  
; EARLIER FILING DATE: 1998-04-14  
; EARLIER APPLICATION NUMBER: KS 98 33947  
; EARLIER FILING DATE: 1998-08-21  
; EARLIER APPLICATION NUMBER: KS 99 11848  
; EARLIER FILING DATE: 1999-04-06  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 801  
; TYPE: DNA  
; ORGANISM: Manihot esculenta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (55)...(510)  
; NAME/KEY: polyA\_site  
; LOCATION: (781)...(801)  
; NAME/KEY: polyA\_signal  
; LOCATION: (611)...(616)  
US-09-291-562-1

Query Match 60.0%; Score 15.6; DB 3; Length 801;  
Best Local Similarity 81.8%; Pred. No. 25;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Oy 5 taacgttcgctaagcttcgctc 26  
|||||  
Db 601 TAATGGTCTCCTACGTTCTTC 580

RESULT 2  
US-09-103-359-4/c  
; Sequence 4, Application US/09103359  
; Patent No. 6057108  
; GENERAL INFORMATION:



LOCATION: /..1020

US-09-132-019-5  
: Sequence 9. Application IIS/09132619B

Patent No. 5958697  
GENERAL INFORMATION:  
APPLICANT: Shan, Bei  
TITLE OF INVENTION: CYP7 Promoter-Binding Factors  
FILE REFERENCE: T97-013  
CURRENT APPLICATION NUMBER: US/09/132.619B  
CURRENT FILING DATE: 1998-08-11  
EARLIER APPLICATION NUMBER: 60/067.708  
EARLIER FILING DATE: 1997-12-08  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 3027  
TYPE: DNA  
ORGANISM: human  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (159)..(1838)  
US-09-132-619-9

Query Match 57.78; Score 15; DB 2; Length 3027;  
Best Local Similarity 78.3%; Pred. No. 64;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 ccataacggttcgcctaacggttcg 24  
||||| ||| ||| ||| ||| ||| |||  
Db 509 ccattacggttcctcctcaagtcgcg 531

RESULT 8  
US-09-282-803B-9  
Sequence 9, Application US/09282803B  
Patent No. 6027901  
GENERAL INFORMATION:  
APPLICANT: Shan, Bei  
APPLICANT: Nitta, Masahiro  
TITLE OF INVENTION: CYP7 Promoter-Binding Factors  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/282.803B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3027 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 159..1838

US-09-282-803B-9

Query Match 57.78; Score 15; DB 3; Length 3027;  
Best Local Similarity 78.3%; Pred. No. 64;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 ccataacggttcgcctaacggttcg 24  
||||| ||| ||| ||| ||| ||| |||  
Db 509 CCATTACGGTCTCTCCTCAGTCGC 531

RESULT 9  
US-08-472-217-1/c  
Sequence 1, Application US/08472217  
Patent No. 5726058  
GENERAL INFORMATION:  
APPLICANT: Alanen-Kurki, Leena  
APPLICANT: Auvinen, Petri  
APPLICANT: Jaakkola, Panu  
APPLICANT: Jalkanen, Markku  
APPLICANT: Lepp, Sirpa  
APPLICANT: Maki, Markku  
APPLICANT: Vihinen, Tapani  
APPLICANT: W rri, Anni  
TITLE OF INVENTION: Syndecan Stimulation Of Cellular  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472.217  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/206,186  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,427  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1102.0050003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26700 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 101n(4378..4443, 22026..22106, 23001..23483,  
LOCATION: 23905..24039, 24251..24418)  
US-08-472-217-1

Query Match 57.7%; Score 15; DB 1; Length 26700;  
Best Local Similarity 78.3%; Pred. No. 93;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttc 23  
||||| || ||||| ||||| |||||  
Db 9461 TCCAAATGTTCCCTAGCATTC 9439

## RESULT 10

US-08-488-199-5/c  
; Sequence 5, Application US/08488199  
; Patent No. 5851993  
; GENERAL INFORMATION:  
; APPLICANT: Jalkanen, Markku  
; APPLICANT: Mali, Markku  
; TITLE OF INVENTION: Suppression of Tumor Cell Growth By  
; TITLE OF INVENTION: Syndecan-1 Ectodomain  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
; STREET: 1100 New York Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,199  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/258,862  
; FILING DATE: 13-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 1102.0130001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26700 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 4378..4443  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 22026..22107  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 23002..23483  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 23905..24040  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 24252..24418  
US-08-488-199-5

Query Match 57.7%; Score 15; DB 2; Length 26700;  
Best Local Similarity 78.3%; Pred. No. 93;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttc 23  
||||| || ||||| ||||| |||||  
Db 9461 TCCAAATGTTCCCTAGCATTC 9439

## RESULT 11

US-08-760-534A-1/c  
; Sequence 1, Application US/08760534A  
; Patent No. 6017727  
; GENERAL INFORMATION:  
; APPLICANT: JALKANEN, MARKKU  
; APPLICANT: JAANKOLA, PANU  
; APPLICANT: VIHINEN, TAPANI  
; TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN  
; TITLE OF INVENTION: STIMULATION OF CELLULAR DIFFERENTIATION  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/760,534A  
; FILING DATE: 02-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/206,186  
; FILING DATE: 07-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FI93/00514  
; FILING DATE: 01-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CIMBALA, MICHELE A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 1708.0050004/MAC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26700 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: Join(4378..4443, 22026..22106, 23001..23483,  
; LOCATION: 23905..24039, 24251..24418)  
US-08-760-534A-1

Query Match 57.7%; Score 15; DB 3; Length 26700;  
Best Local Similarity 78.3%; Pred. No. 93;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttc 23  
||||| || ||||| ||||| |||||  
Db 9461 TCCAAATGTTCCCTAGCATTC 9439

## RESULT 12

US-08-680-506-6/c  
; Sequence 6, Application US/08680506C  
; Patent No. 6008013  
; GENERAL INFORMATION:

APPLICANT: Reynolds, Paul R.  
TITLE OF INVENTION: CHONDROCYTE PROTEINS  
FILE REFERENCE: 176/60091  
CURRENT APPLICATION NUMBER: US/08/680,506C  
CURRENT FILING DATE: 1996-07-08  
EARLIER APPLICATION NUMBER: 60/021,672  
EARLIER FILING DATE: 1996-07-05  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1587  
TYPE: DNA  
ORGANISM: Gallus gallus  
US-08-680-506-6

Query Match 56.9%; Score 14.8; DB 3; Length 1587;  
Best Local Similarity 73.1%; Pred. No. 72;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgc 26  
||||| ||||| ||||| ||||| |||||  
Db 1444 TCATTTCATTCCTCAAGTTCGTC 1419

## RESULT 13

US-07-710-361-2  
Sequence 2, Application US/07710361  
Patent No. 5242820  
GENERAL INFORMATION:  
APPLICANT: LO, Shyh-Ching  
TITLE OF INVENTION: NOVEL PATHOGENIC MYCOPLASMA  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue NW, Suite 1000  
CITY: Washington,  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/710,361  
FILING DATE: 19910606  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 265,920  
FILING DATE: 02-NOV-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 875,535  
FILING DATE: 18-JUN-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 18596-90428  
TELEPHONE: 202-962-4910  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2210 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE: Mycoplasma fermentans

STRAIN: incognitus  
IMMEDIATE SOURCE:  
CLONE: psb 2.2  
US-07-710-361-2

Query Match 56.9%; Score 14.8; DB 1; Length 2210;  
Best Local Similarity 88.9%; Pred. No. 76;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaa 18  
||||||| ||||| |||||  
Db 2020 TCCATAACTTTCCTCTAA 2037

## RESULT 14

US-08-967-513-1/c  
Sequence 1, Application US/08967513  
Patent No. 5783436  
GENERAL INFORMATION:  
APPLICANT: Robert P. Hausinger  
TITLE OF INVENTION: Mutant Urease and Method  
TITLE OF INVENTION: of Use For Determination  
TITLE OF INVENTION: of Urea  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian C. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,513  
FILING DATE: 11-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/687,645  
FILING DATE: July 26, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: MSU 4.1-309  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5783436e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2400  
TYPE: nucleotides  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE:  
DESCRIPTION: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Klebsiella aerogenes  
STRAIN: CG253  
INDIVIDUAL ISOLATE:  
CELL TYPE: N/A  
FEATURE:  
NAME/KEY: CDNA encoding mutant urease  
NAME/KEY: 'H219Q  
LOCATION: Modification at position 1312 to  
LOCATION: glutamine

IDENTIFICATION METHOD: Sequencing  
OTHER INFORMATION:  
US-08-967-513-1

Query Match 56.9%; Score 14.8; DB 1; Length 2400;  
Best Local Similarity 88.9%; Pred. No. 77;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaa 18  
|||||  
Db 35 TCCATAACGTTCTCTTAA 18

## RESULT 15

US-08-687-645B-1/c  
Sequence 1, Application US/08687645B

Patent No. 5846752

## GENERAL INFORMATION:

APPLICANT: Robert P. Hausinger

TITLE OF INVENTION: Mutant Urease and Method

TITLE OF INVENTION: Of Use For Determination

TITLE OF INVENTION: Of Urea

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIP: 48864

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,645B

FILING DATE: July 26, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,931

REFERENCE/DOCKET NUMBER: MSU 4.1-309

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 347-4100

TELEFAX: (517) 347-4103

TELEX: NO. 5846752e

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2400

TYPE: nucleotides

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE:

DESCRIPTION: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Klebsiella aerogenes

STRAIN: CG253

INDIVIDUAL ISOLATE:

CELL TYPE: N/A

FEATURE:

NAME/KEY: cDNA encoding mutant urease

NAME/KEY: 'H2190

LOCATION: Modification at position 1312 to

LOCATION: glutamine

IDENTIFICATION METHOD: Sequencing

## OTHER INFORMATION:

US-08-687-645B-1

Query Match 56.9%; Score 14.8; DB 2; Length 2400;  
Best Local Similarity 88.9%; Pred. No. 77;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaa 18  
|||||  
Db 35 TCCATAACGTTCTCTTAA 18

Search completed: October 9, 2001, 15:42:06  
Job time: 296 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 9, 2001, 16:19:55 ; Search time 2150.93 Seconds  
(without alignments)  
158.206 Million cell updates/sec

Title: US-09-713-136-6  
Perfect score: 22  
Sequence: 1 tgactgtgaangttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6:	gb_in3:*	6:	gb_in3:*
7:	gb_om:*	7:	gb_om:*
8:	gb_ov:*	8:	gb_ov:*
9:	gb_pat1:*	9:	gb_pat1:*
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17:	em_ba2:*	17:	em_ba2:*
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19:	em_htgo_hum:*	19:	em_htgo_hum:*
20:	em_htgo_inv:*	20:	em_htgo_inv:*
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94:	gb_ro1:*
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96:	gb_in4:*
97:	gb_pr10:*
98:	em_ba3:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
1	21	95.5	22	9	AX036946	AX036946 Sequence
2	21	95.5	22	10	AX083678	AX083678 Sequence
3	21	95.5	22	10	AX083680	AX083680 Sequence
4	20	90.9	145939	79	AL158143	AL158143 Homo sapi
5	19.4	88.2	22	9	AX036945	AX036945 Sequence
6	19.4	88.2	22	9	AX046993	AX046993 Sequence
7	19.4	88.2	22	10	AX083675	AX083675 Sequence
8	19.4	88.2	22	10	AX083681	AX083681 Sequence



9 18.4 83.6 22 10 AX083682 Sequence  
c 10 18.4 83.6 4334 85 AB033099 Homo sapi  
11 18.4 83.6 109120 79 AL157945 Homo sapi  
12 18.4 83.6 110762 81 AL391244 Homo sapi  
13 18.4 83.6 197748 70 AC026283 Homo sapi  
c 14 18.4 83.6 197748 70 AC026283 Homo sapi  
15 18.4 81.8 108055 61 AC009521 Homo sapi  
16 18.4 81.8 168601 86 AC008123 Homo sapi  
c 17 18.4 81.8 169423 74 AC069309 Mus muscu  
18 18.4 81.8 169532 62 AC012513 Homo sapi  
19 17.8 80.9 22 9 AX036944 Sequence  
20 17.8 80.9 22 9 AX036952 Sequence  
21 17.8 80.9 22 10 AX083676 Sequence  
c 22 17.8 80.9 152318 66 AC021766 Homo sapi  
23 17.8 80.9 190866 64 AC015954 Homo sapi  
c 24 17.4 79.1 1754 4 AB029058 Anthocida  
c 25 17.4 79.1 102798 78 AL138730 Homo sapi  
c 26 17.4 79.1 135714 90 AL160037 Human DNA  
c 27 17.4 79.1 142172 69 AC025957 Homo sapi  
c 28 17.4 79.1 178593 83 AP003376 Oryza sat  
c 29 17.4 77.3 98411 87 AC010289 Homo sapi  
c 30 17.4 77.3 151620 65 AC018589 Homo sapi  
c 31 17.4 77.3 189697 61 AC010542 Homo sapi  
c 32 16.8 76.4 488 9 A64089 Sequence 15  
c 33 16.8 76.4 521 93 HSPAL9B5 278909 H.sapiens f  
34 16.8 76.4 642 71 AC032512 Giardial 1  
35 16.8 76.4 781 71 AC035787 Giardial 1  
36 16.8 76.4 858 72 AC064490 Giardial 1  
37 16.8 76.4 895 93 HSA279145 A1279145 Homo sapi  
38 16.8 76.4 913 9 AR074152 Sequence  
39 16.8 76.4 1014 72 AC048567 Giardial 1  
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41 16.8 76.4 5068 85 AB051476 Homo sapi  
42 16.8 76.4 7207 93 HSA238520 A1238520 Homo sapi  
43 16.8 76.4 8077 94 HML5A3B X84014 M.musculus  
44 16.8 76.4 10818 1 AE000829 AE000829 Methanoba  
45 16.8 76.4 74992 74 AC069574 Homo sapi

ALIGNMENTS

RESULT 1  
AX036946  
LOCUS AX036946 22 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 3 from Patent FR2790955.  
ACCESSION AX036946  
VERSION AX036946.1 GI:11226374  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Carpentier,A.  
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;  
ASSIST PUBL HOPITAUX DE PARIS (FR)  
FEATURES Location/Qualifiers  
source  
1..22  
/organism="synthetic construct"  
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/note="oligodesoxynucleotide"  
6 a 4 c 6 g  
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Query Match 95.5%; Score 21; DB 9; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaangttccagatga 22  
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Db 1 TGACTGTGAACGTTCCAGATGA 22  
RESULT 2  
AX083678  
LOCUS AX083678 22 bp DNA PAT 28-FEB-2001  
DEFINITION Sequence 4 from Patent WO0112223.  
ACCESSION AX083678  
VERSION AX083678.1 GI:13185410  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS van Nest,G.  
JOURNAL Methods of modulating an immune response using immunostimulatory s  
FEATURES Location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 TGACTGTGAANGTTCCAGATGA 22  
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AX083680  
LOCUS AX083680 22 bp DNA PAT 28-FEB-2001  
DEFINITION Sequence 6 from Patent WO0112223.  
ACCESSION AX083680  
VERSION AX083680.1 GI:13185412  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS van Nest,G.  
JOURNAL Methods of modulating an immune response using immunostimulatory s  
FEATURES Location/Qualifiers  
source  
1..22  
/organism="synthetic construct"  
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6 a 3 c 6 g  
BASE COUNT 6 a 3 c 6 g  
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 TGACTGTGAANGTTCCAGATGA 22  
RESULT 4  
AL158143

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LOCUS       ALL58143       145939 bp       DNA             HTG             08-APR-2001
DEFINITION  Homo sapiens chromosome X clone RP5-1074I8, *** SEQUENCING IN
            PROGRESS ***, 17 unordered pieces.
ACCESSION   ALL58143
VERSION     ALL58143.12  GI:13567909
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 145939)
REFERENCE   1 (bases 1 to 145939)
AUTHORS     Mclay,K
TITLE       Direct Submission
JOURNAL     Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On 9, 2001 this sequence version replaced gi:9931672.
            ----- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ----- Project Information
            Center project name: dj107418
            ----- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator ET-amersham; 7% of reads Chemistry:
            Dye-terminator Big Dye; 92% of reads
            Consensus quality: 137464 bases at least Q40
            Consensus quality: 141229 bases at least Q30
            Consensus quality: 143037 bases at least Q20
            Insert size: 144339; sum-of-contigs
            Insert size: 111741; 30.4% error; agarose-fp
            Quality coverage: 6.03x in Q20 bases; sum-of-contigs Quality
            coverage: 9.27x in Q20 bases; agarose-fp
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 17 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            1 3024: contig of 3024 bp in length
            *
            3025 3124: gap of 100 bp
            *
            3125 10834: contig of 7710 bp in length
            *
            10835 10934: gap of 100 bp
            *
            10935 13595: contig of 2661 bp in length
            *
            13596 13695: gap of 100 bp
            *
            13696 16092: contig of 2397 bp in length
            *
            16093 16192: gap of 100 bp
            *
            16193 22530: contig of 6338 bp in length
            *
            22531 22630: gap of 100 bp
            *
            22631 27253: contig of 4623 bp in length
            *
            27254 27353: gap of 100 bp
            *
            27354 30261: contig of 2908 bp in length
            *
            30262 30361: gap of 100 bp
            *
            30362 33611: contig of 3250 bp in length
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            33612 33711: gap of 100 bp
            *
            33712 38262: contig of 4551 bp in length
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            38263 38362: gap of 100 bp
            *
            38363 40615: contig of 2253 bp in length
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            40616 40715: gap of 100 bp
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            40716 44299: contig of 3584 bp in length
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            44300 44399: gap of 100 bp
            *
            44400 47229: contig of 2830 bp in length
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            47230 47329: gap of 100 bp
            *
            47330 52776: contig of 5447 bp in length
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            52777 52876: gap of 100 bp
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            52877 60226: contig of 7350 bp in length
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            60227 60326: gap of 100 bp
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ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 22)
AUTHORS      Carpentier,A.
JOURNAL      Patent: FR 2790955-A 2 22-SEP-2000;
              ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES     Location/Qualifiers
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Query Match      88.2%; Score 19.4; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
    ||||| ||||| ||||| |||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 6
LOCUS      AX046993 22 bp DNA PAT 15-DEC-2000
DEFINITION Sequence 2 from Patent WO0067787.
ACCESSION  AX046993
VERSION     AX046993.1 GI:11876420
KEYWORDS    synthetic construct.
SOURCE      synthetic construct.
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 22)
AUTHORS      Moss,R.B.
TITLE        Hiv immunogenic compositions and methods
JOURNAL      Patent: WO 0067787-A 2 16-NOV-2000;
              THE IMMUNE RESPONSE CORPORATION (US)
FEATURES     Location/Qualifiers
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="phosphorothioate-modified synthetic
              oligodeoxynucleotide"
BASE COUNT   6 a 3 c 7 g 6 t
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Query Match      88.2%; Score 19.4; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
    ||||| ||||| ||||| |||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 7
LOCUS      AX083675 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 1 from Patent WO0112223.
ACCESSION  AX083675
VERSION     AX083675.1 GI:13185407
KEYWORDS    synthetic construct.
SOURCE      synthetic construct.
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 22)
AUTHORS      van Nest,G.
TITLE        Methods of modulating an immune response using immunostimulatory s
              equences and compositions for use therein
JOURNAL      Patent: WO 0112223-A 1 22-FEB-2001;
              Dynavax Technologies Corporation (US)
FEATURES     Location/Qualifiers
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              /note="5-bromocytosine"
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BASE COUNT   6 a 2 c 7 g 6 t 1 others
ORIGIN

Query Match      88.2%; Score 19.4; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
    ||||| ||||| ||||| |||||
Db 1 TGACTGTGAANGTTTCGAGATGA 22

RESULT 9
LOCUS      AX083682 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 8 from Patent WO0112223.
ACCESSION  AX083682
VERSION     AX083682.1 GI:13185414
KEYWORDS    synthetic construct.
SOURCE      synthetic construct.
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 22)
AUTHORS      van Nest,G.
TITLE        Methods of modulating an immune response using immunostimulatory s
              equences and compositions for use therein
JOURNAL      Patent: WO 0112223-A 8 22-FEB-2001;
              Dynavax Technologies Corporation (US)
FEATURES     Location/Qualifiers
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              /note="5-bromocytosine"
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BASE COUNT   6 a 2 c 7 g 6 t 1 others
ORIGIN

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BASE COUNT
ORIGIN

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Best Local Similarity 90.9%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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|||||
Db 1 TGACTGTGAANGTTTGAGATGA 22

RESULT 10
AB033099/c 4334 bp mRNA PRI 11-NOV-1999
LOCUS
DEFINITION Homo sapiens mRNA for KIAA1273 protein, partial cds.
ACCESSION AB033099
VERSION AB033099.1 GI:6382027
KEYWORDS
SOURCE Homo sapiens brain cDNA to mRNA, clone_lib:pb1uescriptII SK plus
clone:hK09394.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (sites)
Nagase,T., Ishikawa,K., Kikuno,R., Hirotsawa,M., Nomura,N. and
Ohara,O.
Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
DNA Res. 6 (5), 337-345 (1999)
20039619
2 (bases 1 to 4334)
Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
Submitted (04-OCT-1999) to the DDBJ/EMBL/GenBank databases. Osamu
Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology;
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdna.info@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/,
Tel:+81-438-52-3913, Fax:+81-438-52-3914)
Location/Qualifiers
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/clone="hK09394"
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463. .2283
/gene="KIAA1273"
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/note="Start codon is not identified."
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/protein_id="BAA86587.1"
/db_xref="GI:6382028"
/translation="SWQMQLEALNLLHTLVWASLRCRAGAVQTQERLSCSAPROVP
AGECALQEYEAQVQLKSEQIRQAQERRKTLSEETROHQAQYQDKLARQTEQD
LKQOLLNEENRQESVQKQEMRRATVERELRHKNEMLRVETEARAKAARE
NADIIREQIIRLKASEHROTLESIRTAGTLCGEGFRAFTDRDKVTATVRGDTLLAVG
VISAKNATVRGRFIEARLGLPSLVRETSLRTVLEALRHPIQVSRRLSRPODVLEGV
VLSPPAARVADRIAATATNTKNGRLRHILLYGPPTGKTLFAKKLALHSGMDYAIM
TGQDVAPMGREGVTAMHLFDWANTSRRLGLLFMDQADAFLEKRAATEISKDLRATLN
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23801 a 31255 c 31398 g 22566 t 100 others
ORIGIN

Query Match 83.6%; Score 18.4; DB 79; Length 109120;
Best Local Similarity 90.5%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatg 21
||||||| | ||||| |||
Db 69219 TGACTGTGCAGGTTCCAGATG 69239

RESULT 12
AL391244 110762 bp DNA HTG 22-MAR-2001
LOCUS Homo sapiens chromosome 1 clone RP4-758J18 map p36.31-36.33, ***
DEFINITION SEQUENCING IN PROGRESS ***, 2 unordered pieces.
ACCESSION AL391244
VERSION AL391244.10 GI:13445424
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEPIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110762)
Direct Submission
Submitted (21-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Mar 24, 2001 this sequence version replaced gi:13274814.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ758J18
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 0% of reads
Chemistry: Dye-terminator ABI; 1% of reads
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-terminator ET-amersham; 8% of reads
Quality: 110363 bases at least Q40
Consensus quality: 110564 bases at least Q30
Consensus quality: 110615 bases at least Q20
Insert size: 110662; sum-of-contigs
Insert size: 116314; 4.8% error; agarose-fp
Quality coverage: 9.10x in Q20 bases; sum-of-contigs Quality
coverage: 10.07x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 102958: contig of 102958 bp in length
* 102959 103058: gap of 100 bp

```

```

FEATURES
    * 103059 110762: contig of 7704 bp in length.
    Location/Qualifiers
        1. 110762
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /chromosome="1"
        /map="p36.31-36.33"
        /clone="RP4-758J18"
        /clone_lib="RPCI-4"
        /clone_1ib="RPCI-4"
        1. 102958
        /note="assembly_fragment:00018
        clone_end:SP6
        vector_side:left
        clone_end:T7
        vector_side:right"
        103059-110762
        /note="assembly_fragment:00253"
BASE COUNT 24820 a 31446 c 31405 g 22991 t 100 others
ORIGIN

Query Match 83.6%; Score 18.4; DB 81; Length 110762;
Best Local Similarity 90.5%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatg 21
||||||| | ||||| |||
Db 47152 TGACTGTGCAGGTTCCAGATG 47172

RESULT 13
AC026283 197748 bp DNA HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 1 clone RP11-421C4, WORKING DRAFT SEQUENCE,
DEFINITION 17 unordered pieces.
ACCESSION AC026283
VERSION AC026283.2 GI:7523967
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197748)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 197748)
Waterston,R.H.
Direct Submission
Submitted (21-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 7, 2000 this sequence version replaced gi:7272307.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0421C04
----- Summary Statistics -----
Sequencing vector: M13; 98%
Sequencing vector: plasmid; 2%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 2% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 186690 bases at least Q40
Consensus quality: 190557 bases at least Q30
Consensus quality: 192407 bases at least Q20
Insert size: 193000; agarose-fp
Insert size: 196148; sum-of-contigs
Quality coverage: 5.63 in Q20 bases; agarose-fp
Quality coverage: 5.60 in Q20 bases; sum-of-contigs

```



\* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

```

1 1057: contig of 1057 bp in length
* 1058 1157: gap of unknown length
* 1158 3482: contig of 2325 bp in length
* 3483 3582: gap of unknown length
* 3583 5498: contig of 1916 bp in length
* 5499 5598: gap of unknown length
* 5599 9301: contig of 3703 bp in length
* 9302 9401: gap of unknown length
* 9402 12779: contig of 3378 bp in length
* 12780 12879: gap of unknown length
* 12880 13898: contig of 3019 bp in length
* 13899 15998: gap of unknown length
* 15999 21627: contig of 5629 bp in length
* 21628 21727: gap of unknown length
* 21728 28379: contig of 6652 bp in length
* 28380 28479: gap of unknown length
* 28480 36334: contig of 7855 bp in length
* 36335 36434: gap of unknown length
* 36435 50851: contig of 14417 bp in length
* 50852 50951: gap of unknown length
* 50952 60828: contig of 9877 bp in length
* 60829 60928: gap of unknown length
* 60929 71240: contig of 10312 bp in length
* 71241 71340: gap of unknown length
* 71341 88918: contig of 17578 bp in length
* 88919 89018: gap of unknown length
* 89019 108716: contig of 19698 bp in length
* 108717 108817: gap of unknown length
* 108818 128174: contig of 19358 bp in length
* 128175 128274: gap of unknown length
* 128275 164210: contig of 35936 bp in length
* 164211 164311: gap of unknown length
* 164311 197748: contig of 33438 bp in length.

```

## FEATURES

```

Source
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-421C4"
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misc_feature
/feature="assembly_name:Contig4"
1158..3482
misc_feature
/feature="assembly_name:Contig5"
3583..5498
misc_feature
/feature="assembly_name:Contig6"
clone_end:SP6
vector_side:left"
5599..9301
misc_feature
/feature="assembly_name:Contig7"
9402..12779
misc_feature
/feature="assembly_name:Contig8"
12880..15898
misc_feature
/feature="assembly_name:Contig9"
clone_end:17
vector_side:right"
15999..21627
misc_feature
/feature="assembly_name:Contig10"
21728..28379
misc_feature
/feature="assembly_name:Contig11"
28480..36334
misc_feature
/feature="assembly_name:Contig12"
36435..50851
misc_feature
/feature="assembly_name:Contig13"
50952..60828
misc_feature
/feature="assembly_name:Contig14"
60929..71240
misc_feature
/feature="assembly_name:Contig15"
71341..88918

```

```

/feature="assembly_name:Contig16"
89019..108716
/feature="assembly_name:Contig17"
108817..128174
/feature="assembly_name:Contig18"
128275..164210
/feature="assembly_name:Contig19"
164311..197748
/feature="assembly_name:Contig20"
42194 a 54729 c 55209 g 44011 t 1605 others
ORIGIN

Query Match      83.6%; Score 18.4; DB 70; Length 197748;
Best Local Similarity 90.5%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatg 21
||||||| | ||||| |||||
Db 160181 TGACTGTGCAGGTTCCAGATG 160161

RESULT 15
AC009521 108055 bp DNA HTG 14-APR-2001
LOCUS Homo sapiens clone Rp5-944N2, WORKING DRAFT SEQUENCE, 4 unordered
DEFINITION pieces.
AC009521
VERSION AC009521.17 GI:9966733
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Bimaga,K., Blakenburg,K., Bonnin,D., Bouck,J.,
Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J.J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jollivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulsegh,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Monabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojass,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,
Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Willamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Zhou,J., Zorrilla,S., Nelson,D.

```

and Gibbs, R.  
Direct Submission  
Unpublished  
JOURNAL  
REFERENCE 2 (bases 1 to 108055)  
AUTHORS Worley, K.C.  
TITLE Direct Submission  
JOURNAL Submitted (26-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
COMMENT On Sep 5, 2000 this sequence version replaced g1:9966185.  
----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information -----  
Center project name: HMHX  
Center clone name: RP5-944N2  
----- Summary Statistics -----  
Sequencing vector: Plasmid; M77789  
Sequencing vector: M13; L08821  
Chemistry: Dye-terminator Big Dye; 87% of reads  
Chemistry: Dye-terminator Big Dye; 87% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 105193 bases at least Q40  
Consensus quality: 105945 bases at least Q30  
Consensus quality: 106299 bases at least Q20  
Estimated insert size: 105170; sum-of-contigs estimation  
Quality coverage: 7.7x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence.  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 99571: contig of 99571 bp in length  
\* 99572 99671: gap of unknown length  
\* 99672 105349: contig of 5678 bp in length  
\* 105350 105449: gap of unknown length  
\* 105450 106581: contig of 1132 bp in length  
\* 106582 106681: gap of unknown length  
\* 106682 108055: contig of 1374 bp in length.  
FEATURES  
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1..108055  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="RP5-944N2"  
BASE COUNT 30896 a 20974 c 22948 g 32930 t 307 others  
ORIGIN  
  
Query Match 81.8%; Score 18; DB 61; Length 108055;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 tgactgtgaangttccaga 19  
|||||||  
Db 64387 TCACGTGTAATGTTCCAGA 64405



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:22 ; Search time 6788.49 Seconds  
(without alignments)  
30.635 Million cell updates/sec

Title: US-09-713-136-6  
Perfect score: 22  
Sequence: 1 tgaactgtgaangttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
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3: gb\_est3.\*  
4: gb\_est4.\*  
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6: gb\_est6.\*  
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 238: gb\_est169:\*  
 239: gb\_est170:\*  
 240: gb\_est171:\*  
 241: gb\_est172:\*  
 242: gb\_est173:\*  
 243: gb\_est174:\*  
 244: gb\_est175:\*  
 245: gb\_est176:\*  
 246: gb\_est177:\*  
 247: gb\_est178:\*  
 248: gb\_est179:\*  
 249: gb\_est180:\*  
 250: gb\_est181:\*  
 251: gb\_est182:\*  
 252: gb\_est183:\*  
 253: gb\_est184:\*  
 254: gb\_est185:\*  
 255: gb\_est186:\*  
 256: gb\_est187:\*  
 257: gb\_est188:\*  
 258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.



(pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tadb/bac\_ends/mouse/bac\_end\_intro.html Plate: 143 row: A column: 3 Seq primer: SP6 Class: BAC ends.

## FEATURES

source  
Location/Qualifiers  
1. .514  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-143A3"  
/clone\_lib="RPCI-23"  
/sex="Female"  
/lab\_host="DH10B"

/note="Organ: Kidney/brain; Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT  
ORIGIN

91 a 122 c 163 g 138 t  
Query Match 83.6%; Score 18.4; DB 240; Length 514;  
Best Local Similarity 90.5%; Pred. No. 1.3e+02; Length 514;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaangttccagatga 22

DB 113 GGCTGTGAATGTTCCAGATGA 133

## RESULT 3

AW610890  
LOCUS  
DEFINITION  
un13e10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone  
IMAGE:2395242 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW610890 537 bp mRNA EST 23-MAR-2000  
un13e10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone  
IMAGE:2395242 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Other ESTs: un13e10.x1  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:1013390  
Seq primer: custom primer used  
High quality sequence stop: 512.  
Location/Qualifiers  
1. .537  
/organism="Mus musculus"  
/db\_xref="taxon:10090"

/clone="IMAGE:2395242"  
/clone\_lib="Sugano mouse kidney mkia"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG); Site\_2: DraIII (CACTGTGTG); 1st strand cDNA was primed with an oligo(dT) primer  
[ATGTGGCTTTTITTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor (TGTGGCTTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACTGTGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAGGTGG and 3' end primer CACCTGAGCTCGAGACACA."

BASE COUNT 110 a 157 c 130 g 140 t  
ORIGIN

Query Match 83.6%; Score 18.4; DB 118; Length 537;  
Best Local Similarity 90.5%; Pred. No. 1.4e+02; Length 537;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaangttccagatga 22

DB 401 GGCTGTGAATGTTCCAGATGA 421

## RESULT 4

AU017198/c  
LOCUS  
DEFINITION  
AU017198 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone  
J0735G04 3', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AU017198 542 bp mRNA EST 15-OCT-1998  
AU017198 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone  
J0735G04 3', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Query Match 83.6%; Score 18.4; DB 107; Length 542;  
Best Local Similarity 90.5%; Pred. No. 1.4e+02; Length 542;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaangttccagatga 22

DB 113 GGCTGTGAATGTTCCAGATGA 421



High quality sequence stop: 681.  
 Location/Qualifiers  
 1. .681  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4504324"  
 /clone\_lib="NIH\_MGC\_94"  
 /tissue\_type="retina"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site.1: NotI;  
 Site.2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC library."

BASE COUNT 128 a 167 c 222 g 164 t  
 ORIGIN

Query Match 83.6%; Score 18.4; DB 175; Length 681:  
 Best Local Similarity 90.5%; Pred. No. 1.4e-02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 2 gactgtgaangttccagatga 22  
 ||||| ||||| ||||| |||||  
 Db 519 GCGTGTGAATGTTCCAGATGA 539

RESULT 9  
 BF178492  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

BF178492 705 bp mRNA EST 31-OCT-2000  
 601807652F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:4038564 4  
 mRNA sequence.  
 BF178492  
 BF178492.1 GI:11056634  
 EST.  
 house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

1. (bases 1 to 705)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@remail.nih.gov  
 Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9317 row: g column: 13  
 High quality sequence stop: 652.

High quality sequence stop: 652.  
 Location/Qualifiers  
 1. .705  
 /organism="Mus musculus"  
 /strain="C57/B6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4038564"  
 /clone\_lib="NCI\_CGAP\_Mam5"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;  
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Robin Humphreys,  
 NIH"

BASE COUNT 134 a 172 c 234 g 165 t  
 ORIGIN



High quality sequence stop: 460.

# FEATURES

Location/Qualifiers  
1..528

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3296174"

/clone\_lib="NCI\_CGAP\_CLL1"

/tissue\_type="B-cell, chronic lymphocytic leukemia"

/lab\_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCCGATGCTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

140 a 107 c 123 g 158 t

# BASE COUNT

ORIGIN

Query Match 80.9%; Score 17.8; DB 138; Length 528;

Best Local Similarity 86.4%; Pred. No. 2.6e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22

||||| 1 |||||||

Db 449 TGCTGTGTATGTTCCAGATGA 470

# RESULT 13

AA094019

LOCUS

DEFINITION c11619.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens

CDNA 5', mRNA sequence.

ACCESSION AA094019

VERSION AA094019.1 GI:1639612

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 105)

Liew,C.C.

CDNAs from fetal heart (1996)

unpublished (1996)

Contact: Liew CC

Department of Laboratory Medicine and Pathobiology

University of Toronto

Banting Institute, 100 College St., Toronto, Ontario, M5G1L5

Tel: 4169788758

Fax: 4169785650

Email: liewcc@utcc.utoronto.ca

PCR Primers

FORWARD: 5' GCCAGCTCGAAATTAACCCCTCACTAAAGG 3'

BACKWARD: 5' CCAGTGAATGTAATACGACTCACTATAGGCG 3'

Seq primer: 5' GAAATTAACCCCTCACTAAAGG 3'.

# FEATURES

source

Location/Qualifiers

1..105

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="Human fetal heart, Lambda ZAP Express"

/lab\_host="E. coli XL1-Blue"

/note="Vector: Lambda ZAP Express; Site\_1: EcoRI; Site\_2:

XhoI; mRNA was purified from human fetal hearts (8-10

weeks). cDNA was synthesized using a XhoI-Oligo dT

adaptor-primer. EcoRI adaptors were ligated, followed by

digestion with XhoI, for directional cloning into

predigested lambda ZAP Express."

31 a 21 c 16 g 37 t

# BASE COUNT

ORIGIN

Query Match 79.1%; Score 17.4; DB 2; Length 105;

Best Local Similarity 90.0%; Pred. No. 3e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagat 20

||||| 1 |||||||

Db 43 TGACTGTGAACCTTCAGAT 62

# RESULT 14

AI898251

LOCUS

DEFINITION AI898251 384 bp mRNA EST 27-JUL-1999

EST267694 tomato ovary, TAMU Lycopersicon esculentum cDNA clone

CLD32012, mRNA sequence.

ACCESSION AI898251

VERSION AI898251.1 GI:5604153

KEYWORDS EST.

SOURCE tomato.

ORGANISM

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 384)

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.

, Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman

, C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley

, S.D. and Giovannoni,J.

Generation of ESTs from tomato carpel tissue

unpublished (1999)

Contact: David Frisch

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 4366

Fax: 864 656 4293

Email: dfrisch@CLEMSON.EDU

5 prime sequence.

FEATURES

source

Location/Qualifiers

1..384

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="CLD32012"

/clone\_lib="tomato ovary, TAMU"

/tissue\_type="carpel"

/dev\_stage="5 days pre-anthesis to 5 days post-anthesis"

/lab\_host="XL1-Blue MRF"

/note="Vector: pBlueScript SK(-); Site\_1: EcoRI; Site\_2:

XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and

directionally cloned cDNA in vector Lambda ZAP II with 5'

and 3' ends located at the EcoRI and XhoI sites,

respectively. 103 a 64 c 86 g 131 t

BASE COUNT

ORIGIN

Query Match 79.1%; Score 17.4; DB 103; Length 384;

Best Local Similarity 90.0%; Pred. No. 3.9e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagat 20

||||| 1 |||||||

Db 122 TGACTTTGAAGGTTCCAGAT 141

# RESULT 15

AI489944

LOCUS

DEFINITION AI489944 559 bp mRNA EST 29-JUN-1999

EST248283 tomato ovary, TAMU Lycopersicon esculentum cDNA clone

CLD14114, mRNA sequence.

ACCESSION AI489944



```

VERSION  AI489944.1  GI:4385315
KEYWORDS
SOURCE   tomato...
ORGANISM Lycopersicon esculentum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
          Lycopersicon.
REFERENCE 1 (bases 1 to 559)
AUTHORS   Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
          , Liang,P., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
          ,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
          ,S.D. and Giovannoni,J.
TITLE     Generation of ESTs from tomato carpel tissue
JOURNAL   Unpublished (1999)
COMMENT   Contact: David Frisch
          Clemson University Genomics Institute
          Clemson University
          100 Jordan Hall, Clemson, SC 29634, USA
          Tel: 864 656 4366
          Fax: 864 656 4293
          Email: dfrisch@CLEMSON.EDU.

FEATURES             source
     1..559
            /organism="Lycopersicon esculentum"
            /cultivar="TA96"
            /db_xref="taxon:4081"
            /clone="cLED14114"
            /clone_lib="tomato ovary, TAMU"
            /tissue_type="carpel"
            /dev_stage="5 days pre-anthesis to 5 days post-anthesis"
            /lab_host="XLI-Blue MRF"
            /note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
            XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and
            directionally cloned cDNA in vector Lambda ZAP II with 5',
            and 3' ends located at the EcoRI and XhoI sites,
            respectively."
BASE COUNT  157 a   98 c   128 g   176 t
ORIGIN

Query Match      79.1%; Score 17.4; DB 21; Length 559;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1  tgactgtggaangttccagat 20
        ||||| ||||| ||||| |||||
Db      141 TGACTTTGAGGTTCCAGAT 160

```

Search completed: October '9, 2001, 18:20:24  
 Job time: 9794 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds  
(without alignments)  
26.779 Million cell updates/sec

Title: US-09-713-136-6  
Perfect score: 22  
Sequence: 1 tgactgtgaangttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues  
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0601.\*  
1: /SID8/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SID8/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SID8/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SID8/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SID8/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SID8/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SID8/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SID8/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SID8/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SID8/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SID8/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SID8/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SID8/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SID8/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
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17: /SID8/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SID8/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SID8/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SID8/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SID8/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SID8/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	95.5	22	20	AAV80099	Immunomodulatory o
2	21	95.5	22	20	AAV80101	Immunomodulatory o
3	21	95.5	22	21	AAA96254	Sequence of a stab
4	21	95.5	22	21	AAA38068	Immunostimulatory
5	21	95.5	22	21	AAA38070	Immunostimulatory
6	21	95.5	22	21	AAZ55877	Immunomodulatory o
7	21	95.5	22	22	AAF77043	Immunostimulatory
8	21	95.5	22	22	AAF77045	Immunostimulatory
9	19.4	88.2	22	19	AAV32079	Nucleotide sequenc
10	19.4	88.2	22	20	AAV36624	ISS-ODN DY1018 nuc
11	19.4	88.2	22	20	AAV80097	Immunomodulatory o

12	19.4	88.2	22	20	AAV80102	Immunomodulatory o
13	19.4	88.2	22	20	AAV80103	Immunomodulatory o
14	19.4	88.2	22	21	AAV64051	Immunostimulatory
15	19.4	88.2	22	21	AAA96253	Sequence of a stab
16	19.4	88.2	22	21	AAA90458	CpG adjuvant oligo
17	19.4	88.2	22	21	AAA14467	Immunostimulatory
18	19.4	88.2	22	21	AAA38065	Immunostimulatory
19	19.4	88.2	22	21	AAA38071	Immunostimulatory
20	19.4	88.2	22	21	AAA38072	Immunostimulatory
21	19.4	88.2	22	21	AAZ55876	Immunomodulatory o
22	19.4	88.2	22	21	AAZ55880	Immunomodulatory o
23	19.4	88.2	22	22	AAF77040	Immunomodulatory D
24	19.4	88.2	22	22	AAF77046	Immunostimulatory
25	19.4	88.2	22	22	AAZ29800	Cholera toxin immu
26	19.4	88.2	22	22	AAZ29800	Oligonucleotide OD
27	19.4	88.2	22	22	AAZ29377	CG motif and CFA c
28	18.6	84.5	22	22	AAF77047	Immunostimulatory
29	18.4	83.6	22	21	AAZ55881	Immunomodulatory o
30	17.8	80.9	22	19	AAV32080	Nucleotide sequenc
31	17.8	80.9	22	20	AAV36625	ISS-ODN mutant DY1
32	17.8	80.9	22	20	AAV55797	Immunostimulatory
33	17.8	80.9	22	20	AAV55788	Immunostimulatory
34	17.8	80.9	22	20	AAV80105	Oligo used in expe
35	17.8	80.9	22	20	AAV80096	Immunomodulatory o
36	17.8	80.9	22	20	AAV80104	Oligo used in expe
37	17.8	80.9	22	21	AAV64052	Non-CpG control ph
38	17.8	80.9	22	21	AAV86252	Sequence of a stab
39	17.8	80.9	22	21	AAV96250	Sequence of a stab
40	17.8	80.9	22	21	AAA14468	Inactive immunost
41	17.8	80.9	22	21	AAV38066	Immunostimulatory
42	17.8	80.9	22	22	AAF77041	Immunostimulatory
43	16.8	76.4	488	18	AAV91140	Strawberry fruit r
44	16.8	76.4	913	19	AAV23881	Plant CCR enzyme D
45	16.8	76.4	913	20	AAZ06885	Pine cinnamoyl-CoA

## ALIGNMENTS

## RESULT 1

AAV80099  
ID AAV80099 standard; DNA; 22 BP.  
XX AAV80099;  
AC AAV80099;  
XX  
DT 12-MAR-1999 (first entry)  
XX  
DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

OS Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
PT contain an immune-stimulating octanucleotide sequence; for treating  
PT cancer, allergic and infectious diseases

XX Claim 8; Page 29; 63pp; English.

PS The invention relates to immunomodulatory oligonucleotides that comprise

CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,

CC GAGGTTC, and GAGGTTCG. The immunomodulatory sequences are used to treat

CC patients needing immune regulation, such as those suffering from cancer,

CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the

CC oligonucleotide; and determining the relative amount of Th1-biased

CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent

CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

SQ

Query Match 95.5%; Score 21; DB 20; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.17;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22

||||| ||||| ||||| |||||

Db 1 tgactgtgaacgttccagatga 22

||||| ||||| ||||| |||||

RESULT 2

AAV80101

ID AAV80101 standard; DNA; 22 BP.

XX

AC AAV80101;

XX

DT 12-MAR-1999 (first entry)

XX

DE Immunomodulatory oligo comprising an ISS sequence.

XX

KW Immunomodulatory; immunostimulating; octanucleotide; immune regulation;

KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;

KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;

KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 11

FT /\*tag= a

FT /\*note= "5-bromocytosine"

XX

PN WO9855495-A2.

XX

PD 10-DEC-1998.

XX

PF 05-JUN-1998; 98WO-US11578.

XX

PR 06-JUN-1997; 97US-0048793.

XX

PA (DYNA-) DYNAX TECHNOLOGIES CORP.

XX

PI Dina D, Roman M, Schwartz D;

XX

DR WPI; 1999-059898/05.

XX

PT Immunostimulatory oligonucleotides regulate the immune system - and

PT contain an immune-stimulating octanucleotide sequence; for treating

PT cancer, allergic and infectious diseases

XX

PS Claim 22; Page 30; 63pp; English.

XX

CC The invention relates to immunomodulatory oligonucleotides that comprise

CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,

CC GAGGTTC, and GAGGTTCG. The immunomodulatory sequences are used to treat

CC patients needing immune regulation, such as those suffering from cancer,

CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the

CC oligonucleotide; and determining the relative amount of Th1-biased

CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent

CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

SQ

Query Match 95.5%; Score 21; DB 20; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.17;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22

||||| ||||| ||||| |||||

Db 1 tgactgtgaacgttccagatga 22

||||| ||||| ||||| |||||

RESULT 3

AAA96254

ID AAA96254 standard; DNA; 22 BP.

XX

AC AAA96254;

XX

DT 08-FEB-2001 (first entry)

XX

DE Sequence of a stabilised oligonucleotide with antitumour activity.

XX

KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;

KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.

XX

OS Synthetic.

XX

PN WO200056342-A2.

XX

PD 28-SEP-2000.

XX

PF 17-MAR-2000; 2000WO-FR00676.

XX

PR 19-MAR-1999; 99FR-0003433.

XX

PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX

PI Carpentier A;

XX

DR WPI; 2000-602192/57.

XX

PT Use of stabilized oligonucleotides as antitumor agents, particularly

PT against nervous system tumors, have optimal activity and are not toxic

XX

PS Example 13; Page 46; 57pp; French.

XX

CC The present sequence represents a stabilised oligonucleotide which has

CC antitumour activity. The oligonucleotide comprises an octamer motif

CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where

CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are

CC immunostimulatory, and are not toxic. They may be adapted for use in

CC animals or humans. The stabilised oligonucleotides are used for

CC treating tumours of any type and any degree of anaplasia, particularly

CC human tumours in the peripheral or central nervous systems, specifically

CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.

XX

SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.17;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttccagatga 22

RESULT 4  
 AAA38068  
 ID AAA38068 standard; DNA: 22 BP.  
 XX AC AAA38068;  
 XX DT 24-AUG-2000 (first entry)  
 XX DE Immunostimulatory sequence (ISS) #4.  
 XX KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
 KW development; ss.  
 XX OS Synthetic.  
 XX PN WO200021556-A1.  
 XX PD 20-APR-2000.  
 XX PF 08-OCT-1999; 99WO-US23677.  
 XX PR 09-OCT-1998; 98US-0103733.  
 XX PR 07-OCT-1999; 99US-0415186.  
 XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX PI Tighe H, Raz E, Schwartz D, Takabayashi K;  
 XX WPI; 2000-317846/27.  
 XX PT Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual -  
 XX PS Disclosure; Page 16; 65pp; English.

The present invention relates to an immunostimulatory composition comprising a human immunodeficiency virus (HIV) antigen, and an immunomodulatory polynucleotide comprising an immunostimulatory sequence (ISS). This sequence represents an ISS that can be used in the composition. An immunostimulatory composition which comprises a gp120 conjugated to an immunomodulatory polynucleotide, or is proximately associated to it and not conjugated, is used for modulating or stimulating a specific immune response against gp120 in an individual by producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It is also used for suppressing or delaying development of HIV infection in an individual infected with HIV or an individual at risk of infection with HIV, respectively. It is also used for treating an individual infected with HIV in need of immune modulation.

Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.17;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttccagatga 22

RESULT 5  
 AAA38070  
 ID AAA38070 standard; DNA: 22 BP.  
 XX AC AAA38070;  
 XX DT 24-AUG-2000 (first entry)  
 XX DE Immunostimulatory sequence (ISS) #6.  
 XX KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
 KW development; ss.  
 XX OS Synthetic.  
 XX PN WO200021556-A1.  
 XX PD 20-APR-2000.  
 XX PF 08-OCT-1999; 99WO-US23677.  
 XX PR 09-OCT-1998; 98US-0103733.  
 XX PR 07-OCT-1999; 99US-0415186.  
 XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX PI Tighe H, Raz E, Schwartz D, Takabayashi K;  
 XX WPI; 2000-317846/27.  
 XX PT Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual -  
 XX PS Disclosure; Page 16; 65pp; English.

The present invention relates to an immunostimulatory composition comprising a human immunodeficiency virus (HIV) antigen, and an immunomodulatory polynucleotide comprising an immunostimulatory sequence (ISS). This sequence represents an ISS that can be used in the composition. An immunostimulatory composition which comprises a gp120 conjugated to an immunomodulatory polynucleotide, or is proximately associated to it and not conjugated, is used for modulating or stimulating a specific immune response against gp120 in an individual by producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It is also used for suppressing or delaying development of HIV infection in an individual infected with HIV or an individual at risk of infection with HIV, respectively. It is also used for treating an individual infected with HIV in need of immune modulation.

Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.17;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttccagatga 22

RESULT 6  
 AA255877  
 ID AA255877 standard; DNA: 22 BP.

```

XX AC AA255877;
XX DT 10-APR-2000 (first entry)
XX DE Immunomodulatory oligonucleotide SEQ ID NO: 2.
XX KW Immunomodulation; immunostimulatory sequence; adjuvant;
XX KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
XX KW asthma; immunosuppression; 5-bromocytosine; ss.
XX OS Mus musculus.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT modified_base 1..22
XX FT /*tag= a
XX FT /note= "Phosphorothioate linkages"
XX FT misc_feature 9..16
XX FT /*tag= b
XX FT /note= "Immunostimulatory sequence (ISS)"
XX FT modified_base 11
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "5-bromocytosine"
XX PN WO9962923-A2.
XX XX
XX PD 09-DEC-1999.
XX PF
XX PF 04-JUN-1999; 99WO-US12538.
XX PR 05-JUN-1998; 98US-0088310.
XX PR 01-JUN-1999; 99US-0324191.
XX XX
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX PI Schwartz D;
XX XX
XX DR WPI; 2000-105687/09.
XX XX
XX PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
XX PT response, e.g. to tumor antigens
XX XX
XX PS Claim 29; Page 35; 54pp; English.
XX XX
XX CC Sequences AA255876-255877 and AA255880-255886 represent immunomodulatory
XX CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
XX CC AACGTC, AACGTT, AGCGTC, AGCGTT, AGCGTC, GACGTC, GACGTT, GCGGTT,
XX CC AACGTTCC and GACGTTCC). The invention relates to oligonucleotides
XX CC comprising one or more ISSs, where the ISS comprises at least
XX CC one modified cytosine with an electron-withdrawing moiety at
XX CC position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886
XX CC contain ISSs comprising at least one bromocytosine, whereas sequence
XX CC AA255876 contains an unmodified ISS. The immunomodulatory
XX CC oligonucleotides have an adjuvant-like effect: when formulated with an
XX CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
XX CC and induce a Th1-type immune response (activation of cytotoxic T cells),
XX CC while simultaneously downregulating the Th2-type response. The Th1
XX CC response is particularly effective for control of viruses and
XX CC intracellular parasites. The immunomodulatory oligonucleotides are used,
XX CC particularly when formulated with an antigen or a facilitator, for
XX CC modulating immune responses. Such compositions may be used in tumor
XX CC therapy, in treatment of allergy (including asthma), for inducing a
XX CC vigorous cellular response (against a virus, bacterium, fungus or
XX CC protozoan), and also in contraceptive vaccines based on sperm antigens.
XX XX
XX SQ Sequence 22 BP; 6 A; 3 C; 6 G; 6 T; 1 other;

```

```

Query Match 95.5%; Score 21; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 tgactgtgaangttccagatga 22
Db 1 tgactgtgaangttccagatga 22

RESULT 7
AAAF77043
ID AA255877 standard; DNA; 22 BP.
XX AC AA255877;
XX DT 15-MAY-2001 (first entry)
XX DE Immunostimulatory DNA #3.
XX KW Modulate; immune; antigen; immunostimulatory; ds.
XX OS Synthetic.
XX PN WO200112223-A2.
XX PD 22-FEB-2001.
XX PF 18-AUG-2000; 2000WO-US22835.
XX PR 19-AUG-1999; 99US-0149768.
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX PI Van Nest G;
XX DR WPI; 2001-211136/21.
XX PT Modulating immune response to a second antigen in humans involves
XX PT administering an immunostimulatory polynucleotide comprising an
XX PT immunostimulatory sequence and a first antigen
XX PS Disclosure; Page 15; 63pp; English.
XX CC The present invention relates to modulating an immune response to
XX CC a second antigen in an individual, involving
XX CC administering to the individual an immunomodulatory polynucleotide
XX CC comprising an immunostimulatory sequence (ISS) and a first antigen.
XX SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 22; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.17;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
Db 1 tgactgtgaangttccagatga 22

RESULT 8
AAAF77045
ID AA255877 standard; DNA; 22 BP.
XX AC AA255877;
XX DT 15-MAY-2001 (first entry)
XX DE Immunostimulatory DNA #5.
XX KW Modulate; immune; antigen; immunostimulatory; ds.
XX OS Synthetic.
XX PN WO200112223-A2.

```

PD 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US22835.

XX 19-AUG-1999; 99US-0149768.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Van Nest G;

XX WPI; 2001-211136/21.

XX Modulating immune response to a second antigen in humans involves

PT administering an immunostimulatory polynucleotide comprising an

PT immunostimulatory sequence and a first antigen

XX

XX Disclosure; Page 15; 63pp; English.

XX The present invention relates to modulating an immune response to

CC a second antigen in an individual, involving

CC administering to the individual an immunomodulatory polynucleotide

CC comprising an immunostimulatory sequence (ISS) and a first antigen.

XX

XX Sequence 22 BP; 6 A; 3 C; 6 G; 6 T; 1 other;

Query Match 95.5%; Score 21; DB 22; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.17;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22

Db 1 tgactgtgaabgtccagatga 22

RESULT 9

AAV32079

ID AAV32079 standard; DNA; 22 BP.

XX

AC AAV32079;

XX

DT 09-SEP-1998 (first entry)

XX

DE Nucleotide sequence of DY1018.

XX

XX DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;

KW immunisation; anaphylaxis; IgE; retinopathies; ss.

KW

XX synthetic.

OS

XX Key Location/Qualifiers

FH modified\_base 1..22

FT /\*tag= a

FT /note= "phosphothioate backbone"

FT

XX

PN W09816247-A1.

XX

XX 23-APR-1998.

XX

XX 09-OCT-1997; 97WO-US19004.

XX

XX 11-OCT-1996; 96US-0028118.

PR

XX (REGC ) UNIV CALIFORNIA.

XX

XX Carson DA, Raz E, Roman M;

PI

XX WPI; 1998-261028/23.

DR

XX

XX New immunomodulatory compositions - comprising an antigen conjugated

PT to a polynucleotide that contains an immunostimulatory sequence

XX

XX Example 1; Page 36; 69pp; English.

XX This is the nucleotide sequence of DY1018, which is conjugated to

CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule

CC (IMM), which comprises an antigen conjugated to a polynucleotide

CC (PN) that contains at least one immunostimulatory nucleotide sequence

CC (ISS). The conjugate synergistically boost the magnitude of the host

CC immune response against an antigen to a level greater than the host

CC immune response to either the IMM, antigen or ISS-PN alone. These

CC responses to ISS-PN/IMM conjugates are particularly acute during

CC the important early phase of the host immune response to an antigen.

CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular

CC (Th1 type) immune responses of the host. Thus, use of the method to

CC boost the immune responsiveness of a host to subsequent challenge by a

CC sensitising antigen without immunisation avoids the risk of

CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE

CC production in response to the antigen challenge. The conjugates can

CC also be used to combat pathogenic infection and to stimulate

CC therapeutic angiogenesis to treat conditions in which localised blood

CC flow plays a significant etiological role, e.g. retinopathies.

XX

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 19; Length 22;

Best Local Similarity 90.9%; Pred. No. 1;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 10

AAAX36624

ID AAX36624 standard; DNA; 22 BP.

XX

AC AAX36624;

XX

DT 09-JUL-1999 (first entry)

XX

DE ISS-ODN DY1018 nucleotide sequence.

XX

KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;

KW granulocyte-mediated tissue inflammation; Th2 type immune response;

KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;

KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;

KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;

KW eosinophilic fasciitis; therapy; ss.

XX

OS Synthetic.

XX

XX W09911275-A2.

XX

PD 11-MAR-1999.

XX

XX 04-SEP-1998; 98WO-US18382.

PF

XX 05-SEP-1997; 97US-0927120.

PR

XX (REGC ) UNIV CALIFORNIA.

PA

XX Ray E;

PI

XX WPI; 1999-312404/26.

DR

XX Reducing antigen-stimulated granulocyte-mediated inflammation

PT

XX Example 2; Page 30; 69pp; English.

PS

XX This is the ISS-ODN DY1018 nucleotide sequence.

CC The invention relates to a method for preventing or reducing

CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,

CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:

CC (a) reduction in, or the absence of, a Th2 type immune response is  
 CC measured; or (b) there is a reduction or absence of other clinical signs  
 CC of inflammation in the host after antigen challenge. The method is used  
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
 CC and to modulate the host's immune responsiveness to an antigen,  
 CC particularly where the subject suffers from asthma, nasal polyposis,  
 CC eosinophilic fasciitis, atopic dermatitis, allergic conjunctivitis,  
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
 CC antigen immunisation, the method is an antigen-independent method  
 CC and avoids host production of both interleukin-4 (IL-4), which carries  
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
 CC adhesion to endothelia.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 20; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
 ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 11  
 AAV80097  
 ID AAV80097 standard; DNA; 22 BP.  
 XX  
 AC AAV80097;  
 DT 12-MAR-1999 (first entry)  
 DE Immunomodulatory oligo comprising an ISS sequence.  
 XX Immunomodulatory; Immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.  
 XX Synthetic.  
 OS  
 XX WO9855495-A2.  
 PN 10-DEC-1998.  
 PD  
 XX 05-JUN-1998; 98WO-US11578.  
 PF  
 XX 06-JUN-1997; 97US-0048793.  
 PR  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 PI Dina D. Roman M. Schwartz D;  
 XX WPI: 1999-059898/05.  
 DR  
 XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases  
 XX  
 PS Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,  
 CC GAGGTTC, and GAGGTTCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 20; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
 ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 12  
 AAV80102  
 ID AAV80102 standard; DNA; 22 BP.  
 XX  
 AC AAV80102;  
 DT 12-MAR-1999 (first entry)  
 DE Immunomodulatory oligo comprising an ISS sequence.  
 XX Immunomodulatory; Immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.  
 XX Synthetic.  
 OS  
 XX WO9855495-A2.  
 PN 10-DEC-1998.  
 PD  
 XX 05-JUN-1998; 98WO-US11578.  
 PF  
 XX 06-JUN-1997; 97US-0048793.  
 PR  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 PI Dina D. Roman M. Schwartz D;  
 XX WPI: 1999-059898/05.  
 DR  
 XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases  
 XX  
 PS Claim 23; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,  
 CC GAGGTTC, and GAGGTTCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 20; Length 22;  
Best Local Similarity 90.9%; Pred. No. 1;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaacgttcgagatga 22

## RESULT 13

AAV80103  
ID AAV80103 standard; DNA; 22 BP.

XX AC AAV80103;

DT 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.  
XX OS Synthetic.

XX Key Location/Qualifiers

FT modified\_base 11

FT /\*tag= a  
FT /note= "5-bromocytosine"

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
PT contain an immune-stimulating octanucleotide sequence; for treating  
PT cancer, allergic and infectious diseases

PS Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
CC patients needing immune regulation, such as those suffering from cancer,  
CC an allergic disease and asthma. They are also used to prevent infectious  
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
CC Schistosoma. The immunomodulatory sequences are used to screen for human  
CC immunostimulatory activity by incubating macrophage cells and the  
CC oligonucleotide; and determining the relative amount of Th1-biased  
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 20; Length 22;  
Best Local Similarity 90.9%; Pred. No. 1;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaacgttcgagatga 22

## RESULT 14

AAV80103  
ID AAC64051 standard; DNA; 22 BP.

XX AC AAC64051;

XX 15-FEB-2001 (first entry)

XX Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.

XX CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;  
KW enhanced antigen presentation; antigen-presenting cell; APC;  
KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;  
KW vaccine; ss.

XX OS Synthetic.

XX WO200062787-A1.

XX 26-OCT-2000.

XX 11-APR-2000; 2000WO-US09664.

XX 15-APR-1999; 99US-0292278.

XX (REGC ) UNIV CALIFORNIA.

XX Raz E, Martin-Orozco E;

XX WPI; 2000-679548/66.

XX Enhancing antigen-presentation capabilities of T-cells for cancer  
PT immunotherapy, by contacting cells with an immunostimulatory  
PT oligonucleotide

XX Example I; Page 18; 42pp; English.

XX The invention relates to a method of inducing activation of T-cells  
CC to respond to an antigen, comprising contacting antigen-presenting cells  
CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs  
CC thus treated have enhanced antigen presenting capabilities compared to  
CC antigen-activated APCs. APCs with enhanced antigen-presentation  
CC capabilities then present the antigen to T-cells. The method is useful  
CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour  
CC antigen presenting capacity of tumour cells, thereby inducing T-cell  
CC activation, and is therefore useful for treating tumours. Additionally,  
CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.  
CC ISS-ODN treated APCs are induced to take up antigen through upregulation  
CC of Fc-receptor expression, to present antigen through upregulation of  
CC major histocompatibility complex (MHC) Class I and II expression and  
CC cold expression, to produce co-stimulatory factors (B7 and CD40), to  
CC provide cell-to-cell adhesion through upregulation of intercellular  
CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory  
CC cytokine production, all at levels greater than that achieved through  
CC contact of APC with antigen alone. The present sequence represents  
CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the  
CC invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 21; Length 22;  
Best Local Similarity 90.9%; Pred. No. 1;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



```

Oy 1 tgactgtgaangttccagatga 22
    ||||| |||| |||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 15
AAA96253
ID AAA96253 standard; DNA; 22 BP.
XX
AC AAA96253;
XX
DT 08-FEB-2001 (first entry)
DE
DE
XX Sequence of a stabilised oligonucleotide with antitumour activity.
KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.
XX
OS Synthetic.
XX
PN WO200056342-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-FR00676.
XX
PR 19-MAR-1999; 99FR-0003433.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
PI Carpentier A;
XX
DR WPI; 2000-602192/57.
XX
PT Use of stabilised oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic
PT
XX
PS Example 2; Page 16; 57pp; French.
XX
CC The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octamer motif
CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
CC immunostimulatory, and are not toxic. They may be adapted for use in
CC animals or humans. The stabilised oligonucleotides are used for
CC treating tumours, of any type and any degree of anaplasia, particularly
CC human tumours in the peripheral or central nervous systems, specifically
CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

```

Query Match 88.2%; Score 19,4; DB 21; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 tgactgtgaangttccagatga 22
    ||||| |||| |||| |||||
Db 1 tgactgtgaacgttcgagatga 22

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Search completed: October 9, 2001, 16:26:51  
 Job time: 2981 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:47 ; Search time 10334.3 Seconds  
(without alignments)  
31.457 Million cell updates/sec

Title: US-09-713-136-6  
Perfect score: 22  
Sequence: 1 tgcgtgtgaangttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues  
Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA\_Main.\*  
1: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*  
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8: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq.\*  
9: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq.\*  
10: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq.\*  
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24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*  
25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*  
26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*  
27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*  
28: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq.\*  
29: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq.\*  
30: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq.\*  
31: /cgn2\_6/ptodata/1/pna/US098\_COMB.seq.\*  
32: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq.\*  
33: /cgn2\_6/ptodata/1/pna/US098B\_COMB.seq.\*  
34: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq.\*  
35: /cgn2\_6/ptodata/1/pna/US098D\_COMB.seq.\*  
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37: /cgn2\_6/ptodata/1/pna/US098F\_COMB.seq.\*  
38: /cgn2\_6/ptodata/1/pna/US098G\_COMB.seq.\*  
39: /cgn2\_6/ptodata/1/pna/US098H\_COMB.seq.\*  
40: /cgn2\_6/ptodata/1/pna/US098I\_COMB.seq.\*  
41: /cgn2\_6/ptodata/1/pna/US098J\_COMB.seq.\*  
42: /cgn2\_6/ptodata/1/pna/US098K\_COMB.seq.\*  
43: /cgn2\_6/ptodata/1/pna/US098L\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	95.5	22	16	US-09-296-477-6
2	21	95.5	22	16	US-09-296-477-12
3	21	95.5	22	17	US-09-324-191A-2
4	21	95.5	22	18	US-09-415-186-4
5	21	95.5	22	18	US-09-415-186-6
6	21	95.5	22	25	US-09-642-492-6
7	21	95.5	22	25	US-09-642-492-6
8	21	95.5	22	28	US-09-713-136-4
9	21	95.5	22	28	US-09-713-136-6
10	19.4	88.2	22	1	PCT-US00-18229-32
11	19.4	88.2	22	1	PCT-US00-35064-1
12	19.4	88.2	22	1	PCT-US01-03029-2
13	19.4	88.2	22	1	PCT-US01-03029-2
14	19.4	88.2	22	1	PCT-US01-06034-1
15	19.4	88.2	22	1	PCT-US01-06034-1
16	19.4	88.2	22	1	PCT-US01-10118-1
17	19.4	88.2	22	1	PCT-US01-10118-3
18	19.4	88.2	22	1	PCT-US01-11290-1
19	19.4	88.2	22	1	PCT-US01-11290-2
20	19.4	88.2	22	1	PCT-US01-14508-1
21	19.4	88.2	22	1	PCT-US01-14508-1
22	19.4	88.2	22	1	PCT-US01-14508-1
23	19.4	88.2	22	13	US-09-296-477-12
24	19.4	88.2	22	15	US-09-167-039-19
25	19.4	88.2	22	15	US-09-235-742-19
26	19.4	88.2	22	16	US-09-296-477-2
27	19.4	88.2	22	16	US-09-296-477-15
28	19.4	88.2	22	17	US-09-308-036A-1
29	19.4	88.2	22	17	US-09-324-191A-1
30	19.4	88.2	22	17	US-09-324-191A-5
31	19.4	88.2	22	17	US-09-347-343-32
32	19.4	88.2	22	17	US-09-397-198-1
33	19.4	88.2	22	18	US-09-415-186-1
34	19.4	88.2	22	18	US-09-415-186-7
35	19.4	88.2	22	18	US-09-470-382-69
36	19.4	88.2	22	22	US-09-565-906-2
37	19.4	88.2	22	22	US-09-570-325-19
38	19.4	88.2	22	25	US-09-642-492-1
39	19.4	88.2	22	25	US-09-642-492-7
40	19.4	88.2	22	28	US-09-700-354-1
41	19.4	88.2	22	28	US-09-713-136-1
42	19.4	88.2	22	28	US-09-713-136-7
43	19.4	88.2	22	29	US-09-746-130-1
44	19.4	88.2	22	29	US-09-746-130-2
45	19.4	88.2	22	31	US-09-828-505-2

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## ALIGNMENTS

RESULT 1  
US-09-296-477-6  
; Sequence 6, Application US/09296477A  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, E.  
; APPLICANT: SCHWARTZ, D.  
; APPLICANT: ROMAN, M.  
; APPLICANT: DINA, D.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,  
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE  
; FILE REFERENCE: 377882000420  
; CURRENT APPLICATION NUMBER: US/09/296,477A  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: 09/092,329  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 60/048,793  
; EARLIER FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-296-477-6

Query Match 95.5%; Score 21; DB 16; Length 22;  
Best Local Similarity 95.5%; Pred. No. 4.3;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaangttccagatga 22

RESULT 2  
US-09-296-477-12  
; Sequence 12, Application US/09296477A  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, E.  
; APPLICANT: SCHWARTZ, D.  
; APPLICANT: ROMAN, M.  
; APPLICANT: DINA, D.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,  
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE  
; FILE REFERENCE: 377882000420  
; CURRENT APPLICATION NUMBER: US/09/296,477A  
; CURRENT FILING DATE: 1999-04-22  
; EARLIER APPLICATION NUMBER: 09/092,329  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 60/048,793  
; EARLIER FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (11)...(11)  
; OTHER INFORMATION: 5-bromocytosine  
US-09-296-477-12

Query Match 95.5%; Score 21; DB 16; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaangttccagatga 22

RESULT 3  
US-09-324-191A-2  
; Sequence 2, Application US/09324191A  
; GENERAL INFORMATION:  
; APPLICANT: Schwartz, David  
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH  
; TITLE OF INVENTION: MODIFIED BASES AND METHODS OF USE THEREOF  
; FILE REFERENCE: 377882000200  
; CURRENT APPLICATION NUMBER: US/09/324,191A  
; CURRENT FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: 60/088,310  
; PRIOR FILING DATE: 1998-06-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
; NAME/KEY: modified\_base  
; LOCATION: (11)...(11)  
; OTHER INFORMATION: 5-bromocytosine  
US-09-324-191A-2

Query Match 95.5%; Score 21; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaangttccagatga 22

RESULT 4  
US-09-415-186-4  
; Sequence 4, Application US/09415186  
; GENERAL INFORMATION:  
; APPLICANT: Tighe, Helen  
; APPLICANT: Raz, Eval  
; APPLICANT: Schwartz, David  
; APPLICANT: Takabayashi, Kenji  
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 377882000700  
; CURRENT APPLICATION NUMBER: US/09/415,186  
; CURRENT FILING DATE: 1999-10-07  
; EARLIER APPLICATION NUMBER: 60/103,733  
; EARLIER FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-415-186-4

Query Match 95.5%; Score 21; DB 18; Length 22;

Best Local Similarity 95.5%; Pred. No. 4.3;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaacgttccagatga 22

## RESULT 5

US-09-415-186-6  
; Sequence 6, Application US/09415186  
; GENERAL INFORMATION:  
; APPLICANT: Tighe, Helen  
; APPLICANT: Raz, Eyal  
; APPLICANT: Schwartz, David  
; APPLICANT: Takabayashi, Kenji  
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 377882000700  
; CURRENT APPLICATION NUMBER: US/09/415,186  
; CURRENT FILING DATE: 1999-10-07  
; EARLIER APPLICATION NUMBER: 60/103,733  
; EARLIER FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-415-186-6

Query Match 95.5%; Score 21; DB 18; Length 22;  
Best Local Similarity 95.5%; Pred. No. 4.3;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaabgttccagatga 22

## RESULT 6

US-09-642-492-4  
; Sequence 4, Application US/09642492  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, G.  
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE  
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE  
; FILE REFERENCE: 377882000800  
; CURRENT APPLICATION NUMBER: US/09/642,492  
; CURRENT FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/149,768  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-642-492-4

Query Match 95.5%; Score 21; DB 25; Length 22;  
Best Local Similarity 95.5%; Pred. No. 4.3;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||

Db 1 tgactgtgaacgttccagatga 22

## RESULT 7

US-09-642-492-6  
; Sequence 6, Application US/09642492  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, G.  
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE  
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE  
; FILE REFERENCE: 377882000800  
; CURRENT APPLICATION NUMBER: US/09/642,492  
; CURRENT FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/149,768  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (11)...(11)  
; OTHER INFORMATION: N = 5-bromocytosine  
; OTHER INFORMATION: Synthetic construct  
US-09-642-492-6

Query Match 95.5%; Score 21; DB 25; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaangttccagatga 22

## RESULT 8

US-09-713-136-4  
; Sequence 4, Application US/09713136  
; GENERAL INFORMATION:  
; APPLICANT: Tuck, Stephen  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: Immunomodulatory Compositions Containing  
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Method:  
; TITLE OF INVENTION: Of Use Thereof  
; FILE REFERENCE: 377882001500  
; CURRENT APPLICATION NUMBER: US/09/713,136  
; CURRENT FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: 60/165,467  
; PRIOR FILING DATE: 1999-11-15  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-713-136-4

Query Match 95.5%; Score 21; DB 28; Length 22;  
Best Local Similarity 95.5%; Pred. No. 4.3;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaacgttccagatga 22

RESULT 9  
US-09-713-136-6  
; Sequence 6, Application US/09713136  
; GENERAL INFORMATION:  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: Immunomodulatory Compositions Containing  
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods  
; TITLE OF INVENTION: Of Use Thereof  
; FILE REFERENCE: 377882001500  
; CURRENT APPLICATION NUMBER: US/09/713,136  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: 60/165,467  
; PRIOR FILING DATE: 1999-11-15  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
; NAME/KEY: modified\_base  
; LOCATION: (11)...(0)  
; OTHER INFORMATION: N = 5-bromocytosine  
US-09-713-136-6

Query Match 95.5%; Score 21; DB 28; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaangttccagatga 22

RESULT 10  
PCT-US00-18229-32  
; Sequence 32, Application PC/TUS0018229  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Kobayashi, Hiroko  
; TITLE OF INVENTION: Method for Enhancing an Immune Response  
; FILE REFERENCE: 6510-189W01  
; CURRENT APPLICATION NUMBER: PCT/US00/18229  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
PCT-US00-18229-32

Query Match 88.2%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaangttccagatga 22

RESULT 11  
PCT-US00-35064-1  
; Sequence 1, Application PC/TUS0035064  
; GENERAL INFORMATION:

; APPLICANT: Raz, Eyal  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Method for Preventing an Anaphylactic  
; TITLE OF INVENTION: Reaction  
; FILE REFERENCE: 06510/201W01  
; CURRENT APPLICATION NUMBER: PCT/US00/35064  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/171,830  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule  
PCT-US00-35064-1

Query Match 88.2%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaangttccagatga 22

RESULT 12  
PCT-US00-35064-2  
; Sequence 2, Application PC/TUS0035064  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Method for Preventing an Anaphylactic  
; TITLE OF INVENTION: Reaction  
; FILE REFERENCE: 06510/201W01  
; CURRENT APPLICATION NUMBER: PCT/US00/35064  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/171,830  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutant  
PCT-US00-35064-2

Query Match 88.2%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaangttccagatga 22

RESULT 13  
PCT-US01-03029-1  
; Sequence 1, Application PC/TUS0103029  
; GENERAL INFORMATION:  
; APPLICANT: Eyal Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi  
; APPLICANT: Dennis A. Carson  
; TITLE OF INVENTION: Immunomodulatory Polynucleotides In  
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen

; FILE REFERENCE: 06510/166W01  
; CURRENT APPLICATION NUMBER: PCT/US01/03029  
; CURRENT FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/179,353  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory sequence  
PCT-US01-03029-1

Query Match 88.2%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaaggttcgagatga 22

RESULT 14  
PCT-US01-03029-2  
; Sequence 2, Application PC/TUS0103029  
; GENERAL INFORMATION:  
; APPLICANT: Eval Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi  
; APPLICANT: Dennis A. Carson  
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in  
; FILE REFERENCE: 06510/166W01  
; CURRENT APPLICATION NUMBER: PCT/US01/03029  
; CURRENT FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/179,353  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Control sequence  
PCT-US01-03029-2

Query Match 88.2%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaaggttcgagatga 22

RESULT 15  
PCT-US01-06034-1  
; Sequence 1, Application PC/TUS0106034  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eval  
; APPLICANT: Rachmilewitz, Daniel  
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
; FILE REFERENCE: 6510-202W0  
; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
; OTHER INFORMATION: oligonucleotide primer  
; OTHER INFORMATION: oligonucleotide primer  
PCT-US01-06034-1

Query Match 88.2%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22  
|||||  
Db 1 tgactgtgaaggttcgagatga 22

Search completed: October 9, 2001, 21:12:47  
Job time: 20072 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:22 ; Search time 1391.6 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-09-713-136-6  
Perfect score: 22  
Sequence: 1 tgactgtgaangttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq1:\*  
7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq2:\*  
8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	22	7 US-09-802-518-4	Sequence 4, Appli
2	21	95.5	22	7 US-09-802-518-6	Sequence 6, Appli
3	21	95.5	22	7 US-09-802-359-4	Sequence 4, Appli
4	21	95.5	22	7 US-09-802-359-6	Sequence 6, Appli
5	21	95.5	22	7 US-09-802-376-4	Sequence 4, Appli
6	21	95.5	22	7 US-09-802-376-6	Sequence 6, Appli
7	19.4	88.2	22	7 US-09-802-518-1	Sequence 1, Appli
8	19.4	88.2	22	7 US-09-802-518-7	Sequence 7, Appli
9	19.4	88.2	22	7 US-09-802-359-1	Sequence 1, Appli
10	19.4	88.2	22	7 US-09-802-359-7	Sequence 7, Appli
11	19.4	88.2	22	7 US-09-802-376-1	Sequence 1, Appli
12	19.4	88.2	22	7 US-09-802-376-7	Sequence 7, Appli
13	18.4	83.6	22	7 US-09-802-518-8	Sequence 8, Appli
14	18.4	83.6	22	7 US-09-802-359-8	Sequence 8, Appli
15	18.4	83.6	22	7 US-09-802-376-8	Sequence 8, Appli
16	18	81.8	24853	7 US-09-764-874-10235	Sequence 10235, A
17	18	81.8	32212	7 US-09-764-874-10236	Sequence 10236, A
18	17.8	80.9	22	6 US-09-770-943-1	Sequence 1, Appli
19	17.8	80.9	22	6 US-09-770-943-2	Sequence 2, Appli
20	17.8	80.9	22	6 US-09-770-943-10	Sequence 10, Appli
21	17.8	80.9	22	7 US-09-802-518-2	Sequence 2, Appli
22	17.8	80.9	22	7 US-09-802-518-10	Sequence 10, Appli
23	17.8	80.9	22	7 US-09-802-359-2	Sequence 2, Appli
24	17.8	80.9	22	7 US-09-802-359-9	Sequence 9, Appli
25	17.8	80.9	22	7 US-09-802-376-2	Sequence 2, Appli

Sequence 9, Appli  
Sequence 31, App  
Sequence 10462, A  
Sequence 10373, A  
Sequence 2667, Ap  
Sequence 39362, A  
Sequence 7434, Ap  
Sequence 25567, A  
Sequence 20696, A  
Sequence 33706, A  
Sequence 25491, A  
Sequence 25115, A  
Sequence 40617, A  
Sequence 17824, A  
Sequence 40571, A  
Sequence 40550, A  
Sequence 36285, A  
Sequence 36273, A  
Sequence 40494, A  
Sequence 7398, Ap

26 17.8 80.9 22 7 US-09-802-376-9  
27 17.8 80.9 252 5 US-09-825-790-331  
28 17.3 77.3 303 7 US-09-850-147-10462  
29 16.8 76.4 132 7 US-09-724-750-10373  
30 16.8 76.4 171 7 US-09-764-874-2667  
31 16.8 76.4 207 8 US-09-253-457-39362  
32 16.8 76.4 268 8 US-09-253-456-7434  
33 16.8 76.4 308 8 US-09-253-456-25567  
34 16.8 76.4 310 8 US-09-253-457-20696  
35 16.8 76.4 312 7 US-09-540-213-33706  
36 16.8 76.4 318 8 US-09-253-456-25491  
37 16.8 76.4 321 8 US-09-253-456-25115  
38 16.8 76.4 338 8 US-09-253-457-40617  
39 16.8 76.4 345 6 US-09-909-629-17824  
40 16.8 76.4 347 8 US-09-253-457-40571  
41 16.8 76.4 350 8 US-09-253-457-40550  
42 16.8 76.4 352 8 US-09-253-378-36285  
43 16.8 76.4 357 8 US-09-253-378-36273  
44 16.8 76.4 361 8 US-09-253-457-40494  
45 16.8 76.4 368 8 US-09-253-456-7398

## ALIGNMENTS

RESULT 1  
US-09-802-518-4  
; Sequence 4, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-4

Query Match 95.5%; Score 21; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.33;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttccagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaangttccagatga 22

RESULT 2  
US-09-802-518-6  
; Sequence 6, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-6

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
DB 1 tgactgtgaangttccagatga 22

RESULT 3
US-09-802-359-4
; Sequence 4, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-4

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.33;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
DB 1 tgactgtgaacgttccagatga 22

RESULT 4
US-09-802-359-6
; Sequence 6, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-359-6

; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-6

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
DB 1 tgactgtgaangttccagatga 22

RESULT 5
US-09-802-376-4
; Sequence 4, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-4

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.33;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
DB 1 tgactgtgaacgttccagatga 22

RESULT 6
US-09-802-376-6
; Sequence 6, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-376-6
```



Query Match 95.5%; Score 21; DB 7; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
DB 1 tgactgtgaangttccagatga 22  
|||||

## RESULT 7

US-09-802-518-1  
; Sequence 1, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-1

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 2.2;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
DB 1 tgactgtgaangttccagatga 22  
|||||

## RESULT 8

US-09-802-518-7  
; Sequence 7, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-518-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
DB 1 tgactgtgaangttccagatga 22  
|||||

## RESULT 9

US-09-802-359-1  
; Sequence 1, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-359-1

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 2.2;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
DB 1 tgactgtgaangttccagatga 22  
|||||

## RESULT 10

US-09-802-359-7  
; Sequence 7, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-359-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22  
|||||  
DB 1 tgactgtgaangttccagatga 22  
|||||

## RESULT 11

```
US-09-802-376-1
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; APPLICANT: Van Nest, Gary
; PRIORITY FILING DATE: 2001-03-09
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIORITY FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   ||||| ||||| ||||| |||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 12
US-09-802-376-7
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; APPLICANT: Van Nest, Gary
; PRIORITY FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-376-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   ||||| ||||| ||||| |||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 13
US-09-802-518-8
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,518
; APPLICANT: Van Nest, Gary
; PRIORITY FILING DATE: 2001-03-09
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
```

```
US-09-802-376-8
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; APPLICANT: Van Nest, Gary
; PRIORITY FILING DATE: 2001-03-09
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIORITY FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-376-8

Query Match      83.6%; Score 18.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   ||||| ||||| ||||| |||||
DB 1 tgactgtgaangttngagatga 22

RESULT 14
US-09-802-359-8
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; APPLICANT: Van Nest, Gary
; PRIORITY FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-359-8

Query Match      83.6%; Score 18.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   ||||| ||||| ||||| |||||
DB 1 tgactgtgaangttngagatga 22

RESULT 15
US-09-802-376-8
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; APPLICANT: Van Nest, Gary
; PRIORITY FILING DATE: 2001-03-09
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
```

```
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-8
```

```
Query Match      83.6%; Score 18.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
Db 1 tgactgtgaangttngagatga 22
```

```
Search completed: October 9, 2001, 21:36:22
Job time: 21242 sec
```

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:06 ; Search time 217.64 Seconds  
(without alignments)  
19.136 Million cell updates/sec

Title: US-09-713-136-6

Perfect score: 22  
Sequence: 1 tgactgtgaangttccagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A-COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B-COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B-COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS-COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.8	80.9	22	4	US-09-092-314-1
2	17.8	80.9	22	4	US-09-092-314-2
3	17.8	80.9	22	4	US-09-092-314-10
4	16.8	76.4	913	2	US-08-975-316-61
5	16.2	74.5	1166	1	US-08-121-063-7
6	16.2	73.6	22	4	US-09-092-314-3
7	16.2	73.6	22	4	US-09-092-314-4
8	15.8	71.8	588	3	US-08-965-904B-1
9	15.8	71.8	773	3	US-08-934-131-2
10	15.4	70.0	1876	3	US-08-714-918-33
11	15.4	70.0	1876	4	US-09-265-315-33
12	15.4	70.0	1876	4	US-09-265-315-33
13	15.4	70.0	1876	4	US-09-266-417-33
14	15.4	70.0	10207	1	US-08-920-812-2
15	15.4	70.0	10207	1	US-08-920-827-2
16	15.4	70.0	10207	1	US-08-921-177-2
17	15.4	70.0	10207	1	US-08-362-577C-2
18	15.4	70.0	10207	2	US-08-920-828-2
19	15.2	69.1	2694	3	US-08-975-703-5
20	15.2	69.1	2694	4	US-08-515-884-5
21	14.8	67.3	27	2	US-08-308-952-18
22	14.8	67.3	27	4	US-09-124-141-27
23	14.8	67.3	660	1	US-08-325-553-28
24	14.8	67.3	660	2	US-08-394-152A-28
25	14.8	67.3	2088	1	US-08-164-839-7
26	14.8	67.3	2088	1	US-08-583-799-7
27	14.8	67.3	2921	1	US-08-164-839-9

Sequence 9, Appli  
Sequence 38, Appli  
Sequence 7, Appli  
Sequence 8, Appli  
Sequence 17, Appli  
Sequence 17, Appli  
Sequence 7, Appli  
Sequence 27, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 7, Appli

#### ALIGNMENTS

RESULT 1  
US-09-092-314-1  
; Sequence 1, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-1

Query Match 80.9%; Score 17.8; DB 4; Length 22;  
Best Local Similarity 86.4%; Pred. No. 1;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttccagatga 22  
Db 1 tgactgtgaaggttagatga 22

RESULT 2  
US-09-092-314-2  
; Sequence 2, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1009c1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-316-61

Query Match 76.4%; Score 16.8; DB 2; Length 913;
Best Local Similarity 85.7%; Pred. No. 6.9;
Matches 18; Conservative 0; Mismatches 3; Indels

QY 2 gactgtgaangttccagatga 22
   |||||  || |||||
Db 513 GACTGTGAATTTACACATGA 533

RESULT 5
US-08-121-063-7
; Sequence 7, Application US/08121063
; Patent No. 5446143
; GENERAL INFORMATION:
; APPLICANT: Simpson, Evan R.
; APPLICANT: Mahendroo, Mala
; APPLICANT: Mendelson, Carole R.
; TITLE OF INVENTION: Adipose-Specific Promoter Regions of
; TITLE OF INVENTION: Human Aromatase Cytochrome P450 gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,063
; FILING DATE: 14-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSD:351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

```

LENGTH: 1166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-121-063-7

Query Match 74.5%; Score 16.4; DB 1; Length 1166;  
Best Local Similarity 89.5%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ctgtggaangttccagatga 22  
||||| ||||| ||  
Db 525 CTGTGAAGTTCAGAGA 543

RESULT 6  
US-09-092-314-3  
; Sequence 3, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-3

Query Match 73.6%; Score 16.2; DB 4; Length 22;  
Best Local Similarity 81.8%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tgactgtgaangttccagatga 22  
||||| || |||||  
Db 1 tgactgtgaaccttagagatga 22

RESULT 7  
US-09-092-314-4  
; Sequence 4, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-4

Query Match 73.6%; Score 16.2; DB 4; Length 22;  
Best Local Similarity 81.8%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tgactgtgaangttccagatga 22  
||||| || |||||  
Db 1 tgactgtgaaccttagagatga 22

RESULT 8  
US-08-965-904B-1  
; Sequence 1, Application US/08965904B  
; Patent No. 6030811  
; GENERAL INFORMATION:  
; APPLICANT: CHABOT-FLETCHER, MARIE  
; APPLICANT: ANDERSON, KAREN M.  
; TITLE OF INVENTION: A HUMAN MYOTROPHIN CLONE,  
; TITLE OF INVENTION: HSABH01  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/965,904B  
; FILING DATE: 07-NOV-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030,677  
; FILING DATE: 13-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Prestia, Paul F.  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: ATG-50026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0700  
; TELEX: 846189  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 588 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-965-904B-1

Query Match 71.8%; Score 15.8; DB 3; Length 588;  
Best Local Similarity 85.0%; Pred. No. 21;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 gactgtgaangttccagatg 21  
||||| || |||||  
Db 341 GACTGTGAAGGCCCATG 360

RESULT 9  
US-08-934-131-2  
; Sequence 2, Application US/08934131

Patent No. 6153423  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer  
APPLICANT: Corley, Nell  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: HUMAN MYOTROPHIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Inocyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
FILING DATE: Filed Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0387 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-05  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 773 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGNOT22  
CLONE: 2591910  
US-08-934-131-2

Query Match 71.8%; Score 15.8; DB 3; Length 773;  
Best Local Similarity 85.0%; Pred. No. 22;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 gactgtgaangttccagatg 21  
||||||| | |||||  
Db 544 GACTGTGAAGCCCGAGATG 563

RESULT 10  
US-08-714-918-33/C  
Sequence 33, Application US/08714918  
Patent No 6037123  
GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Ving  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/714,918  
FILING DATE: September 13, 1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,102  
FILING DATE: December 22, 1995  
APPLICATION NUMBER: 60/003,798  
FILING DATE: September 15, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 222/005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1876 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-714-918-33

Query Match 70.0%; Score 15.4; DB 3; Length 1876;  
Best Local Similarity 88.9%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaangttccaga 19  
||||||| | |||||  
Db 844 GACTGTAAATGTTCCAGA 827

RESULT 11  
US-09-265-315-33/C  
Sequence 33, Application US/09265315  
Patent No. 6187341  
GENERAL INFORMATION:  
APPLICANT: Benton, Bret  
APPLICANT: Lee, Ving J.  
APPLICANT: Malouin, Francois  
APPLICANT: Martin, Patrick K.  
APPLICANT: Schmid, Molly B.  
APPLICANT: Sun, Dongxu  
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
ACTIVE ON STAPHYLOCOCCUS AUREUS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/265.315  
;; FILING DATE: March 9, 1999  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/714, 918  
;; FILING DATE: September 13, 1996  
;; APPLICATION NUMBER: 60/009,102  
;; FILING DATE: December 22, 1995  
;; APPLICATION NUMBER: 60/003,798  
;; FILING DATE: September 15, 1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 240/247  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 33:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1876 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-09-265-315-33

Query Match 70.0%; Score 15.4; DB 4; Length 1876;  
Best Local Similarity 88.9%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaangttccaga 19  
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Db 844 GACTGTAATGTTCCAGA 827

RESULT 12  
US-09-265-315-33/c  
; Sequence 33, Application US/09265315  
; Patent No. 6187541  
; GENERAL INFORMATION:  
; APPLICANT: Benton, Bret  
; APPLICANT: Lee, Ving J.  
; APPLICANT: Malouin, Francois  
; APPLICANT: Martin, Patrick K.  
; APPLICANT: Schmid, Molly B.  
; APPLICANT: Sun, Dongxu  
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
; TITLE OF INVENTION: TARGET GENES  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/265.315  
; FILING DATE: March 9, 1999  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/714, 918  
; FILING DATE: September 13, 1996

;; APPLICATION NUMBER: 60/009,102  
;; FILING DATE: December 22, 1995  
;; APPLICATION NUMBER: 60/003,798  
;; FILING DATE: September 15, 1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 240/247  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 33:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1876 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-09-265-315-33

Query Match 70.0%; Score 15.4; DB 4; Length 1876;  
Best Local Similarity 88.9%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaangttccaga 19  
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Db 844 GACTGTAATGTTCCAGA 827

RESULT 13  
US-09-266-417-33/c  
; Sequence 33, Application US/09266417  
; Patent No. 6228588  
; GENERAL INFORMATION:  
; APPLICANT: Benton, Bret  
; APPLICANT: Lee, Ving J.  
; APPLICANT: Malouin, Francois  
; APPLICANT: Martin, Patrick K.  
; APPLICANT: Schmid, Molly B.  
; APPLICANT: Sun, Dongxu  
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS  
; TITLE OF INVENTION: TARGET GENES  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/266.417  
; FILING DATE: March 9, 1999  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/714, 918  
; FILING DATE: September 13, 1996  
; APPLICATION NUMBER: 60/009,102  
; FILING DATE: December 22, 1995  
; APPLICATION NUMBER: 60/003,798  
; FILING DATE: September 15, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327



REFERENCE/DOCKET NUMBER: 240/248  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1876 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-266-417-33

Query Match 70.0%; Score 15.4; DB 4; Length 1876;  
Best Local Similarity 88.9%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttccaga 19  
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Db 844 GACTGTAATGTTCCAGA 827

RESULT 14  
US-08-920-812-2/c  
Sequence 2, Application US/08920812  
Patent No. 5763188  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
APPLICANT: Matsuhisa, Akio  
APPLICANT: Uehara, Hirotsugu  
APPLICANT: Eda, Soji  
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/920.812  
FILING DATE: 29-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,577  
FILING DATE: 27-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures, Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 19036/32420  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORGANISM: Staphylococcus aureus  
STRAIN: Clinical Isolate SA-24  
US-08-920-812-2

Query Match 70.0%; Score 15.4; DB 1; Length 10207;  
Best Local Similarity 88.9%; Pred. No. 58;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttccaga 19  
||||| || |||||  
Db 68 GACTGTAATGTTCCAGA 51

RESULT 15  
US-08-920-827-2/c  
Sequence 2, Application US/08920827  
Patent No. 5770375  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
APPLICANT: Matsuhisa, Akio  
APPLICANT: Uehara, Hirotsugu  
APPLICANT: Eda, Soji  
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/920.827  
FILING DATE: 29-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,577  
FILING DATE: 27-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures, Li-Hsien  
REGISTRATION NUMBER: 33,547  
REFERENCE/DOCKET NUMBER: 19036/32420  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORGANISM: Staphylococcus aureus  
STRAIN: Clinical Isolate SA-24  
US-08-920-827-2

Query Match 70.0%; Score 15.4; DB 1; Length 10207;  
Best Local Similarity 88.9%; Pred. No. 58;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttccaga 19  
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Db 68 GACTGTAATGTTCCAGA 51

Search completed: October 9, 2001, 15:42:08  
Job time: 298 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:20:15 ; Search time 2150.93 Seconds  
(without alignments)  
158.206 Million cell updates/sec

Title: US-09-713-136-7  
Perfect score: 22  
Sequence: 1 tgactgtgaangttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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  - 2: gb\_ba2:\*
  - 3: gb\_ba3:\*
  - 4: gb\_in1:\*
  - 5: gb\_in2:\*
  - 6: gb\_in3:\*
  - 7: gb\_ov:\*
  - 8: gb\_ov:\*
  - 9: gb\_pat1:\*
  - 10: gb\_pat2:\*
  - 11: gb\_ph:\*
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  - 13: gb\_pl2:\*
  - 14: gb\_pl3:\*
  - 15: gb\_pl4:\*
  - 16: em\_ba1:\*
  - 17: em\_ba2:\*
  - 18: em\_fun:\*
  - 19: em\_htgo\_hum:\*
  - 20: em\_htgo\_inv:\*
  - 21: em\_htgo\_rod:\*
  - 22: em\_htg\_hum1:\*
  - 23: em\_htg\_hum2:\*
  - 24: em\_htg\_hum3:\*
  - 25: em\_htg\_hum4:\*
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  - 27: em\_htg\_hum6:\*
  - 28: em\_htg\_hum7:\*
  - 29: em\_htg\_hum8:\*
  - 30: em\_htg\_inv1:\*
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  - 33: em\_htg\_rod:\*
  - 34: em\_hum1:\*
  - 35: em\_hum2:\*
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  - 40: em\_hum7:\*
  - 41: em\_in:\*
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- 54: gb\_sts2:\*
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- 56: gb\_sy:\*
- 57: gb\_un:\*
- 58: gb\_vl:\*
- 59: gb\_vl2:\*
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- 62: gb\_htg3:\*
- 63: gb\_htg4:\*
- 64: gb\_htg5:\*
- 65: gb\_htg6:\*
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- 67: gb\_htg8:\*
- 68: gb\_htg9:\*
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- 70: gb\_htg11:\*
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- 82: gb\_htg23:\*
- 83: gb\_htg24:\*
- 84: gb\_htg25:\*
- 85: gb\_pr1:\*
- 86: gb\_pr2:\*
- 87: gb\_pr3:\*
- 88: gb\_pr4:\*
- 89: gb\_pr5:\*
- 90: gb\_pr6:\*
- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_ro1:\*
- 95: gb\_ro2:\*
- 96: gb\_in4:\*
- 97: gb\_pr10:\*
- 98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	21	95.5	22	9	AX036945 Sequence
2	21	95.5	22	9	AX046993 Sequence
3	21	95.5	22	10	AX083675 Sequence
4	21	95.5	22	10	AX083681 Sequence
5	20	90.9	22	10	AX083682 Sequence
6	19.4	88.2	22	9	AX036944 Sequence
7	19.4	88.2	22	9	AX036946 Sequence
8	19.4	88.2	22	10	AX083676 Sequence

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9 19.4 88.2 22 10 AX083678 Sequence
10 19.4 88.2 22 10 AX083680 Sequence
11 18.4 83.6 145939 79 AL158143 Homo sapi
12 18.4 83.6 165337 70 AC027442 Homo sapi
13 18.4 83.6 209777 69 AC024934 Homo sapi
14 17.8 80.9 22 9 AX036952 Sequence
15 17.8 80.9 12545 6 CEF42G10
16 17.4 79.1 102798 78 AL138730 Homo sapi
17 17.4 79.1 135714 90 AL160037 Homo sapi
18 17.4 79.1 183869 73 AC068700 Homo sapi
19 16.8 76.4 929 53 CDS07553J
20 16.8 76.4 992 53 CDS0740C
21 16.8 76.4 2355 89 AK001312 Homo sapi
22 16.8 76.4 2442 89 AK001749 Homo sapi
23 16.8 76.4 2448 5 AF034078 Caenorhab
24 16.8 76.4 2502 91 BC002736 Homo sapi
25 16.8 76.4 2896 85 AB046637 Macaca fa
26 16.8 76.4 4334 85 AB033099 Homo sapi
27 16.8 76.4 13495 1 AE001805 Thermotog
28 16.8 76.4 29548 6 CEF19B6
29 16.8 76.4 49523 90 AL358135 Human DNA
30 16.8 76.4 82360 13 AP000606 Arabidops
31 16.8 76.4 85335 65 AC019557 Drosophil
32 16.8 76.4 85654 81 AL513169 Homo sapi
33 16.8 76.4 90287 61 AC010018 Drosophil
34 16.8 76.4 109120 79 AL157945 Homo sapi
35 16.8 76.4 110000 83 CEY111B2_4 Continuation (5 of
36 16.8 76.4 110762 81 AL391244 Homo sapi
37 16.8 76.4 122854 77 AC087581 Homo sapi
38 16.8 76.4 125590 6 CEY49E10
39 16.8 76.4 136047 74 AC069470 Arabidops
40 16.8 76.4 139032 87 AC010656 Homo sapi
41 16.8 76.4 140907 90 AL162499 Human DNA
42 16.8 76.4 148984 92 HSI05D16 Human DNA
43 16.8 76.4 152842 73 AC067921 Homo sapi
44 16.8 76.4 157270 89 AF236874 Homo sapi
45 16.8 76.4 159958 91 AP000475 Homo sapi

ALIGNMENTS

RESULT 1
AX036945 22 bp DNA
LOCUS Sequence 2 from Patent FR2790955.
DEFINITION AX036945
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
6 a 3 c 7 g 6 t

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 95.5%; Score 21; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.67;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 4
AX083681 22 bp DNA
LOCUS Sequence 7 from Patent WO0112223.
DEFINITION AX083681
ACCESSION AX083681
VERSION AX083681.1 GI:13185407
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Methods of modulating an immune response using immunostimulatory s
equences and compositions for use therein
Patent: WO 0112223-A 1 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1..22
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/db_xref="taxon:32630"
/note="Synthetic construct"
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BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.67;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 4
AX083681 22 bp DNA
LOCUS Sequence 7 from Patent WO0112223.
DEFINITION AX083681
ACCESSION AX083681
VERSION AX083681.1 GI:11876420
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss,R.B.
JOURNAL Hiv immunogenic compositions and methods
Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="phosphorothioate-modified synthetic
oligodeoxynucleotide"
6 a 3 c 7 g 6 t

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 95.5%; Score 21; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.67;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
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Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 3
AX083675 22 bp DNA
LOCUS Sequence 1 from Patent WO0112223.
DEFINITION AX083675
ACCESSION AX083675
VERSION AX083675.1 GI:13185407
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Methods of modulating an immune response using immunostimulatory s
equences and compositions for use therein
Patent: WO 0112223-A 1 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 3 c 7 g 6 t

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.67;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
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Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 4
AX083681 22 bp DNA
LOCUS Sequence 7 from Patent WO0112223.
DEFINITION AX083681
ACCESSION AX083681
VERSION AX083681.1 GI:11876420
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss,R.B.
JOURNAL Hiv immunogenic compositions and methods
Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="phosphorothioate-modified synthetic
oligodeoxynucleotide"
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BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
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ACCESSION  AX083681
VERSION     AX083681.1  GI:13185413
KEYWORDS   synthetic construct.
SOURCE     synthetic construct
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS    van Nest,G.
TITLE      Methods of modulating an immune response using immunostimulatory s
JOURNAL    Patent: WO 0112223-A 7 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES   Location/Qualifiers
source     1..22
            /organism="synthetic construct"
            /db_xref="taxon:32630"
modified_base 11
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BASE COUNT 6 a 2 c 7 g 6 t 1 others
ORIGIN

Query Match      95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 1 TGACTGTGAANGTTCGAGATGA 22

RESULT 5
LOCUS      AX083682      22 bp      DNA
DEFINITION Sequence 8 from Patent WO0112223.
ACCESSION  AX083682
VERSION    AX083682.1  GI:13185414
KEYWORDS   synthetic construct.
SOURCE     synthetic construct
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS    van Nest,G.
TITLE      Methods of modulating an immune response using immunostimulatory s
JOURNAL    Patent: WO 0112223-A 8 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES   Location/Qualifiers
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            /db_xref="taxon:32630"
modified_base 11
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            /mod_base=OTHER
BASE COUNT 6 a 1 c 7 g 6 t 2 others
ORIGIN

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Best Local Similarity 95.5%; Pred. No. 2.4;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
    |||||
Db 1 TGACTGTGAANGTTCGAGATGA 22

RESULT 6
AX083694
LOCUS      AX083694      22 bp      DNA
DEFINITION Sequence 1 from Patent FR2790955.
ACCESSION  AX083694
VERSION    AX083694.1  GI:11226372
KEYWORDS   synthetic construct.
SOURCE     synthetic construct
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Carpentier,A.
JOURNAL    Patent: FR 2790955-A 1 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES   Location/Qualifiers
source     1..22
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BASE COUNT 7 a 1 c 8 g 6 t
ORIGIN

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Best Local Similarity 90.9%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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    |||||
Db 1 TGACTGTGAAGTTAGAGATGA 22

RESULT 7
LOCUS      AX083696      22 bp      DNA
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION  AX083696
VERSION    AX083696.1  GI:11226374
KEYWORDS   synthetic construct.
SOURCE     synthetic construct
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Carpentier,A.
JOURNAL    Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES   Location/Qualifiers
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            /db_xref="taxon:32630"
            /note="oligodesoxynucleotide"
BASE COUNT 6 a 4 c 6 g 6 t
ORIGIN

Query Match      88.2%; Score 19.4; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
    |||||
Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 8
AX083676
LOCUS      AX083676      22 bp      DNA
DEFINITION Sequence 2 from Patent WO0112223.
ACCESSION  AX083676
VERSION    AX083676.1  GI:13185408
KEYWORDS   synthetic construct.
SOURCE     synthetic construct
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)

```

AUTHORS van Nest,G.  
 TITLE Methods of modulating an immune response using immunostimulatory s  
 sequences and compositions for use therein  
 JOURNAL Patent: WO 0112223-A 2 22-FEB-2001;  
 Dynavax Technologies Corporation (US)  
 FEATURES Location/Qualifiers  
 source 1..22  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Synthetic construct"  
 BASE COUNT 6 a 4 c 7 g 5 t  
 ORIGIN

Query Match 88.2%; Score 19.4; DB 10; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 5.1;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 TGACCGTGAACGTTCCGAGATGA 22

RESULT 9  
 LOCUS AX083678 22 bp DNA PAT 28-FEB-2001  
 DEFINITION Sequence 4 from Patent WO0112223.  
 ACCESSION AX083678  
 VERSION AX083678.1 GI:13185410  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct  
 artificial sequence.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS van Nest,G.  
 TITLE Methods of modulating an immune response using immunostimulatory s  
 sequences and compositions for use therein  
 JOURNAL Patent: WO 0112223-A 2 22-FEB-2001;  
 Dynavax Technologies Corporation (US)  
 FEATURES Location/Qualifiers  
 source 1..22  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Synthetic construct"  
 BASE COUNT 6 a 4 c 6 g 6 t  
 ORIGIN

Query Match 88.2%; Score 19.4; DB 10; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 5.1;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 TGACTGTGAACGTTCCGAGATGA 22

RESULT 10  
 LOCUS AX083680 22 bp DNA PAT 28-FEB-2001  
 DEFINITION Sequence 6 from Patent WO0112223.  
 ACCESSION AX083680  
 VERSION AX083680.1 GI:13185412  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct  
 artificial sequence.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS van Nest,G.  
 TITLE Methods of modulating an immune response using immunostimulatory s  
 sequences and compositions for use therein  
 JOURNAL Patent: WO 0112223-A 6 22-FEB-2001;  
 Dynavax Technologies Corporation (US)

FEATURES Location/Qualifiers  
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 /organism="synthetic construct"  
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 modified\_base 11  
 /note="5-bromocytosine"  
 /mod\_base=OTHER  
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Query Match 88.2%; Score 19.4; DB 10; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 TGACTGTGAANGTTCCAGATGA 22

RESULT 11  
 LOCUS AL158143 145939 bp DNA HTG 08-APR-2001  
 DEFINITION Homo sapiens chromosome X clone RP5-107418, \*\*\* SEQUENCING IN  
 PROGRESS \*\*\*, 17 unordered pieces.  
 ACCESSION AL158143  
 VERSION AL158143.12 GI:13567909  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 145939)  
 AUTHORS McIay,K.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk  
 COMMENT On Apr 9, 2001 this sequence version replaced gi:9931672.  
 ----- Genome Center  
 Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: dJ107418  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Sequencing vector: plasmid; L08752; 100% of reads  
 Chemistry: Dye-terminator ET-amersham; 7% of reads Chemistry:  
 Dye-terminator Big Dye; 92% of reads  
 Consensus quality: 137464 bases at least Q40  
 Consensus quality: 141229 bases at least Q30  
 Consensus quality: 143037 bases at least Q20  
 Insert size: 144339; sum-of-contigs  
 Insert size: 111741; 30.4% error; agarose-fp  
 Quality coverage: 6.03x in Q20 bases; sum-of-contigs Quality  
 coverage: 9.27x in Q20 bases; agarose-fp  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 17 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 3024: contig of 3024 bp in length  
 \* 3025 3124: gap of 100 bp  
 \* 3125 10834: contig of 7710 bp in length  
 \* 10835 10934: gap of 100 bp  
 \* 10935 13595: contig of 2661 bp in length  
 \* 13596 13695: gap of 100 bp



Consensus quality: 160628 bases at least Q20  
 Insert size: 170000; agarose-fp  
 Insert size: 162337; sum-of-contigs  
 Quality coverage: 3.6 in Q20 bases; agarose-fp  
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs

\*\*\*\*\*  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 31 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1105: contig of 1105 bp in length  
 \* 1106 1205: gap of 100 bp  
 \* 1206 2479: contig of 1274 bp in length  
 \* 2480 2579: gap of 100 bp  
 \* 2580 4211: contig of 1632 bp in length  
 \* 4212 4311: gap of 100 bp  
 \* 4312 5781: contig of 1470 bp in length  
 \* 5782 5881: gap of 100 bp  
 \* 5882 7830: contig of 1949 bp in length  
 \* 7831 7930: gap of 100 bp  
 \* 7931 9913: contig of 1983 bp in length  
 \* 9914 10013: gap of 100 bp  
 \* 10014 12486: contig of 2473 bp in length  
 \* 12487 12586: gap of 100 bp  
 \* 12587 15592: contig of 3006 bp in length  
 \* 15593 15692: gap of 100 bp  
 \* 15693 19721: contig of 4029 bp in length  
 \* 19722 19821: gap of 100 bp  
 \* 19822 23269: contig of 3448 bp in length  
 \* 23270 23369: gap of 100 bp  
 \* 23370 26785: contig of 3416 bp in length  
 \* 26786 26885: gap of 100 bp  
 \* 26886 30363: contig of 3478 bp in length  
 \* 30364 30463: gap of 100 bp  
 \* 30464 33964: contig of 3501 bp in length  
 \* 33965 34064: gap of 100 bp  
 \* 34065 37794: contig of 3730 bp in length  
 \* 37795 37894: gap of 100 bp  
 \* 37895 43354: contig of 5460 bp in length  
 \* 43355 43454: gap of 100 bp  
 \* 43455 47839: contig of 4385 bp in length  
 \* 47840 47939: gap of 100 bp  
 \* 47940 53326: contig of 5387 bp in length  
 \* 53327 53426: gap of 100 bp  
 \* 53427 58576: contig of 5150 bp in length  
 \* 58577 58676: gap of 100 bp  
 \* 58677 64554: contig of 5878 bp in length  
 \* 64555 64654: gap of 100 bp  
 \* 64655 68538: contig of 3884 bp in length  
 \* 68539 68638: gap of 100 bp  
 \* 68639 74650: contig of 6012 bp in length  
 \* 74651 74750: gap of 100 bp  
 \* 74751 80037: contig of 5287 bp in length  
 \* 80038 80137: gap of 100 bp  
 \* 80138 85646: contig of 5509 bp in length  
 \* 85647 85746: gap of 100 bp  
 \* 85747 92718: contig of 6972 bp in length  
 \* 92719 92818: gap of 100 bp  
 \* 92819 101098: contig of 8280 bp in length  
 \* 101099 101198: gap of 100 bp  
 \* 101199 108560: contig of 7362 bp in length  
 \* 108561 108660: gap of 100 bp  
 \* 108661 118118: contig of 9458 bp in length  
 \* 118119 118218: gap of 100 bp  
 \* 118219 128612: contig of 10394 bp in length  
 \* 128613 128712: gap of 100 bp  
 \* 128713 139860: contig of 11148 bp in length  
 \* 139861 139960: gap of 100 bp  
 \* 139961 151029: contig of 11069 bp in length

FEATURES  
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 /clone\_lib="RPC1-11 Human Male BAC"  
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 1206..2479  
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 2580..4211  
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Query Match 83.6%; Score 18.4; DB 70; Length 165337;  
 Best Local Similarity 90.5%; Pred. No. 33;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22  
|||||  
Db 34792 GACTGTGAAGTTTGAGATGA 34812

RESULT 13  
AC024934  
LOCUS Homo sapiens chromosome 12 clone RP11-329A19, WORKING DRAFT  
DEFINITION  
AC024934  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE HTG; HTGS-PHASE1; HTGS-DRAFT.  
ORGANISM human.

AC024934 209777 bp DNA HTG 30-DEC-2000  
Homo sapiens chromosome 12 clone RP11-329A19, WORKING DRAFT  
SEQUENCE, 14 unordered pieces.

HTG; HTGS-PHASE1; HTGS-DRAFT.

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 209777)  
Muzny,D.M., Adams,C., Adlo-Oduola,B., Ali-osman,F.R., Allen,C.,  
Alabrooks,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbara,J.,  
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,  
Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,  
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,  
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,  
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,  
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,  
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,  
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,  
Duggan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,  
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Hollins,B., Honsl,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,  
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,  
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Ma,J., Maheshwari,M., Mapue,P., Martin,R., Martindale,A.,  
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,  
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,  
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,  
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,  
Ogih,M., Okuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,  
Peery,J., Perez,L., Peters,L., Picketts,R., Primus,E., Pu,L.L.,  
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,  
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitaishvili,N.,  
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,  
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,  
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,  
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,  
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,  
Watlington,S., Williams,G., Williamson,A., Wleciyk,R., Wooden,S.,  
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.  
and Gibbs,R.

Direct Submission  
Unpublished  
2 (bases 1 to 209777)  
Worley,K.C.  
Direct Submission  
Submitted (03-MAR-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Dec 29, 2000 this sequence version replaced gi:11192044.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu

FEATURES  
source  
1. 209777  
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/chromosome="12"  
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ORIGIN

Query Match 83.6%; Score 18.4; DB 69; Length 209777;  
Best Local Similarity 90.5%; Pred. No. 33;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22  
|||||  
Db 76399 GACTGTGAAGTTTGAGATGA 76419

RESULT 14  
AX036952



**LOCUS** AX036952 22 bp DNA 16-NOV-2000  
**DEFINITION** Sequence 9 from Patent FR2790955.  
**ACCESSION** AX036952  
**VERSION** AX036952.1 GI:11226380  
**SOURCE** synthetic construct.  
**ORGANISM** artificial construct.  
**REFERENCE** 1 (bases 1 to 22)  
**AUTHORS** Carpentier,A.  
**JOURNAL** Patent: FR 2790955-A 9 22-SEP-2000;  
ASSIST PUBL HOPITAUX DE PARIS (FR)  
**FEATURES** Location/Qualifiers  
1..22  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
7 a 2 c 6 g 7 t  
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**ORIGIN**  
1 tgactgtgaangttcagatga 22  
|||||  
1 TGACTGTGAACGTTATAGATGA 22  
|||||

**Query Match** 80.9%; Score 17.8; DB 9; Length 22;  
**Best Local Similarity** 86.4%; Pred. No. 39;  
**Matches** 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy** 1 tgactgtgaangttcagatga 22  
|||||  
**Db** 1 TGACTGTGAACGTTATAGATGA 22  
|||||

**RESULT** 15  
**CER42G10/c**  
**LOCUS** CER42G10 12545 bp DNA INV 25-OCT-2000  
**DEFINITION** Caenorhabditis elegans cosmid F42G10, complete sequence.  
**ACCESSION** 248230  
**VERSION** 248230.1 GI:668329  
**KEYWORDS** HTG; Arg-tRNA; MiToGen activated protein kinase; Transfer RNA.  
**SOURCE** Caenorhabditis elegans.  
**ORGANISM** Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.  
1 (bases 1 to 12545)  
none.

**REFERENCE** 1  
**AUTHORS** Harris,B.R.  
**TITLE** Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium  
**JOURNAL** Science 282 (5396), 2012-2018 (1998)  
**MEDLINE** 99069613  
**REMARK** The C. elegans Sequencing Consortium.  
Erratum: [published errata appear in Science 1999 Jan 1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep 3;285(5433):1493]  
2 (bases 1 to 12545)  
Harris,B.R.

**REFERENCE** 2  
**AUTHORS** Direct Submission  
**TITLE** Submitted (12-FEB-1995) Nematode Sequencing Project, Sanger Centre,  
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,  
Washington University, St. Louis, MO 63110, USA. E-mail:  
jesse@sanger.ac.uk or tw@nematode.wustl.edu  
**JOURNAL** Coding sequences below are predicted from computer analysis, using  
predictions from Genefinder (P. Green, U. Washington), and other  
available information.  
Current sequence finishing criteria for the C. elegans genome  
sequencing consortium are that all bases are either sequenced  
unambiguously on both strands, or on a single strand with both a  
dye primer and dye terminator reaction, from distinct subclones.  
Exceptions are indicated by an explicit note.  
**IMPORTANT:** This sequence is not the entire insert of clone F42G10.  
It may be shorter because we only sequence overlapping sections  
once, or longer because we arrange for a small overlap between  
neighbouring submissions.  
The true left end of clone F42G10 is at 9861 in  
sequence 248006.  
The true right end of clone F42G10 is at 102 in

sequence 295122.  
The true right end of clone F19C6 is at 104 in this sequence. The  
start of this sequence (1..104) overlaps with the end of sequence  
248006.  
The end of this sequence (12448..12545) overlaps with the start of  
sequence 295122.  
For a graphical representation of this sequence and its analysis  
see: http://wormbase.sanger.ac.uk/per1/ace/elegans/seq/sequence?  
name=F42G10.

**FEATURES** Location/Qualifiers  
1..12545  
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4533..4658,5035..5087,5537..5600))  
/genes="F42G10.1"  
complement(join(1923..1983,2244..2767,2819..2932,  
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cDNA EST yk24a6.5 comes from this gene"  
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CHEQHYTSFTSFVQFHITAAASGLSFNTONEITHISVFTMNPIDAPKSVDOFLYVL  
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/codon\_start=1  
/protein\_id="CAA88264.1"  
/db\_xref="GI:3877043"  
/db\_xref="SWISS-PROT:Q20347"  
/translation="MVQEDDENLRNSLRPTSLSTRPTSLSVNGNEKTIPEESVLRS  
LSGTGLKYDPDEHLTYFSSANLQDLAIGNFCTVYKMRHKETGLIAVKTRCNI  
GHEQIRLLREHDTIVKSKGPNIVKFIYFSEGDCWICMELMGLISMLLYKRVYVM  
KNSRLENVVGHTVCTVDALDYKELKELIIRHVDVPSNILDGTCVGLCGICGO  
LSESFARKTAGCQPLVAPERITSOKYDVRSDVSLGILTYEATGKFPYQEMNSLF  
DQIATYVSGDPPILHPSDDDFHVSPLVKTFCITLTKDRHRPKYDTLKSFDYRIYA  
VAGPEIEAKRILGVEAIDIRNHPVDHRC"  
join(complement(1308..1367),complement(1111..1227)).

**trna**  
/genes="F42G10.tl"  
/notes="ACG Arg R-trna  
predicted using tRNAscan-SE-1.11  
preliminary prediction  
similar to tRNA-Arg"  
complement(2120..2192)  
/genes="F42G10.tl"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
/notes="contains similarity to Pfam domain: PF00069  
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E-value=1.1e-55, N=1"  
/codon\_start=1  
/protein\_id="CAA88264.1"  
/db\_xref="GI:3877043"  
/db\_xref="SWISS-PROT:Q20347"  
/translation="MVQEDDENLRNSLRPTSLSTRPTSLSVNGNEKTIPEESVLRS  
LSGTGLKYDPDEHLTYFSSANLQDLAIGNFCTVYKMRHKETGLIAVKTRCNI  
GHEQIRLLREHDTIVKSKGPNIVKFIYFSEGDCWICMELMGLISMLLYKRVYVM  
KNSRLENVVGHTVCTVDALDYKELKELIIRHVDVPSNILDGTCVGLCGICGO  
LSESFARKTAGCQPLVAPERITSOKYDVRSDVSLGILTYEATGKFPYQEMNSLF  
DQIATYVSGDPPILHPSDDDFHVSPLVKTFCITLTKDRHRPKYDTLKSFDYRIYA  
VAGPEIEAKRILGVEAIDIRNHPVDHRC"  
join(complement(1308..1367),complement(1111..1227)).

**gene**  
/genes="F42G10.tl"  
/notes="ACG Arg R-trna  
predicted using tRNAscan-SE-1.11  
preliminary prediction  
similar to tRNA-Arg"  
complement(2120..2192)  
/genes="F42G10.tl"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
/notes="contains similarity to Pfam domain: PF00069  
(Eukaryotic protein kinase domain), Score=196.8,  
E-value=1.1e-55, N=1"  
/codon\_start=1  
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/db\_xref="SWISS-PROT:Q20347"  
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LSGTGLKYDPDEHLTYFSSANLQDLAIGNFCTVYKMRHKETGLIAVKTRCNI  
GHEQIRLLREHDTIVKSKGPNIVKFIYFSEGDCWICMELMGLISMLLYKRVYVM  
KNSRLENVVGHTVCTVDALDYKELKELIIRHVDVPSNILDGTCVGLCGICGO  
LSESFARKTAGCQPLVAPERITSOKYDVRSDVSLGILTYEATGKFPYQEMNSLF  
DQIATYVSGDPPILHPSDDDFHVSPLVKTFCITLTKDRHRPKYDTLKSFDYRIYA  
VAGPEIEAKRILGVEAIDIRNHPVDHRC"  
join(complement(1308..1367),complement(1111..1227)).

**gene**  
/genes="F42G10.tl"  
/notes="ACG Arg R-trna  
predicted using tRNAscan-SE-1.11  
preliminary prediction  
similar to tRNA-Arg"  
complement(2120..2192)  
/genes="F42G10.tl"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
/notes="contains similarity to Pfam domain: PF00069  
(Eukaryotic protein kinase domain), Score=196.8,  
E-value=1.1e-55, N=1"  
/codon\_start=1  
/protein\_id="CAA88264.1"  
/db\_xref="GI:3877043"  
/db\_xref="SWISS-PROT:Q20347"  
/translation="MVQEDDENLRNSLRPTSLSTRPTSLSVNGNEKTIPEESVLRS  
LSGTGLKYDPDEHLTYFSSANLQDLAIGNFCTVYKMRHKETGLIAVKTRCNI  
GHEQIRLLREHDTIVKSKGPNIVKFIYFSEGDCWICMELMGLISMLLYKRVYVM  
KNSRLENVVGHTVCTVDALDYKELKELIIRHVDVPSNILDGTCVGLCGICGO  
LSESFARKTAGCQPLVAPERITSOKYDVRSDVSLGILTYEATGKFPYQEMNSLF  
DQIATYVSGDPPILHPSDDDFHVSPLVKTFCITLTKDRHRPKYDTLKSFDYRIYA  
VAGPEIEAKRILGVEAIDIRNHPVDHRC"  
join(complement(1308..1367),complement(1111..1227)).

**CDS**  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
/notes="contains similarity to Pfam domain: PF00069  
(Eukaryotic protein kinase domain), Score=196.8,  
E-value=1.1e-55, N=1"  
/codon\_start=1  
/protein\_id="CAA88264.1"  
/db\_xref="GI:3877043"  
/db\_xref="SWISS-PROT:Q20347"  
/translation="MVQEDDENLRNSLRPTSLSTRPTSLSVNGNEKTIPEESVLRS  
LSGTGLKYDPDEHLTYFSSANLQDLAIGNFCTVYKMRHKETGLIAVKTRCNI  
GHEQIRLLREHDTIVKSKGPNIVKFIYFSEGDCWICMELMGLISMLLYKRVYVM  
KNSRLENVVGHTVCTVDALDYKELKELIIRHVDVPSNILDGTCVGLCGICGO  
LSESFARKTAGCQPLVAPERITSOKYDVRSDVSLGILTYEATGKFPYQEMNSLF  
DQIATYVSGDPPILHPSDDDFHVSPLVKTFCITLTKDRHRPKYDTLKSFDYRIYA  
VAGPEIEAKRILGVEAIDIRNHPVDHRC"  
join(complement(1308..1367),complement(1111..1227)).

**CDS**  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/genes="F42G10.2"  
/notes="contains similarity to Pfam domain: PF00069  
(Eukaryotic protein kinase domain), Score=196.8,  
E-value=1.1e-55, N=1"  
/codon\_start=1  
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/db\_xref="SWISS-PROT:Q20347"  
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GHEQIRLLREHDTIVKSKGPNIVKFIYFSEGDCWICMELMGLISMLLYKRVYVM  
KNSRLENVVGHTVCTVDALDYKELKELIIRHVDVPSNILDGTCVGLCGICGO  
LSESFARKTAGCQPLVAPERITSOKYDVRSDVSLGILTYEATGKFPYQEMNSLF  
DQIATYVSGDPPILHPSDDDFHVSPLVKTFCITLTKDRHRPKYDTLKSFDYRIYA  
VAGPEIEAKRILGVEAIDIRNHPVDHRC"  
join(complement(1308..1367),complement(1111..1227)).

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Query Match      80.9%  Score 17.8;  DB 6;  Length 12545;
Best Local Similarity 86.4%  Pred. No. 59;
Matches 19;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy      1  tgactgtgaangttcgcagatga  22
        |||||  ||  |||  |||||
Db      10445  TGACTGTCAAAGTTGGAGATGA  10424

Search completed: October 9, 2001, 16:20:28
Job time: 2598 sec

```

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:24 ; Search time 6788.49 Seconds  
(without alignments)  
30.635 Million cell updates/sec

Title: US-09-713-136-7

Perfect score: 22

Sequence: 1 tgactgtgaangttcgagatga 22.

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_estl1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
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22: gb\_est22:\*  
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258: gb_est189:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



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Query Match      80.9%; Score 17.8; DB 107; Length 479;
Best Local Similarity 86.4%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||| ||||| ||| ||||| |||
Db 299 TGAGTGTGAATGTAGAGATGA 320

RESULT 3
CNS05PD9/c
LOCUS
DEFINITION
  CNS05PD9 972 bp DNA 26-MAY-2000
  Tetraodon nigroviridis genome survey sequence T7 end of clone
  005F08 of library A from Tetraodon nigroviridis, genomic survey
  sequence.
ACCESSION
  ALJ47814
VERSION
  ALJ47814.1 GI:8241584
KEYWORDS
  GSS; genome survey sequence.
SOURCE
  Tetraodon nigroviridis.
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
  Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
  Tetraodontidae; Tetraodon.
REFERENCE
  1 (bases 1 to 972)
  Roest-Crollius H., Jaillon O., Dasilva C., Fizames C., Fisher C.,
  Bouneau L., Billault A., Quetier F., Saurin W., Bernot A. and
  Weissenbach J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
  Unpublished
  2 (bases 1 to 972)
  Roest-Crollius H., Jaillon O., Dasilva C., Fizames C., Fisher C.,
  Bouneau L., Billault A., Quetier F., Saurin W., Bernot A. and
  Weissenbach J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
  Unpublished
  3 (bases 1 to 972)
  Direct Submission
  Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
  This sequence is a single read and was generated as part of a large
  scale clone-end sequencing project of the Tetraodon nigroviridis
  genome. For more information, please take a look at
  http://www.genoscope.cns.fr/Tetraodon.
FEATURES
  source
  1..972
    /organism="Tetraodon nigroviridis"
    /db_xref="taxon:99883"
    /clone_lib="A"
    /clone_lib="A"
    /note="Genoscope sequence ID : COAA005DC04C1-end : T7"
BASE COUNT 195 a 268 c 199 g 297 t 13 others
ORIGIN
Query Match      80.9%; Score 17.8; DB 222; Length 972;
Best Local Similarity 86.4%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||| ||||| ||| ||||| |||
Db 46 TGCCTGTGAGGTCGAGATGA 25

RESULT 4
CNS027SC
LOCUS
DEFINITION
  CNS027SC 934 bp DNA GSS
  Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
  243B23 of library G from Tetraodon nigroviridis, genomic survey
  sequence.
ACCESSION
  AA236074
VERSION
  AA236074.1 GI:1860512
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
  1 (bases 1 to 202)
  NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapsb@mail.nih.gov

```

```

sequence.
AL185061
VERSION
  AL185061.1 GI:7823165
KEYWORDS
  GSS; genome survey sequence.
SOURCE
  Tetraodon nigroviridis.
ORGANISM
  Tetraodon nigroviridis.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
  Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
  Tetraodontidae; Tetraodon.
REFERENCE
  1 (bases 1 to 934)
  Roest-Crollius H., Jaillon O., Dasilva C., Fizames C., Fisher C.,
  Bouneau L., Billault A., Quetier F., Saurin W., Bernot A. and
  Weissenbach J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
  Unpublished
  2 (bases 1 to 934)
  Roest-Crollius H., Jaillon O., Dasilva C., Bouneau L., Fisher C.,
  Bernot A., Fizames C., Wincker P., Brottier P., Quetier F.,
  Saurin W. and Weissenbach J.
  Human gene number estimate provided by genome wide analysis using
  Tetraodon nigroviridis DNA sequence
  Unpublished
  3 (bases 1 to 934)
  Direct Submission
  Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
  This sequence is a single read and was generated as part of a large
  scale clone-end sequencing project of the Tetraodon nigroviridis
  genome. For more information, please take a look at
  http://www.genoscope.cns.fr/Tetraodon.
FEATURES
  source
  1..934
    /organism="Tetraodon nigroviridis"
    /db_xref="taxon:99883"
    /clone_lib="G"
    /clone_lib="G"
    /note="Genoscope sequence ID : COAG243CAL2SP1-end :
    PUC-ori"
BASE COUNT 226 a 216 c 224 g 259 t 9 others
ORIGIN
Query Match      77.3%; Score 17; DB 220; Length 934;
Best Local Similarity 85.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 actgtgaangttcgagatga 22
   ||||| ||| ||| ||| |||
Db 254 ACTGTGAATGTGCGGATGA 273

RESULT 5
AA236074
LOCUS
DEFINITION
  AA236074 202 bp mRNA EST 13-AUG-1997
  zs05a04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684270 5'
  similar to SW:KELC_DROME Q04652 RING CANAL PROTEIN ;, mRNA
  sequence.
ACCESSION
  AA236074
VERSION
  AA236074.1 GI:1860512
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
  1 (bases 1 to 202)
  NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapsb@mail.nih.gov

```







house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 286)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MG1:908579  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 273.

## FEATURES

```

1. 286
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1396863"
/clone_lib="Soares_mammary_gland_NBMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notice="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTATACCAACTCTGAAGTCGGAGCGCCGGAATGCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

```

BASE COUNT	68 a	67 c	80 g	71 t
ORIGIN				

Query Match 76.4%; Score 16.8; DB 16; Length 286;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy . 2 gactgtgaangttcgagatga 22  
||||||| ||||| |||  
Db 105 GACTGTGAAACTTCGAGCTGA 125

RESULT 10	AA45764	297 bp	mRNA	EST	04-AUG-1997
LOCUS	AA45764				
DEFINITION	vc63b04.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:779215 5', mRNA sequence.				

AA443764  
AA445764.1  
EST.

KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

MUS MUSCULUS  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 297)  
REFERENCE  
AUTHORS  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project  
Unpublished (1996)

Contact: Marra M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
Fax: 314 286 1810

Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:472071

Seq primer: -40m13 fwd. ET from Amersham.

FEATURES	SOURCE
1. <b>Geographical Location:</b> The study was conducted in a rural area of a developing country, where access to healthcare services is limited.	Local Health Center
2. <b>Study Population:</b> The study included 100 participants, primarily women, who were selected through a random sampling method.	Community Health Workers
3. <b>Data Collection:</b> Data was collected through a series of interviews and a structured questionnaire, covering various aspects of the participants' health and lifestyle.	Research Team
4. <b>Analysis:</b> The data was analyzed using statistical software, with a focus on identifying trends and correlations between different variables.	Statistical Software
5. <b>Findings:</b> The study revealed that a significant portion of the population had limited knowledge of basic health practices, which could lead to preventable health issues.	Research Team
6. <b>Conclusion:</b> The study concluded that there is a need for targeted health education programs to improve the health outcomes of the community.	Research Team

I. 0297  
 organism="Mus musculus"  
 strain="B6D F1J"  
 db\_xref="taxon:10090"  
 clone\_image:779215  
 clone\_name=Knowles Solt  
 tissue\_type="embryo"  
 dev\_stage="2-cell"  
 lab\_host="DH108"  
 note="Organ: embryo; ve  
 Site\_1: MluI; Site\_2: Sa  
 mRNA prepared from 13.50  
 SalI(dT): 5'-CGGTCCACCGT  
 were cloned into the Mlu  
 pBluescribe vector usin  
 Average insert size: 1.6  
 73 c 76 q: 1.6

[illegible]

Query Match

Best Local Similarity 85.7%; pred. No. 2.9e+02;  
Mismatches 0; Mismatches 3; Indels 0; Gaps 0;

Qv 2 qactqtqaanqttcqaaatga 22

Db 219 GAATGTGAAGGTTCTAGATGA 239

RESULT 11

AV189436

AV189436	360 bp	EST	22-JUL-1999
LOCUS	AV189436	unpublished cDNA:Strain N2 hermaphrodite	
DEFINITION	AV189436	embryo <i>Caenorhabditis elegans</i> cDNA clone yk536b7 5', mRNA sequence.	
ACCESSION	AV189436		
VERSION	AV189436.1	GI:5571419	
KEYWORDS	EST.		
SOURCE	<i>Caenorhabditis elegans</i> .		
ORGANISM	<i>Caenorhabditis elegans</i>		
	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae.		

## REFERENCE

## REFERENCES

## CONCLUSION

**ENTER**

# TITLE

**JOURNAL  
COMMENT**

COMMENT

```

FEATURES
  source
    Location/Qualifiers
      1. 360
      /organism="Caenorhabditis elegans"
      /strain="N2"
      /db_xref="taxon:6239"
      /clone="YK536B7"
      /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
      hermaphrodite embryo"
      /sex="hermaphrodite"
      /dev_stage="embryo"
      111 a 68 c 89 g 92 t
BASE COUNT
ORIGIN

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Best Local Similarity 85.7%; Pred. No. 3.e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatg 21
    ||| ||||| ||||| |||||
Db 151 TCAGTGTGATAGTTCGAGATG 171

RESULT 12
BE428418 398 bp mRNA EST 26-JUL-2000
LOCUS MTD006.G10F990616 ITEC MTD Durum Wheat Root Library Triticum
DEFINITION turgidum subsp. durum cDNA clone MTD006.G10, mRNA sequence.
ACCESSION BE428418
VERSION BE428418.1 GI:9426261
KEYWORDS EST.
SOURCE durum wheat.
ORGANISM Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE
  1 (bases 1 to 398)
  Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
  ,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
  Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
  Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,T.,
  Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
  Sorrells,M., Warburton,M. and Wenzel,G.
  International Triticeae EST Cooperative (ITEC): Production of
  Expressed Sequence Tags for Species of the Triticeae
  Unpublished (2000)
  Contact: Joudrier P
  INRA, Unite de Biochimie et Biologie Molculaire des Cereales
  2, place VIALA, 34060 Montpellier cedex 01 FRANCE
  Tel: 33 4 99 61 23 84
  Fax: 33 4 99 61 23 48
  Email: joudrier@enscm.inra.fr
  International Triticeae EST Cooperative (ITEC)
  http://wheat.pw.usda.gov/genome.
  Location/Qualifiers
    1. 398
    /organism="Triticum turgidum subsp. durum"
    /cultivar="Silliana"
    /db_xref="taxon:4567"
    /clone="MTD006.G10"
    /clone_lib="ITEC MTD Durum Wheat Root Library"
    /tissue_type="root"
    /dev_stage="3-day-old seedling, water-stressed"
    /note="vector: pSPORT1; T7 primers used. See pSPORT1
    polylinker site. 0.3-2.0 kbp average insert size."
    99 a 77 c 104 g 118 t
BASE COUNT
ORIGIN

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Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatg 21
    ||| ||||| ||||| |||||
Db 147 TCAGTGTGATGTCGAGATG 167

FEATURES
  source
    Location/Qualifiers
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      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone_lib="EN0086"
      /dev_stage="Adult"
      /note="Organ: lung_normal; vector: puc18; Site_1: SmaI;
      Site_2: SmaI; A mini-library was made by cloning products
      derived from ORESTES PCR (U.S. Letters Patent application
      No. 196,716 - Ludwig Institute for Cancer Research)
      profiles into the pUC 18 vector. Reverse transcription of
      tissue mRNA and cDNA amplification were performed under
      low stringency conditions."
      85 a 117 c 135 g 97 t
BASE COUNT
ORIGIN

Query Match 76.4%; Score 16.8; DB 170; Length 434;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatg 21
    ||| ||||| ||||| |||||
Db 147 TCAGTGTGATGTCGAGATG 167

RESULT 14
AI597068/c 441 bp mRNA EST 21-APR-1999
LOCUS AI597068/c
DEFINITION VJ44e09.xl Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:931912 3', mRNA sequence.
ACCESSION AI597068

```

Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogiwara, Y.,  
Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,  
Sorrells, M., Warburton, M. and Wenzel, G.  
International Triticeae EST Cooperative (ITEC): Production of  
Expressed Sequence Tags for Species of the Triticeae  
Unpublished (2000)  
Contact: Schuch W  
Zeneca Wheat Improvement Centre, Norwich Research Park  
Colney Lane, Norwich NR4 7UH UNITED KINGDOM  
Tel: 44 1603 250 2600  
Fax: 44 1603 250 699  
Email: wolfgang.schuch@zeneca.com  
International Triticeae EST Cooperative (ITEC)  
http://wheat.pw.usda.gov/genome.  
Location/Qualifiers  
1. 474  
/organism="Triticum aestivum"  
/cultivar="Novosibirskaya 67"  
/db\_xref="taxon:4565"  
/clone="WNR021.G5"  
/clone\_lib="ITEC WMR Wheat Root Library"  
/tissue\_type="root"  
/note="W13 Reverse sequencing primer used for 5' end of  
clone."

BASE COUNT 119 a 87 c 127 g 141 t  
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Query Match 76.4%; Score 16.8; DB 167; Length 474;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 gactgtgaangttcgagatga 22  
||||| ||||| ||||| |||||  
DB 350 GACGGTGAAGTTAGAGATGA 370

Search completed: October 9, 2001, 18:20:25  
Job time: 9795 sec

Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogiwara, Y.,  
Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,  
Sorrells, M., Warburton, M. and Wenzel, G.  
International Triticeae EST Cooperative (ITEC): Production of  
Expressed Sequence Tags for Species of the Triticeae  
Unpublished (2000)  
Contact: Schuch W  
Zeneca Wheat Improvement Centre, Norwich Research Park  
Colney Lane, Norwich NR4 7UH UNITED KINGDOM  
Tel: 44 1603 250 2600  
Fax: 44 1603 250 699  
Email: wolfgang.schuch@zeneca.com  
International Triticeae EST Cooperative (ITEC)  
http://wheat.pw.usda.gov/genome.  
Location/Qualifiers  
1. 474  
/organism="Triticum aestivum"  
/cultivar="Novosibirskaya 67"  
/db\_xref="taxon:4565"  
/clone="WNR021.G5"  
/clone\_lib="ITEC WMR Wheat Root Library"  
/tissue\_type="root"  
/note="W13 Reverse sequencing primer used for 5' end of  
clone."

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Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 gactgtgaangttcgagatga 22  
||||| ||||| ||||| |||||  
DB 116 GGCTGTGATGTTCCACAGATGA 96

Search completed: October 9, 2001, 18:20:25  
Job time: 9795 sec

Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogiwara, Y.,  
Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,  
Sorrells, M., Warburton, M. and Wenzel, G.  
International Triticeae EST Cooperative (ITEC): Production of  
Expressed Sequence Tags for Species of the Triticeae  
Unpublished (2000)  
Contact: Schuch W  
Zeneca Wheat Improvement Centre, Norwich Research Park  
Colney Lane, Norwich NR4 7UH UNITED KINGDOM  
Tel: 44 1603 250 2600  
Fax: 44 1603 250 699  
Email: wolfgang.schuch@zeneca.com  
International Triticeae EST Cooperative (ITEC)  
http://wheat.pw.usda.gov/genome.  
Location/Qualifiers  
1. 474  
/organism="Triticum aestivum"  
/cultivar="Novosibirskaya 67"  
/db\_xref="taxon:4565"  
/clone="WNR021.G5"  
/clone\_lib="ITEC WMR Wheat Root Library"  
/tissue\_type="root"  
/note="W13 Reverse sequencing primer used for 5' end of  
clone."

BASE COUNT 103 a 144 c 111 g 82 t  
ORIGIN  
Query Match 76.4%; Score 16.8; DB 22; Length 441;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 gactgtgaangttcgagatga 22  
||||| ||||| ||||| |||||  
DB 116 GGCTGTGATGTTCCACAGATGA 96

Search completed: October 9, 2001, 18:20:25  
Job time: 9795 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds  
(without alignments)  
26.779 Million cell updates/sec

Title: US-09-713-136-7

Perfect score: 22  
Sequence: 1 tgactgtgaangttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_0601:.\*  
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT:.\*  
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3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT:.\*  
4: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT:.\*  
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8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT:.\*  
9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT:.\*  
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14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT:.\*  
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19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT:.\*  
20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT:.\*  
21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT:.\*  
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	22	19	AAV32079
2	21	95.5	22	20	AAV36624
3	21	95.5	22	20	AAV80097
4	21	95.5	22	20	AAV80102
5	21	95.5	22	20	AAV80103
6	21	95.5	22	21	AAC64051
7	21	95.5	22	21	AAV80103
8	21	95.5	22	21	AAV80103
9	21	95.5	22	21	AAV80103
10	21	95.5	22	21	AAV80103
11	21	95.5	22	21	AAV80103

12	21	95.5	22	21	AAA38072	Immunostimulatory
13	21	95.5	22	21	AAV55876	Immunomodulatory o
14	21	95.5	22	21	AAV55880	Immunomodulatory o
15	21	95.5	22	22	AAV77040	Immunostimulatory
16	21	95.5	22	22	AAV77046	Immunostimulatory
17	21	95.5	22	22	AAV29800	Cholera toxin immu
18	21	95.5	22	22	AAV29800	Oligonucleotide OD
19	21	95.5	22	22	AAV29800	CG motif and CFA c
20	20.2	91.8	22	22	AAV77047	Immunostimulatory
21	20	90.9	22	21	AAV55881	Immunomodulatory o
22	19.4	88.2	22	19	AAV32080	Nucleotide sequenc
23	19.4	88.2	22	20	AAV36625	ISS-ODN mutant DY1
24	19.4	88.2	22	20	AAV55797	Immunostimulatory
25	19.4	88.2	22	20	AAV55788	Immunostimulatory
26	19.4	88.2	22	20	AAV80105	Oligo used in expe
27	19.4	88.2	22	20	AAV80096	Immunomodulatory o
28	19.4	88.2	22	20	AAV80099	Immunomodulatory o
29	19.4	88.2	22	20	AAV80101	Immunomodulatory o
30	19.4	88.2	22	20	AAV80104	Oligo used in expe
31	19.4	88.2	22	21	AAV64052	Non-Cpg control ph
32	19.4	88.2	22	21	AAV64052	Sequence of a stab
33	19.4	88.2	22	21	AAV6254	Sequence of a stab
34	19.4	88.2	22	21	AAV14468	Inactive immunosti
35	19.4	88.2	22	21	AAV38066	Immunostimulatory
36	19.4	88.2	22	21	AAV38068	Immunostimulatory
37	19.4	88.2	22	21	AAV38070	Immunostimulatory o
38	19.4	88.2	22	21	AAV55877	Immunostimulatory
39	19.4	88.2	22	22	AAV77041	Immunostimulatory
40	19.4	88.2	22	22	AAV77043	Immunostimulatory
41	19.4	88.2	22	22	AAV77045	Immunostimulatory
42	17.8	80.9	22	20	AAV55790	Immunostimulatory
43	17.8	80.9	22	20	AAV55791	Immunostimulatory
44	17.8	80.9	22	20	AAV80106	Oligo used in expe
45	17.8	80.9	22	22	AAV92378	CG motif and CFA c

ALIGNMENTS

RESULT 1  
AAV32079  
ID AAV32079 standard; DNA; 22 BP.  
XX  
AC AAV32079;  
XX  
DT 09-SEP-1998 (first entry)  
XX  
DE Nucleotide sequence of DY1018.  
XX  
KW DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;  
KW immunisation; anaphylaxis; IgE; retinopathies; ss.  
XX  
OS synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..22  
FT /\*tag= a  
FT /note= "phosphothioate backbone"  
XX  
XX  
XX WO9816247-A1.  
XX  
XX 23-APR-1998.  
XX  
XX 09-OCT-1997; 97NO-US19004.  
XX  
XX 11-OCT-1996; 96US-0028118.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Carson DA, Raz E, Roman M;  
XX WPI, 1998-261028/23.  
XX

PT New Immunomodulatory compositions - comprising an antigen conjugated  
 PT to a polynucleotide that contains an immunostimulatory sequence

XX Example 1; Page 36; 69pp; English.

CC This is the nucleotide sequence of DY1018, which is conjugated to  
 CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule  
 CC (IMM), which comprises an antigen conjugated to a polynucleotide  
 CC (PN) that contains at least one immunostimulatory nucleotide sequence  
 CC (ISS). The conjugate synergistically boost the magnitude of the host  
 CC immune response against an antigen to a level greater than the host  
 CC immune response to either the IMM, antigen or ISS-PN alone. These  
 CC responses to ISS-PN/IMM conjugates are particularly acute during  
 CC the important early phase of the host immune response to an antigen.  
 CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular  
 CC (Th1 type) immune responses of the host. Thus, use of the method to  
 CC boost the immune responsiveness of a host to subsequent challenge by a  
 CC sensitising antigen without immunisation avoids the risk of  
 CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE  
 CC production in response to the antigen challenge. The conjugates can  
 CC also be used to combat pathogenic infection and to stimulate  
 CC therapeutic angiogenesis to treat conditions in which localised blood  
 CC flow plays a significant etiological role, e.g. retinopathies.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 19; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.14;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcgagatga 22

# RESULT 2

AAX36624  
 ID AAX36624 standard; DNA; 22 BP.

XX AC AAX36624;

XX 09-JUL-1999 (first entry)

XX ISS-ODN DY1018 nucleotide sequence.

XX Antigen-stimulated inflammation; immunostimulatory oligonucleotide;  
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;  
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;  
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;  
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;  
 KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.

XX WO9911275-A2.

XX 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18382.

XX 05-SEP-1997; 97US-0927120.

XX (REGC ) UNIV CALIFORNIA.

XX Ray E;

XX WPI; 1999-312404/26.

XX Reducing antigen-stimulated granulocyte-mediated inflammation

XX Example 2; Page 30; 69pp; English.

CC This is the ISS-ODN DY1018 nucleotide sequence.  
 CC The invention relates to a method for preventing or reducing  
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:  
 CC (a) reduction in, or the absence of, a Th2 type immune response is  
 CC measured; or (b) there is a reduction or absence of other clinical signs  
 CC of inflammation in the host after antigen challenge. The method is used  
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
 CC and to modulate the host's immune responsiveness to an antigen,  
 CC particularly where the subject suffers from asthma, nasal polyposis,  
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
 CC antigen immunisation, the method is an antigen-independent method,  
 CC and avoids host production of both interleukin-4 (IL-4), which carries  
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
 CC adhesion to endothelia.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.14;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcgagatga 22

# RESULT 3

AAV80097

ID AAV80097 standard; DNA; 22 BP.

XX AC AAV80097;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,  
 CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. NO. 0.14; Mismatches 1; Indels 0; Gaps 0;  
 Matches 21; Conservative 0;

OY 1 tgactgtgaangttcgagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 4  
 AAV80102  
 ID AAV80102 standard; DNA; 22 BP.  
 XX  
 AC AAV80102;

DT 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 11  
 FT /\*tag= a  
 FT /note= "5-bromocytosine"

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 23; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. NO. 0.14; Mismatches 1; Indels 0; Gaps 0;  
 Matches 21; Conservative 0;

OY 1 tgactgtgaangttcgagatga 22  
 |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 5  
 AAV80103  
 ID AAV80103 standard; DNA; 22 BP.  
 XX  
 AC AAV80103;

DT 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 11  
 FT /\*tag= a  
 FT /note= "5-bromocytosine"

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,  
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

```

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
Query Match 95.5%; Score 21; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
AAC64051
ID AAC64051 standard; DNA; 22 BP.
XX AC AAC64051;
XX DT 15-FEB-2001 (first entry)
XX DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
XX KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
XX KW enhanced antigen presentation; antigen-presenting cell; APC;
XX KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
XX KW vaccine; ss.
XX OS Synthetic.
XX PN WO200062787-A1.
XX PD 26-OCT-2000.
XX PP 11-APR-2000; 2000WO-US09664.
XX PR 15-APR-1999; 99US-0292278.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Raz E, Martin-Orozco E;
XX WPI; 2000-679548/66.
XX PT Enhancing antigen-presentation capabilities of T-cells for cancer
XX PT immunotherapy, by contacting cells with an immunostimulatory
XX PT oligonucleotide.
XX PS Example 1; Page 18; 42pp; English.
XX CC The invention relates to a method of inducing activation of T-cells
XX CC to respond to an antigen, comprising contacting antigen-presenting cells
XX CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
XX CC thus treated have enhanced antigen presenting capabilities compared to
XX CC antigen-activated APCs. APCs with enhanced antigen-presentation
XX CC capabilities then present the antigen to T-cells. The method is useful
XX CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
XX CC antigen presenting capacity of tumour cells, thereby inducing T-cell
XX CC activation, and is therefore useful for treating tumours. Additionally,
XX CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
XX CC ISS-ODN treated APCs are induced to take up antigen through upregulation
XX CC of Fc-receptor expression, to present antigen through upregulation of
XX CC major histocompatibility complex (MHC) Class I and II expression and
XX CC CD1d expression, to produce co-stimulatory factors (B7 and CD40), to
XX CC provide cell-to-cell adhesion through upregulation of intercellular
XX CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
XX CC cytokine production, all at levels greater than that achieved through
XX CC contact of APC with antigen alone. The present sequence represents
XX CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the
XX CC invention.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 7
AAA96253
ID AAA96253 standard; DNA; 22 BP.
XX AC AAA96253;
XX DT 08-FEB-2001 (first entry)
XX DE Sequence of a stabilised oligonucleotide with antitumour activity.
XX KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
XX KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.
XX OS Synthetic.
XX PN WO200056342-A2.
XX PD 28-SEP-2000.
XX PP 17-MAR-2000; 2000WO-FR00676.
XX PR 19-MAR-1999; 99FR-0003433.
XX PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX PI Carpentier A;
XX WPI; 2000-602192/57.
XX PT Use of stabilised oligonucleotides as antitumor agents, particularly
XX PT against nervous system tumors, have optimal activity and are not toxic
XX PT .
XX PS Example 2; Page 16; 57pp; French.
XX CC The present sequence represents a stabilised oligonucleotide which has
XX CC antitumour activity. The oligonucleotide comprises an octamer motif
XX CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
XX CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
XX CC immunostimulatory, and are not toxic. They may be adapted for use in
XX CC animals or humans. The stabilised oligonucleotides are used for
XX CC treating tumours, of any type and any degree of anaplasia, particularly
XX CC human tumours in the peripheral or central nervous systems, specifically
XX CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 8
AAA90458
ID AAA90458 standard; DNA; 22 BP.
XX AC AAA90458;

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XX 10-JAN-2001 (first entry)  
 XX CpG adjuvant oligonucleotide, SEQ ID NO:19.  
 XX CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;  
 KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;  
 KW viral infection; bacterial infection; parasitic infection; HCV; HBV;  
 KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;  
 KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;  
 KW rabies virus; cholera; diphtheria; tetanus; pertussis;  
 KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.  
 XX Synthetic.  
 XX WO200050006-A2.  
 XX 31-AUG-2000.  
 XX 09-FEB-2000; 2000WO-US03331.  
 XX 26-FEB-1999; 99US-0121858.  
 XX 29-JUL-1999; 99US-0146391.  
 XX 28-OCT-1999; 99US-0161997.  
 XX (CHIR) CHIRON CORP.  
 XX O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Uguzzoli M, Singh M;  
 PI Barackman J;  
 XX WPI; 2000-587123/55.  
 XX Microemulsion having an adsorbent surface comprising a microdroplet  
 PT emulsion consisting of a metabolizable oil and an emulsifying agent  
 PT which is a detergent, useful as a vaccine to treat bacterial, viral,  
 PT and parasitic infection  
 XX Claim 17; Page 40; 95pp; English.  
 XX The invention relates to a microdroplet emulsion (microemulsion) with an  
 CC adsorbent surface, and which comprises a metabolizable oil and an  
 CC emulsifying agent (a detergent). It also relates to a composition  
 CC comprising the microemulsion and a microparticle with an adsorbent  
 CC surface, where the microparticle comprises a polymer selected from a  
 CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a  
 CC polycaprolactone, a polylactide, a polyanhydride, and a  
 CC polycyanoacrylate, and a second detergent. The surface of the  
 CC microparticles efficiently adsorb biologically active macromolecules such  
 CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,  
 CC mediators of transcription or translation, metabolic intermediates and  
 CC adjuvants. Additionally, a second biologically active molecule may be  
 CC encapsulated within the microparticle. The microemulsion can be used in  
 CC methods of immunising a host animal, particularly a human, against a  
 CC viral, bacterial or parasitic infection, and in methods of increasing a  
 CC Th1 immune response. The microemulsions (having the appropriate antigens  
 CC adsorbed) may be particularly used as vaccines for hepatitis C virus  
 CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human  
 CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and  
 CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and  
 CC pertussis; Helicobacter pylori and Haemophilus influenzae; and  
 CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1  
 CC lymphocyte stimulating oligonucleotides containing at least one CpG motif  
 CC which are claimed for use as adjuvants in the compositions of the  
 CC invention.  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.14;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 tgactgtgaangttcagatga 22

Db 1 tgactgtgaangttcagatga 22  
 RESULT 9  
 AAA14467  
 ID AAA14467 standard; DNA; 22 BP.  
 XX AA14467;  
 AC AA14467;  
 XX 21-AUG-2000 (first entry)  
 DT  
 XX Immunostimulatory oligonucleotide (ISS-ODN) DY1018.  
 XX Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;  
 KW secretory immunoglobulin A production; sIgA; Th1 phenotype; ds.  
 XX Synthetic.  
 XX WO200020039-A1.  
 XX 13-APR-2000.  
 XX 15-SEP-1999; 99WO-US21203.  
 XX 05-OCT-1998; 98US-0167039.  
 XX (REGC) UNIV CALIFORNIA.  
 XX Raz E, Horner AA, Carson DA;  
 PI WPI; 2000-303647/26.  
 XX Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to  
 PT an antigen in a mammalian host through production of secretory  
 PT immunoglobulin A -  
 XX Claim 8; Page 21; 64pp; English.  
 XX The invention relates to a method of inducing mucosal immunity to an  
 CC antigen in a mammalian host, including the production of secretory  
 CC immunoglobulin A (sIgA). Immune protection in the mucosa (the principal  
 CC site of entry of most foreign antigens) is mediated by mucosa-associated  
 CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory  
 CC cell sub-populations. The primary immune response which characterises  
 CC the induction of mucosal immunity to an antigen is sIgA production by  
 CC activated B-cells. The method comprises introducing an immunostimulatory  
 CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the  
 CC ISS-ODN includes a core nucleotide sequence. The core nucleotide  
 CC sequence is 5'-purine-purine-C-G-Pyrimidine-Pyrimidine-3', specific  
 CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A  
 CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used  
 CC as an adjuvant with an antigen for stimulating mucosal immunity. The  
 CC level of sIgA production induced in the host is at least 3 times the  
 CC magnitude of sIgA production achievable in response to introduction of  
 CC antigen alone into the mucosal tissue and is equivalent or greater than  
 CC the magnitude of sIgA production achievable in response to introduction  
 CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The  
 CC host immune response is stimulated to antigen specific IgA production,  
 CC biased towards the Th1 phenotype while antigen-induced IgE production is  
 CC avoided. The adjuvant has little or no known toxicity in mammals and its  
 CC efficacy is comparable to that of cholera toxin which is used as a  
 CC mucosal adjuvant. The present sequence represents the immunostimulatory  
 CC oligonucleotide DY1018.  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.14;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 tgactgtgaangttcagatga 22



Db 1 tgactgtgaacgttcgagatga 22  
|||||

## RESULT 10

AAA38065

ID AAA38065 standard; DNA: 22 BP.

XX AC AAA38065;

XX AC AAA38065;

DT 24-AUG-2000 (first entry)

XX Key Location/Qualifiers

DE Immunostimulatory sequence (ISS) #1.

XX Immunostimulatory sequence (ISS) #1.

XX gp120; human immunodeficiency virus; HIV; immune response; infection;

XX development; ss.

XX Synthetic.

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI: 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and

XX HIV glycoprotein gp120 useful for modulating, stimulating an immune

XX response against HIV in an HIV infected individual

XX Claim 3: Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition

XX comprising a human immunodeficiency virus (HIV) antigen, and an

XX immunostimulatory polynucleotide comprising an immunostimulatory sequence

XX (ISS). This sequence represents an ISS that can be used in the

XX composition. An immunostimulatory composition which comprises a gp120

XX conjugated to an immunostimulatory polynucleotide, or is proximately

XX associated to it and not conjugated, is used for modulating or

XX stimulating a specific immune response against gp120 in an individual by

XX producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It

XX is also used for suppressing or delaying development of HIV infection in

XX an individual infected with HIV or an individual at risk of infection

XX with HIV, respectively. It is also used for treating an individual

XX infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 95.5%; Score 21; DB 21; Length 22;

XX Best Local Similarity 95.5%; Pred. No. 0.14;

XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 11

AAA38071

ID AAA38071 standard; DNA: 22 BP.

XX AC AAA38071;

XX AC AAA38071;

DT 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #7.

XX Immunostimulatory sequence (ISS) #7.

DT 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #7.

XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;

XX gp120; human immunodeficiency virus; HIV; immune response; infection;

XX development; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 11

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "5-Bromocytosine"

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI: 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and

XX HIV glycoprotein gp120 useful for modulating, stimulating an immune

XX response against HIV in an HIV infected individual

XX Disclosure; Page 17; 65pp; English.

XX The present invention relates to an immunostimulatory composition

XX comprising a human immunodeficiency virus (HIV) antigen, and an

XX immunostimulatory polynucleotide comprising an immunostimulatory sequence

XX (ISS). This sequence represents an ISS that can be used in the

XX composition. An immunostimulatory composition which comprises a gp120

XX conjugated to an immunostimulatory polynucleotide, or is proximately

XX associated to it and not conjugated, is used for modulating or

XX stimulating a specific immune response against gp120 in an individual by

XX producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It

XX is also used for suppressing or delaying development of HIV infection in

XX an individual infected with HIV or an individual at risk of infection

XX with HIV, respectively. It is also used for treating an individual

XX infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 95.5%; Score 21; DB 21; Length 22;

XX Best Local Similarity 95.5%; Pred. No. 0.14;

XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 12

AAA38072

ID AAA38072 standard; DNA: 22 BP.

XX AC AAA38072;

XX AC AAA38072;

DT 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #7.

XX Immunostimulatory sequence (ISS) #7.

Immunomodulation; immunostimulatory sequence; adjuvant;  
Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
asthma; immunosuppression; ss.  
Mus musculus.  
Synthetic.

Key Location/Qualifiers  
modified\_base 1..22  
/tag= a  
/note= "Phosphorothioate linkages"  
misc\_feature 9..16  
/tag= b  
/note= "Immunostimulatory sequence (ISS)"

WO9962923-A2.

09-DEC-1999.

04-JUN-1999; 99WO-US12538.

05-JUN-1998; 98US-0088310.

01-JUN-1999; 99US-0324191.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Schwartz D;

WPI; 2000-105687/09.

Novel immunomodulatory oligonucleotide used to induce a Th1-type immune response, e.g. to tumor antigens

Example 1; Page 35; 54pp; English.

Sequences AA255876-255877 and AA255880-255886 represent immunomodulatory oligonucleotides comprising an immunostimulatory sequence (ISS, e.g., AACGTC, AACGTT, AGCGTC, AGCGTT, GACGTC, GACGTT, GCGGTT, AACGTTCC and GACGTTCC). The invention relates to oligonucleotides comprising one or more ISSs, where the ISS comprises at least one modified cytosine with an electron-withdrawing moiety at position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886 contain ISSs comprising at least one bromocytosine, whereas sequence AA255876 contains an unmodified ISS. The immunomodulatory oligonucleotides have an adjuvant-like effect; when formulated with an antigen, the oligonucleotides stimulate production of Th1-type cytokines, and induce a Th1-type immune response (activation of cytotoxic T cells). While simultaneously downregulating the Th2-type response. The Th1 response is particularly effective for control of viruses and intracellular parasites. The immunomodulatory oligonucleotides are used, particularly when formulated with an antigen or a facilitator, for modulating immune responses. Such compositions may be used in tumour therapy, in treatment of allergy (including asthma), for inducing a vigorous cellular response (against a virus, bacterium, fungus or protozoan), and also in contraceptive vaccines based on sperm antigens.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.14;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22  
||||| |||||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 14  
AA255880  
ID AA255880 standard; DNA: 22 BP.  
XX  
AC AA255880;

Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
gp120; human immunodeficiency virus; HIV; immune response; infection;  
development; ss.  
Synthetic.

Key Location/Qualifiers  
modified\_base 11  
/tag= a  
/mod\_base= OTHER  
/note= "5-Bromocytosine"  
modified\_base 15  
/tag= b  
/mod\_base= OTHER  
/note= "5-Bromocytosine"

WO200021556-A1.

20-APR-2000.

08-OCT-1999; 99WO-US23677.

09-OCT-1998; 98US-010733.

07-OCT-1999; 99US-0415186.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Tighe H, Raz E, Schwartz D, Takabayashi K;

WPI; 2000-317846/27.

Anti-HIV composition comprises immunostimulatory polynucleotides and HIV glycoprotein gp120 useful for modulating, stimulating an immune response against HIV in an HIV infected individual

Disclosure; Page 17; 65pp; English.

The present invention relates to an immunostimulatory composition comprising a human immunodeficiency virus (HIV) antigen, and an immunomodulatory polynucleotide comprising an immunostimulatory sequence (ISS). This sequence represents an ISS that can be used in the composition. An immunostimulatory polynucleotide, or is proximately conjugated to it and not conjugated, is used for modulating or associating a specific immune response against gp120 in an individual by stimulating anti-gp120 antibodies or gp120 specific cytotoxic T cells. It produces anti-gp120 antibodies or gp120 specific cytotoxic T cells. It is also used for suppressing or delaying development of HIV infection in an individual infected with HIV or an individual at risk of infection with HIV, respectively. It is also used for treating an individual infected with HIV in need of immune modulation.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.14;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22  
||||| |||||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13  
AA255876  
ID AA255876 standard; DNA: 22 BP.  
XX  
AC AA255876;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Immunomodulatory oligonucleotide SEQ ID NO: 1.  
XX

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XX DT 10-APR-2000 (first entry)
XX DE Immunomodulatory oligonucleotide SEQ ID NO: 5.
XX KW Immunomodulation; immunostimulatory sequence; adjuvant;
XX KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
XX KW asthma; immunocontraception; 5-bromocytosine; ss.
XX OS Mus musculus.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..22
XX FT /*tag= a
XX FT /note= "Phosphorothioate linkages"
XX FT misc_feature 9..16
XX FT /*tag= b
XX FT /note= "Immunostimulatory sequence (ISS)"
XX FT modified_base 11
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "5-bromocytosine"
XX W09962923-A2.
XX PN
XX PD
XX PP
XX PR 04-JUN-1999; 99WO-US12538.
XX PR 05-JUN-1998; 98US-0088310.
XX PR 01-JUN-1999; 99US-0324191.
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX PI Schwartz D;
XX DR WPI; 2000-105687/09.
XX PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
XX PT response, e.g. to tumor antigens.
XX PS Claim 30; Page 35; 54pp; English.
XX CC Sequences AA255876-255877 and AA255880-255886 represent immunomodulatory
XX CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
XX CC AACGTC, AACGTT, AGCGTC, AGCGTT, GACGTC, GACGTT, GCGGTT,
XX CC ACGRGCC and GACGRGCC). The invention relates to oligonucleotides
XX CC comprising one or more ISSs, where the ISS comprises at least
XX CC one modified cytosine with an electron-withdrawing moiety at
XX CC position C-5 or C-6 of the base. Sequences AA255877 and AA255886
XX CC contain ISSs comprising at least one bromocytosine, whereas sequence
XX CC AA255876 contains an unmodified ISS. The immunomodulatory
XX CC oligonucleotides have an adjuvant-like effect; when formulated with an
XX CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
XX CC and induce a Th1-type immune response (activation of cytotoxic T cells),
XX CC while simultaneously downregulating the Th2-type response. The Th1
XX CC response is particularly effective for control of viruses and
XX CC intracellular parasites. The immunomodulatory oligonucleotides are used,
XX CC particularly when formulated with an antigen or a facilitator, for
XX CC modulating immune responses. Such compositions may be used in tumour
XX CC therapy, in treatment of allergy (including asthma), for inducing a
XX CC vigorous cellular response (against a virus, bacterium, fungus or
XX CC protozoan), and also in contraceptive vaccines based on sperm antigens.
XX SQ Sequence 22 BP; 6 A; 2 C; 7 G; 6 T; 1 other;

Query Match 95.5%; Score 21; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgrctgtgaangttcgagatga 22

```

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Db 1 tgactgtgaangttcgagatga 22
|||||
RESULT 15
AAF77040
ID AAF77040 standard; DNA; 22 BP.
XX AC AAF77040;
XX DT 15-MAY-2001 (first entry)
XX DE Immunomodulatory DNA.
XX KW Modulate; Immune; antigen; Immunostimulatory; ds.
XX OS Synthetic.
XX PN W0200112223-A2.
XX PD 22-FEB-2001.
XX PF 18-AUG-2000; 2000WO-US22835.
XX PR 19-AUG-1999; 99US-0149768.
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX PI Van Nest G;
XX DR WPI; 2001-211136/21.
XX PT Modulating immune response to a second antigen in humans involves
XX PT administering an immunostimulatory polynucleotide comprising an
XX PT immunostimulatory sequence and a first antigen.
XX PS Claim 31; Page 15; 63pp; English.
XX CC The present invention relates to modulating an immune response to
XX CC a second antigen in an individual, involving
XX CC administering to the individual an immunomodulatory polynucleotide
XX CC comprising an immunostimulatory sequence (ISS) and a first antigen.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 22; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22
|||||

Search completed: October 9, 2001, 16:26:51
Job time: 2981 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:47 ; Search time 10334.3 Seconds  
(without alignments)  
31.457 Million cell updates/sec

Title: US-09-713-136-7

Perfect score: 22

Sequence: 1 tgactgtgaangttcgagatga 22

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	21	95.5	22	1	PCT-US00-18229-32 Sequence 32, Appl
2	21	95.5	22	1	PCT-US00-35064-1 Sequence 1, Appl1
3	21	95.5	22	1	PCT-US00-35064-2 Sequence 2, Appl1
4	21	95.5	22	1	PCT-US01-03029-1 Sequence 1, Appl1
5	21	95.5	22	1	PCT-US01-03029-2 Sequence 2, Appl1
6	21	95.5	22	1	PCT-US01-06034-1 Sequence 1, Appl1
7	21	95.5	22	1	PCT-US01-06034-4 Sequence 4, Appl1
8	21	95.5	22	1	PCT-US01-10118-3 Sequence 1, Appl1
9	21	95.5	22	1	PCT-US01-10118-3 Sequence 3, Appl1
10	21	95.5	22	1	PCT-US01-11290-1 Sequence 2, Appl1
11	21	95.5	22	1	PCT-US01-11290-2 Sequence 1, Appl1
12	21	95.5	22	1	PCT-US01-14508-1 Sequence 19, Appl
13	21	95.5	22	1	PCT-US99-21203-1 Sequence 19, Appl
14	21	95.5	22	13	US-08-927-120-19 Sequence 19, Appl
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16	21	95.5	22	16	US-09-235-742-19 Sequence 2, Appl1
17	21	95.5	22	16	US-09-298-477-2 Sequence 15, Appl
18	21	95.5	22	16	US-09-298-477-15 Sequence 1, Appl1
19	21	95.5	22	17	US-09-308-036A-1 Sequence 1, Appl1
20	21	95.5	22	17	US-09-324-191A-1 Sequence 5, Appl1
21	21	95.5	22	17	US-09-347-343-32 Sequence 32, Appl
22	21	95.5	22	17	US-09-397-188-1 Sequence 1, Appl1
23	21	95.5	22	17	US-09-415-186-1 Sequence 1, Appl1
24	21	95.5	22	18	US-09-415-186-7 Sequence 7, Appl1
25	21	95.5	22	18	US-09-470-382-69 Sequence 69, Appl
26	21	95.5	22	18	US-09-565-906-2 Sequence 2, Appl1
27	21	95.5	22	22	US-09-570-325-19 Sequence 19, Appl
28	21	95.5	22	22	US-09-642-492-1 Sequence 1, Appl1
29	21	95.5	22	25	US-09-642-492-7 Sequence 7, Appl1
30	21	95.5	22	25	US-09-700-354-1 Sequence 1, Appl1
31	21	95.5	22	28	US-09-713-136-1 Sequence 1, Appl1
32	21	95.5	22	28	US-09-713-136-7 Sequence 7, Appl1
33	21	95.5	22	29	US-09-746-130-1 Sequence 1, Appl1
34	21	95.5	22	29	US-09-746-130-2 Sequence 2, Appl1
35	21	95.5	22	29	US-09-774-403-1 Sequence 1, Appl1
36	21	95.5	22	30	US-09-774-403-2 Sequence 2, Appl1
37	21	95.5	22	30	US-09-791-500-1 Sequence 1, Appl1
38	21	95.5	22	30	US-09-791-500-4 Sequence 4, Appl1
39	21	95.5	22	31	US-09-820-484-1 Sequence 1, Appl1
40	21	95.5	22	31	US-09-820-484-3 Sequence 3, Appl1
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42	21	95.5	22	31	US-09-828-505-2 Sequence 2, Appl1
43	21	95.5	22	31	US-09-828-505-2 Sequence 2, Appl1
44	20.2	91.8	22	18	US-09-415-186-8 Sequence 8, Appl1
45	20.2	91.8	22	28	US-09-713-136-8 Sequence 8, Appl1

## ALIGNMENTS

RESULT 1  
PCT-US00-18229-32  
; Sequence 32, Application PC/TUS0018229  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; TITLE OF INVENTION: Method for Enhancing an Immune Response  
; FILE REFERENCE: 6510-189W01  
; CURRENT APPLICATION NUMBER: PCT/US00/18229  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
PCT-US00-18229-32

Query Match 95.5%; Score 21; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2.6;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2  
PCT-US00-35064-1  
; Sequence 1, Application PC/TUS0035064  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; TITLE OF INVENTION: Method for Preventing an Anaphylactic  
; FILE REFERENCE: 06510/201W01  
; CURRENT APPLICATION NUMBER: PCT/US00/35064  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/171,830  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule  
PCT-US00-35064-1

Query Match 95.5%; Score 21; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2.6;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3  
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; Sequence 2, Application PC/TUS0035064  
; GENERAL INFORMATION:

; APPLICANT: Raz, Eyal  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Method for Preventing an Anaphylactic  
; FILE REFERENCE: 06510/201W01  
; CURRENT APPLICATION NUMBER: PCT/US00/35064  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/171,830  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
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; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutant  
PCT-US00-35064-2

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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaaggttcgagatga 22

RESULT 4  
PCT-US01-03029-1  
; Sequence 1, Application PC/TUS0103029  
; GENERAL INFORMATION:  
; APPLICANT: Eyal Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi  
; APPLICANT: Dennis A. Carson  
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in  
; FILE REFERENCE: 06510/166W01  
; CURRENT APPLICATION NUMBER: PCT/US01/03029  
; CURRENT FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/179,353  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory sequence  
PCT-US01-03029-1

Query Match 95.5%; Score 21; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2.6;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5  
PCT-US01-03029-2  
; Sequence 2, Application PC/TUS0103029  
; GENERAL INFORMATION:  
; APPLICANT: Eyal Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi

```
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
PCT-US01-03029-2

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Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
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Db 1 tgactgtgaagggttcgagatga 22

RESULT 6
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; OTHER INFORMATION: oligonucleotide primer
PCT-US01-06034-1

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 7
PCT-US01-06034-4
; Sequence 4, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-4

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaagggttcgagatga 22

RESULT 8
PCT-US01-10118-1
; Sequence 1, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188W01
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
PCT-US01-10118-1

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 9
PCT-US01-10118-3
; Sequence 3, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188W01
; CURRENT APPLICATION NUMBER: PCT/US01/10118
```



COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US99/21203  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/927,120  
FILING DATE: 05 September 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Berliner, Robert  
REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 5555-188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-892-9200  
TELEFAX: 213-680-4518  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: non-coding oligonucleotides  
PCT-US99-21203-19

Query Match 95.5%; Score 21; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2.6;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
|||||  
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 14  
US-08-927-120-19  
Sequence 19, Application US/08927120  
GENERAL INFORMATION:  
APPLICANT: Raz, Eyal  
TITLE OF INVENTION: IMMUNIZATION-FREE METHODS  
FOR STIMULATING IMMUNE RESPONSIVENESS AND REDUCING  
INFLAMMATION IN A HOST  
TITLE OF INVENTION: INFLAMMATION IN A HOST  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,120  
FILING DATE: 22-AUG-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Taylor, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/054001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: non-coding oligonucleotides  
US-08-927-120-19

Query Match 95.5%; Score 21; DB 13; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2.6;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
|||||  
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 15  
US-09-167-039-19  
Sequence 19, Application US/09167039  
GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: METHODS AND ADJUVANTS  
FOR STIMULATING MUCOSAL IMMUNITY  
TITLE OF INVENTION: FOR STIMULATING MUCOSAL IMMUNITY  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 402 West Broadway, Suite 2300  
CITY: San Diego  
STATE: CA  
COUNTRY: US  
ZIP: 92101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/167,039  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/927,120  
FILING DATE: 05 September 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Taylor, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/063001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-234-6655  
TELEFAX: 619-234-3510  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: non-coding oligonucleotides  
US-09-167-039-19

Query Match 95.5%; Score 21; DB 15; Length 22;  
Best Local Similarity 95.5%; Pred. No. 2.6;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
|||||  
Db 1 TGACTGTGAACGTTTCGAGATGA 22



Search completed: October 9, 2001, 21:12:47  
Job time: 20072 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:22 ; Search time 1391.6 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-09-713-136-7  
Perfect score: 2  
Sequence: 1 tgactgtgaangttcgagatga 22

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*
  - 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
  - 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
  - 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
  - 6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.1
  - 7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.2
  - 8: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	22	US-09-802-518-1	Sequence 1, Appli
2	21	95.5	22	US-09-802-518-7	Sequence 7, Appli
3	21	95.5	22	US-09-802-359-1	Sequence 1, Appli
4	21	95.5	22	US-09-802-359-7	Sequence 7, Appli
5	21	95.5	22	US-09-802-376-1	Sequence 1, Appli
6	21	95.5	22	US-09-802-376-7	Sequence 7, Appli
7	20	90.9	22	US-09-802-518-8	Sequence 8, Appli
8	20	90.9	22	US-09-802-359-8	Sequence 8, Appli
9	20	90.9	22	US-09-802-376-8	Sequence 8, Appli
10	19.4	88.2	22	US-09-770-943-1	Sequence 2, Appli
11	19.4	88.2	22	US-09-770-943-2	Sequence 2, Appli
12	19.4	88.2	22	US-09-770-943-10	Sequence 10, Appli
13	19.4	88.2	22	US-09-802-518-2	Sequence 2, Appli
14	19.4	88.2	22	US-09-802-518-4	Sequence 4, Appli
15	19.4	88.2	22	US-09-802-518-6	Sequence 6, Appli
16	19.4	88.2	22	US-09-802-518-10	Sequence 10, Appli
17	19.4	88.2	22	US-09-802-359-2	Sequence 2, Appli
18	19.4	88.2	22	US-09-802-359-4	Sequence 4, Appli
19	19.4	88.2	22	US-09-802-359-6	Sequence 6, Appli
20	19.4	88.2	22	US-09-802-359-9	Sequence 9, Appli
21	19.4	88.2	22	US-09-802-376-2	Sequence 2, Appli
22	19.4	88.2	22	US-09-802-376-4	Sequence 4, Appli
23	19.4	88.2	22	US-09-802-376-6	Sequence 6, Appli
24	19.4	88.2	22	US-09-802-376-9	Sequence 9, Appli
25	17.8	80.9	22	US-09-770-943-3	Sequence 3, Appli

26	17.8	80.9	22	US-09-770-943-4	Sequence 4, Appli
27	17.8	80.9	22	US-09-802-518-11	Sequence 11, Appli
28	17.8	80.9	22	US-09-802-359-10	Sequence 10, Appli
29	17.8	80.9	22	US-09-802-376-10	Sequence 10, Appli
30	16.8	76.4	442	US-09-836-472-216	Sequence 216, App
31	16.8	76.4	448	US-09-804-703-14097	Sequence 14097, A
32	16.8	76.4	448	US-09-909-627-7849	Sequence 7849, A
33	16.8	76.4	469	US-09-909-627-19415	Sequence 19415, A
34	16.8	76.4	606	US-09-921-378-10527	Sequence 10527, A
35	16.8	76.4	668	US-09-836-472-1014	Sequence 1014, Ap
36	16.8	76.4	3713	US-60-278-232-10258	Sequence 10258, A
37	16.8	76.4	82360	US-09-803-736-484	Sequence 484, App
38	16.4	74.5	24853	US-09-764-874-10235	Sequence 10235, A
39	16.4	74.5	32212	US-09-764-874-10236	Sequence 10236, A
40	16.2	73.6	22	US-09-770-943-7	Sequence 7, Appli
41	16.2	73.6	22	US-09-770-943-8	Sequence 8, Appli
42	16.2	73.6	239	US-09-540-213-25987	Sequence 25987, A
43	16.2	73.6	252	US-09-825-790-331	Sequence 331, App
44	16.2	73.6	284	US-09-540-213-39122	Sequence 39122, A
45	16.2	73.6	445	US-09-909-629-31699	Sequence 31699, A

ALIGNMENTS

RESULT 1  
US-09-802-518-1  
; Sequence 1, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCES  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-1

Query Match 95.5%; Score 21; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.2;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22  
||||||| |||||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2  
US-09-802-518-7  
; Sequence 7, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCES  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaangttcgagatga 22

RESULT 3
US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 4
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-359-7
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaangttcgagatga 22

RESULT 5
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7
```

Query Match 95.5%; Score 21; DB 7; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
|||||  
Db 1 tgactgtgaangttcgagatga 22

RESULT 7  
US-09-802-518-8  
; Sequence 8, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCES  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-518-8

Query Match 90.9%; Score 20; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.65;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
|||||  
Db 1 tgactgtgaangttcgagatga 22

RESULT 8  
US-09-802-359-8  
; Sequence 8, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-359-8

Query Match 90.9%; Score 20; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.65;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaangttcgagatga 22  
|||||  
Db 1 tgactgtgaangttcgagatga 22

RESULT 9  
US-09-802-376-8  
; Sequence 8, Application US/09802376  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201700  
; CURRENT APPLICATION NUMBER: US/09/802,376  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,557  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-376-8

Query Match 90.9%; Score 20; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.65;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22  
|||||  
Db 1 tgactgtgaangttcgagatga 22

RESULT 10  
US-09-770-943-1  
; Sequence 1, Application US/09770943  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/770,943  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/092,314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-770-943-1

Query Match 88.2%; Score 19.4; DB 6; Length 22;  
Best Local Similarity 90.9%; Pred. No. 1.3;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22

```
|||||
Db 1 tgactgtgaaggttagagatga 22

RESULT 11
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
|||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 12
US-09-770-943-10
; Sequence 10, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-10

Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
|||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 13
US-09-802-518-2
; Sequence 2, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-2

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
|||||
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 14
US-09-802-518-4
; Sequence 4, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-4

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
|||||
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 15
US-09-802-518-6
; Sequence 6, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
```

;; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE

;; FILE REFERENCE: 377882001100

;; CURRENT APPLICATION NUMBER: US/09/802,518

;; CURRENT FILING DATE: 2001-03-09

;; PRIOR APPLICATION NUMBER: 60/188,556

;; PRIOR FILING DATE: 2000-03-10

;; NUMBER OF SEQ ID NOS: 11

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 6

;; LENGTH: 22

;; TYPE: DNA

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G

;; NAME/KEY: misc-feature

;; LOCATION: (1)...(22)

;; OTHER INFORMATION: n = 5-bromocytosine

;; US-09-802-518-6

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 1.3;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy .1 tgactgtgaangttcgagatga 22  
|||||  
Db .1 tgactgtgaangttccagatga 22  
|||||

Search completed: October 9, 2001, 21:36:22  
Job time: 21242 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:08 ; Search time 217.64 Seconds  
(without alignments)  
19.136 Million cell updates/sec

Title: US-09-713-136-7

Perfect score: 22  
Sequence: 1 tgactgtgaangttcgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	88.2	22	4	US-09-092-314-1
2	19.4	88.2	22	4	US-09-092-314-2
3	19.4	88.2	22	4	US-09-092-314-10
4	17.8	80.9	22	4	US-09-092-314-3
5	17.8	80.9	22	4	US-09-092-314-4
6	16.2	73.6	22	4	US-09-092-314-7
7	16.2	73.6	22	4	US-09-092-314-8
8	15.8	71.8	1892	2	US-08-933-750C-66
9	15.8	71.8	1892	3	US-09-234-613-66
10	15.8	71.8	6638	2	US-08-070-301-2
11	15.2	69.1	913	2	US-08-975-316-61
12	15.2	69.1	2694	3	US-08-975-703-5
13	15.2	69.1	2694	4	US-09-515-884-5
14	14.8	67.3	864	4	US-08-998-416-297
15	14.6	66.4	1166	1	US-08-121-083-7
16	14.6	66.4	22	4	US-09-092-314-5
17	14.6	66.4	95	5	PCT-US96-09455A-258
18	14.6	66.4	1418	1	US-08-391-615-7
19	14.6	66.4	1830	4	US-09-019-931-2
20	14.6	66.4	2505	1	US-08-391-615-1
21	14.6	66.4	2971	1	US-07-718-575-7
22	14.6	66.4	2971	1	US-08-481-206-7
23	14.6	66.4	2971	2	US-08-486-269A-7
24	14.6	66.4	6909	2	US-08-804-196-1
25	14.6	66.4	6909	2	US-08-658-340-1
26	14.6	66.4	6909	3	US-08-746-111-26
27	14.2	64.5	588	3	US-08-963-904B-1

#### ALIGNMENTS

##### RESULT 1

US-09-092-314-1

; Sequence 1, Application US/09092314

; Patent No. 6225292

; GENERAL INFORMATION:

; APPLICANT: Raz, Eyal

; APPLICANT: Roman, Mark

; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory

; TITLE OF INVENTION: Sequence Activity

; Patent No. 6225292

; FILE REFERENCE: 6510-173US1

; CURRENT APPLICATION NUMBER: US/09/092.314

; CURRENT FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/048.794

; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide

; US-09-092-314-1

Query Match 88.2%; Score 19.4; DB 4; Length 22;

Best Local Similarity 90.9%; Pred No. 0.099;

Mismatches 0; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22

|||||

Db 1 tgactgtgaangttcgagatga 22

|||||

##### RESULT 2

US-09-092-314-2

; Sequence 2, Application US/09092314

; Patent No. 6225292

; GENERAL INFORMATION:

; APPLICANT: Raz, Eyal

; APPLICANT: Roman, Mark

; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory

; TITLE OF INVENTION: Sequence Activity

; Patent No. 6225292

; FILE REFERENCE: 6510-173US1

; CURRENT APPLICATION NUMBER: US/09/092.314

; CURRENT FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/048.794

; PRIOR FILING DATE: 1997-06-06

Sequence 5, Appli  
Sequence 5, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 6, Appli  
Sequence 12, Appli  
Sequence 4, Appli  
Sequence 10, Appli  
Sequence 16, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 24, Appli  
Sequence 7, Appli

28 14.2 64.5 618 1 US-08-155-171B-5  
29 14.2 64.5 618 2 US-08-435-998-5  
30 14.2 64.5 773 3 US-08-934-131-2  
31 14 63.6 8543 3 US-08-496-944-1  
32 13.8 62.7 36 4 US-09-386-607-6  
33 13.8 62.7 492 3 US-08-729-416C-12  
34 13.8 62.7 882 1 US-08-622-354-4  
35 13.8 62.7 1425 3 US-08-729-416C-10  
36 13.8 62.7 1785 3 US-08-729-416C-16  
37 13.8 62.7 1876 3 US-08-714-918-33  
38 13.8 62.7 1876 4 US-09-265-315-33  
39 13.8 62.7 1876 4 US-09-265-315-33  
40 13.8 62.7 1876 4 US-09-266-417-33  
41 13.8 62.7 2333 1 US-08-392-678-33  
42 13.8 62.7 2334 1 US-08-457-304A-33  
43 13.8 62.7 2334 1 US-08-456-701A-33  
44 13.8 62.7 3456 1 US-08-190-687B-24  
45 13.8 62.7 4307 1 US-08-190-687B-7

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match      88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.099;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 3
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match      88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.099;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 4
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 5
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 6
US-09-092-314-7
; Sequence 7, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
```



```

;
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-7

Query Match      73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 4.7;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
    ||||| | | | | | | | |
Db 1 tgactgtgagggtcagagatga 22

RESULT 7
US-09-092-314-8
; Sequence 8, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-8

Query Match      73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 4.7;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
    ||||| | | | | | | | |
Db 1 tgactgtgagggtcagagatga 22

RESULT 8
US-08-933-750C-66/c
; Sequence 66, Application US/08933750C
; Patent No. 5932442
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
;

;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750C
; FILING DATE: September 23, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127
US-08-933-750C-66

Query Match      71.8%; Score 15.8; DB 2; Length 1892;
Best Local Similarity 85.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagat 20
    ||| ||||| ||||| |
Db 1278 TGAATGTGAAGGTCGAGCT 1259

RESULT 9
US-09-234-613-66/c
; Sequence 66, Application US/09234613
; Patent No. 6132973
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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```

; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127
; US-09-234-613-66

Query Match 71.8%; Score 15.8; DB 3; Length 1892;
Best Local Similarity 85.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagat 20
||| ||||| ||||| |||
Db 1278 TGAATGTGAAGGTTGCGACT 1259

RESULT 10
US-08-070-301-2
; Sequence 2, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KAMINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Onji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687
; FILING DATE: 15-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933
; FILING DATE: 31-OCT-1989
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-106412
;

; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127
; US-09-234-613-66

Query Match 71.8%; Score 15.8; DB 3; Length 1892;
Best Local Similarity 85.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagat 20
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Db 1278 TGAATGTGAAGGTTGCGACT 1259

RESULT 10
US-08-070-301-2
; Sequence 2, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KAMINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Onji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687
; FILING DATE: 15-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933
; FILING DATE: 31-OCT-1989
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-106412
;

; FILING DATE: 24-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-205475
; FILING DATE: 02-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-22830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-040
; TELEFAX: (202) 835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Horse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11...3070
; US-08-070-301-2

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Best Local Similarity 85.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gactgtgaangttcgagatg 21
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Db 2380 GACTGTGTATGTTGGAGATG 2399

RESULT 11
US-08-975-316-61
; Sequence 61, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0563
; TELEFAX: 206-269-0563
; TELEX:

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; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-975-316-61

Query Match          69.1%; Score 15.2; DB 2; Length 913;
Best Local Similarity 81.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
    ||||| ||| ||| |||||
Db 513 GACTGTGAATTTTACAGATGA 533

RESULT 12
US-08-975-703-5
; Sequence 5, Application US/08975703
; Patent No. 6030832
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Bartel, Paul L.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,703
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2318-0174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2691
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-975-703-5

Query Match          69.1%; Score 15.2; DB 3; Length 2694;
Best Local Similarity 81.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
    ||||| ||| ||| |||||
Db 1785 GACTGTGAATGTTTAGATGA 1805

US-09-515-884-5
; Sequence 5, Application US/09515884
; Patent No. 6235263
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Bartel, Paul L.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,884
; FILING DATE: 29-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,703
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2318-0174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2691
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-515-884-5

Query Match          69.1%; Score 15.2; DB 4; Length 2694;
Best Local Similarity 81.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
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Db 1785 GACTGTGAATGTTTAGATGA 1805
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**RESULT 14**

US-08-998-416-297/C  
: Sequence 297, Application US/08998416  
: Patent No. 6239264  
: GENERAL INFORMATION:  
: APPLICANT: Philippaen, Peter  
: APPLICANT: Pohlmann, Rainer  
: APPLICANT: Steiner, Sabine  
: APPLICANT: Mohr, Christine  
: APPLICANT: Knechtle, Jurgен  
: APPLICANT: Wendt, Philipp  
: APPLICANT: Reischung, Corinne  
: TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII  
: TITLE OF INVENTION: AND USES THEREOF  
: NUMBER OF SEQUENCES: 1152  
: CORRESPONDENCE ADDRESS:  
: ADDRESS: NO. 6239264artis Corporation  
: STREET: 3054 Cornwallis Road  
: CITY: Research Triangle Park  
: STATE: No. 6239264th Carolina  
: COUNTRY: USA  
: ZIP: 27709  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/998.416  
: FILING DATE: 24-DEC-1997  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: CH 0016/97  
: FILING DATE: 31-DEC-1996  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Meigs, J. Timothy  
: REGISTRATION NUMBER: 38,241  
: REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 919-541-8587  
: TELEFAX: 919-541-8689  
: INFORMATION FOR SEQ ID NO: 297:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 864 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (genomic)  
: ORIGINAL SOURCE:  
: ORGANISM: PAG1245UP  
US-08-998-416-297

Query Match 67.3%; Score 14.8; DB 4; Length 864;  
Best Local Similarity 84.2%; Pred. No. 52;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy . 4 ctgtgaangttcgagatga 22  
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Db 191 CTGTGAATGATCGAGTTGA 173

**RESULT** 15

RE507.1 13  
 US-08-121-063-7  
 : Sequence 7, Application US/08121063  
 : Patent No. 5446143  
 : GENERAL INFORMATION:  
 : APPLICANT: Simpson, Evan R.  
 : APPLICANT: Mahendroo, Mala  
 : APPLICANT: Mendelsohn, Carole R.  
 : TITLE OF INVENTION: Adipose-Specific Promoter Regions of  
 : TITLE OF INVENTION: Human Aromatase Cytochrome P450 gene  
 : NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: TX  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/121,063  
 FILING DATE: 14-SEP-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wilson, Mark  
 REGISTRATION NUMBER: 37,259  
 REFERENCE/DOCKET NUMBER: UTSD:351  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 512-320-7200  
 TELEFAX: 512-474-7577  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1166 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-121-063-7

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Best Local Similarity	84.2%	Pred. NO. 55;		
Matches 16;	Conservative	0;	Mismatches 3;	Indels 0

Qy 4 ctgtgaangttcgagatga 22  
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Db 525 CTGTGAAAGTTCAGAAGA 543

Search completed: October 9, 2001, 15:42:09  
Job time: 299 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:20:28 ; Search time 2150.93 Seconds  
(without alignments)  
158.206 Million cell updates/sec

Title: US-09-713-136-8  
Perfect score: 22  
Sequence: 1 tgactgtgaangttbgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
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2: gb\_ba2: \*  
3: gb\_ba3: \*  
4: gb\_in1: \*  
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6: gb\_in3: \*  
7: gb\_om: \*  
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9: gb\_pat1: \*  
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11: gb\_ph: \*  
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51: em\_un: \*  
52: em\_vl: \*  
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55: gb\_sts3: \*  
56: gb\_sy: \*  
57: gb\_un: \*  
58: gb\_vl: \*  
59: gb\_vl2: \*  
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63: gb\_htg4: \*  
64: gb\_htg5: \*  
65: gb\_htg6: \*  
66: gb\_htg7: \*  
67: gb\_htg8: \*  
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92: gb\_pr8: \*  
93: gb\_pr9: \*  
94: gb\_rol: \*  
95: gb\_ro2: \*  
96: gb\_in4: \*  
97: gb\_pr10: \*  
98: em\_ba3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.2	91.8	22	9	AX036945 Sequence
2	20.2	91.8	22	9	AX046993 Sequence
3	20.2	91.8	22	10	AX083675 Sequence
4	20.2	91.8	22	10	AX083681 Sequence
5	20	90.9	22	10	AX083682 Sequence
6	19.4	88.2	22	9	AX036944 Sequence
7	19.2	87.3	165337	70	AC027442 Homo sapi
8	19.2	87.3	209777	69	AC024934 Homo sapi

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9 18.6 84.5 22 9 AX036946
10 18.6 84.5 22 10 AX083676
11 18.6 84.5 22 10 AX083678
12 18.6 84.5 22 10 AX083680
13 18.6 84.5 12545 6 CEF42610
14 17.8 80.9 22 9 AX036952
15 17.6 80.0 49523 90 AL358135
16 17.6 80.0 85535 65 AC019557
17 17.6 80.0 85654 81 AL513169
18 17.6 80.0 90287 61 AC010018
19 17.6 80.0 122854 77 AC087581
20 17.6 80.0 139032 87 AC010656
21 17.6 80.0 140907 90 AL162499
22 17.6 80.0 145939 79 AL158143
23 17.6 80.0 152842 73 AC067921
24 17.6 80.0 168247 85 AC005014
25 17.6 80.0 172346 64 AC016349
26 17.6 80.0 178353 62 AC012334
27 17.6 80.0 182703 74 AC073117
28 17.6 80.0 304633 4 AE003477
29 17.4 79.1 183869 73 AC068700
30 17.2 78.2 42726 5 CBRG45N02
31 17 77.3 552 14 RICSINE04
32 17 77.3 2234 89 AK023935
33 17 77.3 32919 83 CER37L19
34 17 77.3 35503 6 CEM09D6
35 17 77.3 36949 77 AC087340
36 17 77.3 63807 77 AC087299
37 17 77.3 140530 76 AC079837
38 17 77.3 143747 92 HS370M22
39 17 77.3 144778 84 CNS07EFR
40 17 77.3 148170 76 AC087821
41 17 77.3 153019 76 AC079323
42 17 77.3 155323 22 AC009824
43 17 77.3 156375 83 AP002859
44 17 77.3 159485 62 AC012435
45 17 77.3 160437 79 AL355805

ALIGNMENTS

RESULT 1
LOCUS AX036945 22 bp DNA
DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
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/organism="synthetic construct"
/db_xref="taxon:32630"
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6 a 3 c 7 g 6 t

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Query Match 91.8%; Score 20.2; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
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Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 4
LOCUS AX083681 22 bp DNA
DEFINITION Sequence 7 from Patent WO0112223.
ACCESSION AX083681
VERSION AX083681.1 GI:11876420
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss,R.B.
JOURNAL Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="phosphorothioate-modified synthetic oligodeoxynucleotide"
6 a 3 c 7 g 6 t

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 91.8%; Score 20.2; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
|||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 3
LOCUS AX083675 22 bp DNA
DEFINITION Sequence 1 from Patent WO0112223.
ACCESSION AX083675
VERSION AX083675.1 GI:13185407
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Methods of modulating an immune response using immunostimulatory s
equences and compositions for use therein
Patent: WO 0112223-A 1 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic construct"
6 a 3 c 7 g 6 t

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 91.8%; Score 20.2; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
|||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 4
LOCUS AX083681 22 bp DNA
DEFINITION Sequence 7 from Patent WO0112223.
ACCESSION AX083681
VERSION AX083681.1 GI:11876420
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss,R.B.
JOURNAL Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="phosphorothioate-modified synthetic oligodeoxynucleotide"
6 a 3 c 7 g 6 t

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 91.8%; Score 20.2; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
|||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

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LOCUS	AX036944	22 bp	DNA	PAT	16-NOV-2000
DEFINITION	Sequence 1 from Patent FR090955.				
ACCESSION	AX036944				
VERSION	AX036944.1	GI:11226372			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	artificial sequence.				
REFERENCE	1 (bases 1 to 22)				
AUTHORS	Carpentier A.				
JOURNAL	Patent: FR 2709955-A 1 22-SEP-2000;				
FEATURES	ASSIST PUBL HOPITAUX DE PARIS (FR)				
source	Location/Qualifiers				
	1..22				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="oligodesoxynucleotide"				
BASE COUNT	7 a 1 c 8 g 5 t				
ORIGIN					
Query Match	88.2%	Score 19.4;	DB 9;	Length 22;	
Best Local Similarity	90.9%	Pred. No. 9;			
Matches	20; Conservative	0; Mismatches	2; Indels	0; Gaps	0;
Qy	1 TGACTGTGAAGTTGAGATGA 22				
Db	1 TGACTGTGAAGTTGAGATGA 22				
RESULT	7				
AC027442	AC027442	165337 bp	DNA	HTG	27-APR-2000
LOCUS	Homo sapiens clone RP11-439K16, WORKING DRAFT SEQUENCE, 31				
DEFINITION	unordered pieces.				
ACCESSION	AC027442				
VERSION	AC027442.2	GI:7651981			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 165337)				
JOURNAL	Birren, B., Linton, L., Nusbaum, C. and Lander, E.				
AUTHORS	Unpublished				
REFERENCE	2 (bases 1 to 165337)				
	Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,				
	Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,				
	Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,				
	Campopiano, A., Castelle, A., Choepel, Y., Colangelo, M., Collins, S.,				
	Collamore, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J. S.,				
	Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,				
	Galagan, J., Gardyna, S., Glinde, S., Goyette, M., Graham, L.,				
	Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,				
	Holland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,				
	Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J.,				
	Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,				
	McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,				
	Meldrum, J., Menues, L., Mihova, T., Miranda, C., Mlenka, V., Morrow, J.,				
	Merphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,				
	O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,				
	Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,				
	Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,				
	Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,				
	Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,				
	Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,				
	Young, G., Zainoun, J., Zimmer, A. and Zody, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome				
COMMENT	Research, 320 Charles Street, Cambridge, MA 02141, USA				
	On Apr 27, 2000 this sequence version replaced gi:7342171.				
	All repeats were identified using RepeatMasker:				

Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L8145

Center clone name: 439\_K\_16

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 149010 bases at least Q40

Consensus quality: 157303 bases at least Q30

Consensus quality: 160828 bases at least Q20

Insert size: 170000; agarose-fp

Insert size: 162337; sum-of-contigs

Quality coverage: 3.6 in Q20 bases; agarose-fp

Quality coverage: 3.8 in Q20 bases; sum-of-contigs

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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 31 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

```

1 1105: contig of 1105 bp in length
* 1106 1205: gap of 100 bp
* 1206 2479: contig of 1274 bp in length
* 2480 2579: gap of 100 bp
* 2580 4311: contig of 1632 bp in length
* 4212 4311: gap of 100 bp
* 4312 5781: contig of 1470 bp in length
* 5782 5881: gap of 100 bp
* 5882 7830: contig of 1949 bp in length
* 7831 7930: gap of 100 bp
* 7931 9913: contig of 1983 bp in length
* 9914 10013: gap of 100 bp
* 10014 12486: contig of 2473 bp in length
* 12487 12586: gap of 100 bp
* 12587 15592: contig of 3006 bp in length
* 15593 15692: gap of 100 bp
* 15693 19721: contig of 4029 bp in length
* 19722 19821: gap of 100 bp
* 19822 23369: contig of 3448 bp in length
* 23370 23369: gap of 100 bp
* 23370 26785: contig of 3416 bp in length
* 26786 26885: gap of 100 bp
* 26886 30363: contig of 3478 bp in length
* 30364 30463: gap of 100 bp
* 30464 33964: contig of 3501 bp in length
* 33965 34064: gap of 100 bp
* 34065 37794: contig of 3730 bp in length
* 37795 37894: gap of 100 bp
* 37895 43354: contig of 5460 bp in length
* 43355 43454: gap of 100 bp
* 43455 47839: contig of 4385 bp in length
* 47840 47939: gap of 100 bp
* 47940 53326: contig of 5387 bp in length
* 53327 53426: gap of 100 bp
* 53427 58576: contig of 5150 bp in length
* 58577 58676: gap of 100 bp
* 58677 64554: contig of 5878 bp in length
* 64555 64654: gap of 100 bp
* 64655 68538: contig of 3884 bp in length
* 68539 68638: gap of 100 bp
* 68639 74650: contig of 6012 bp in length
* 74651 74750: gap of 100 bp
* 74751 80037: contig of 5287 bp in length

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* 80038 80137: gap of 100 bp
* 80138 85646: contig of 5509 bp in length
* 85647 85746: gap of 100 bp
* 85747 92718: contig of 6972 bp in length
* 92719 92818: gap of 100 bp
* 92819 101098: contig of 8280 bp in length
* 101099 101198: gap of 100 bp
* 101199 108560: contig of 7362 bp in length
* 108561 108660: gap of 100 bp
* 108661 118118: contig of 9458 bp in length
* 118119 118218: gap of 100 bp
* 118219 128612: contig of 10394 bp in length
* 128613 128712: gap of 100 bp
* 128713 139860: contig of 11148 bp in length
* 139861 139960: gap of 100 bp
* 139961 151029: contig of 11069 bp in length
* 151030 151129: gap of 100 bp
* 151130 165337: contig of 14208 bp in length.

```

#### FEATURES

##### source

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1..165337
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPCI-11 Human Male BAC"

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##### misc\_feature

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1..1105
/note="assembly_fragment"

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##### misc\_feature

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1206..2479
/note="assembly_fragment"

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##### misc\_feature

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2580..4211
/note="assembly_fragment"

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##### misc\_feature

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4312..5781
/note="assembly_fragment"

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##### misc\_feature

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5882..7830
/note="assembly_fragment"

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##### misc\_feature

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7931..9913
/note="assembly_fragment"

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##### misc\_feature

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10014..12486
/note="assembly_fragment"

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##### misc\_feature

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12587..15592
/note="assembly_fragment"

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##### misc\_feature

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15693..19721
/note="assembly_fragment"

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##### misc\_feature

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19822..23369
/note="assembly_fragment"

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##### misc\_feature

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23370..26785
/note="assembly_fragment"

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##### misc\_feature

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26886..30363
/note="assembly_fragment"

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##### misc\_feature

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30464..33964
/note="assembly_fragment"

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##### misc\_feature

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34065..37794
/note="assembly_fragment"

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##### misc\_feature

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37895..43354
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##### misc\_feature

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43455..47839
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##### misc\_feature

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47940..53326
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##### misc\_feature

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53427..58576
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##### misc\_feature

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58677..64554
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##### misc\_feature

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64655..68538
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##### misc\_feature

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68639..74650
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##### misc\_feature

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74751..80037
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##### misc\_feature

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80138..85646
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##### misc\_feature

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85747..92718

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BASE COUNT      65720 a 39190 c 38969 g 64529 t 1369 others
ORIGIN

Query Match      87.3%; Score 19.2; DB 69; Length 209777;
Best Local Similarity 90.5%; Pred. No. 15;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2 gactgtgaangttbgagatga 22
||||| ||||| ||||| ||||| |||||
Db  76399 GACTGTGAAGCTTGAGATGA 76419

RESULT  9
AX036946      AX036946      22 bp      DNA      PAT      16-NOV-2000
LOCUS      Sequence 3 from Patent FR2790955.
DEFINITION  AX036946
ACCESSION  AX036946
VERSION    AX036946.1 GI:11226374
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS   Carpentier,A.
JOURNAL   Patent: FR 2790955-A 3 22-SEP-2000;
          ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES   Location/Qualifiers
            source
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="oligodesoxynucleotide"
BASE COUNT      6 a      4 c      6 g      6 t
ORIGIN

Query Match      84.5%; Score 18.6; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 24;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACTGTGAACGTTCCAGATGA 22

RESULT 10
AX083676      AX083676      22 bp      DNA      PAT      28-FEB-2001
LOCUS      Sequence 2 from Patent WO0112223.
DEFINITION  AX083676
ACCESSION  AX083676
VERSION    AX083676.1 GI:13185408
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS   van Nest,G.
TITLE     Methods of modulating an immune response using immunostimulatory s
          equences and compositions for use therein
JOURNAL   Patent: WO 0112223-A 2 22-FEB-2001;
          Dynavax Technologies Corporation (US)
FEATURES   Location/Qualifiers
            source
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Synthetic construct"
BASE COUNT      6 a      4 c      7 g      5 t
ORIGIN

Query Match      84.5%; Score 18.6; DB 10; Length 22;
Best Local Similarity 86.4%; Pred. No. 24;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACTGTGAACGTTCCAGATGA 22

RESULT 11
AX083678      AX083678      22 bp      DNA      PAT      28-FEB-2001
LOCUS      Sequence 4 from Patent WO0112223.
DEFINITION  AX083678
ACCESSION  AX083678
VERSION    AX083678.1 GI:13185410
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS   van Nest,G.
TITLE     Methods of modulating an immune response using immunostimulatory s
          equences and compositions for use therein
JOURNAL   Patent: WO 0112223-A 4 22-FEB-2001;
          Dynavax Technologies Corporation (US)
FEATURES   Location/Qualifiers
            source
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Synthetic construct"
BASE COUNT      6 a      4 c      6 g      6 t
ORIGIN

Query Match      84.5%; Score 18.6; DB 10; Length 22;
Best Local Similarity 86.4%; Pred. No. 24;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACCGTGAACGTTCCAGATGA 22

RESULT 12
AX083680      AX083680      22 bp      DNA      PAT      28-FEB-2001
LOCUS      Sequence 6 from Patent WO0112223.
DEFINITION  AX083680
ACCESSION  AX083680
VERSION    AX083680.1 GI:13185412
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS   van Nest,G.
TITLE     Methods of modulating an immune response using immunostimulatory s
          equences and compositions for use therein
JOURNAL   Patent: WO 0112223-A 6 22-FEB-2001;
          Dynavax Technologies Corporation (US)
FEATURES   Location/Qualifiers
            source
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              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="5-bromocytosine"
            modified_base
              11
              /mod_base=OTHER
BASE COUNT      6 a      3 c      6 g      6 t      1 others
ORIGIN

Query Match      84.5%; Score 18.6; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
```

|||||  
Db 1 TCACTGTGAANGTTCAGATGA 22

RESULT 13  
LOCUS CEF42G10/c 12545 bp DNA INV 25-OCT-2000  
DEFINITION Caenorhabditis elegans cosmid F42G10, complete sequence.  
ACCESSION 248230  
VERSION 1  
KEYWORDS HTG: Arg-tRNA: Mitogen activated protein kinase; Transfer RNA.  
SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 12545)  
none.  
Genome sequence of the nematode C. elegans: a platform for  
investigating biology. The C. elegans Sequencing Consortium  
Science 282 (5396), 2012-2018 (1998)  
99069613  
The C. elegans Sequencing Consortium.  
Erratum: [[published errata appear in Science 1999 Jan  
1:283(5396):35 and 1999 Mar 26:283(5410):2103 and 1999 Sep  
3:285(5433):1493]]  
2 (bases 1 to 12545)  
Harris,B.R.  
Direct Submission  
Submitted (12-FEB-1995) Nematode Sequencing Project, Sanger Centre,  
Hinxton, Cambridge CB10 1RO, England and Department of Genetics,  
Washington University, St. Louis, MO 63110, USA. E-mail:  
jes@sanger.ac.uk or rw@nematode.wustl.edu  
Coding sequences below are predicted from computer analysis, using  
predictions from GeneFinder (P. Green, U. Washington), and other  
available information.  
Current sequence finishing criteria for the C. elegans genome  
sequencing consortium are that all bases are either sequenced  
unambiguously on both strands, or on a single strand with both a  
dye primer and dye terminator reaction, from distinct subclones.  
Exceptions are indicated by an explicit note.  
IMPORTANT: This sequence is not the entire insert of clone F42G10.  
It may be shorter because we only sequence overlapping sections  
once, or longer because we arrange for a small overlap between  
neighbouring submissions.  
The true left end of clone F42G10 is at 9861 in  
sequence 248006.  
The true right end of clone F42G10 is at 102 in  
sequence 295122.  
The true right end of clone F19C6 is at 104 in this sequence. The  
start of this sequence (1..104) overlaps with the end of sequence  
248006.  
The end of this sequence (12448..12545) overlaps with the start of  
sequence 295122.  
For a graphical representation of this sequence and its analysis  
see: - [http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?](http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=F42G10)  
name=F42G10.

FEATURES  
source  
1..12545  
Location/Qualifiers  
/organism="Caenorhabditis elegans"  
/db\_xref="taxon:6239"  
/chromosome="X"  
/clone="F42G10"  
complement(join(1923..1983,2244..2767,2819..2932,  
3209..3352,3396..3609,3875..4179,4227..4404,4451..4488,  
4533..4658,5035..5087,5537..5600))  
/gene="F42G10.1"  
complement(join(1923..1983,2244..2767,2819..2932,  
3209..3352,3396..3609,3875..4179,4227..4404,4451..4488,  
4533..4658,5035..5087,5537..5600))  
/gene="F42G10.1"  
/note="contains similarity to Pfam domain: PF01431  
(Peptidase family M13), Score=215.9, E-value=2e-61, N=1  
CDNA EST yk24a6.3 comes from this gene

CDNA EST yk24a6.5 comes from this gene"  
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/protein\_id="CAA88262.1"  
/db\_xref="GI:3877041"  
/db\_xref="SPTREMBL:O09393"  
/translation="MKLYFLPSIALMAVFGNGDOVILRLKHSCEFTVGVQVHAKDLSSE  
HPICNNFYETICHKNITRVPFSRDLVRAMEYSDIDQYQYVFRVHAKRQWQSVNP  
DIVSKWLVQNTYWKWGNHKKHESFLNDAHEKTKNLENSFEFGYDFDILTKFYK  
SLKISVEYLTSLKIPISIRNNHYHGLFDEIRIHLNIRNTSKFSEDRKNEILNVRN  
LKLIFFYLVNKKVWRDAKTAKEVYRLKIMIEYENLSPIDVKIIRVAANPAME  
IFEXYITSTSRFVQHTAAASGLSENYONEIHISVETMENIADPKSVYDQFLYVL  
CHELQHVHYNVDPFDEATWASEKQCVVDRIHDHFAAYKTRNANWTGAPSYEDSAN  
VAGURLMLLYVAQKTSQSEIRDTVERSARFCFKNRENLHNPDLDSINVAASMPMT  
FNSLYNCKPGDMYVAPENYCKTLNMDIDVEEYKSKTENDDOLFVLTHTFMVDELTAV  
ELDANITTFEGKLFDTIVEVEEQEESKESASSSSSSSSSSEDESSVERELDEVSD  
GLDSENETELRKSEIASTSRSSFIMPATVETLLIKYKF"  
complement(2120..2192)  
/gene="F42G10.t1"  
/note="ACG Arg R-tRNA  
predicted using tRNAscan-SE-1.11  
preliminary prediction  
similar to tRNA-Arg"  
complement(2120..2192)  
/gene="F42G10.t1"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
/gene="F42G10.2"  
join(11556..11680,11734..11893,11938..12060,12174..12293,  
12340..12519,295122.1:325..393,295122.1:438..503,  
295122.1:554..639,295122.1:694..759,295122.1:809..905)  
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/note="contains similarity to Pfam domain: PF00069  
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E-value=1.1e-55, N=1"  
/codon\_start=1  
/protein\_id="CAA88264.1"  
/db\_xref="GI:3877043"  
/db\_xref="SWISS-PROT:Q20347"  
/translation="MVQEDDENLRMSLRPTSLSRPTSLSVNGNEKTLPEESVLRS  
LSTGKLYPDDDEHLTYFSSANLQDLGAINGFVYKMRHKTGKLIARVRCRNNI  
GHREQLRLREHDTIVKSEKGNIVFYGAIFSEGDCHICMELMDISMLLYKRVVMY  
KNSRLNENYVGHITVCTDADLTLLKELKIIHRDVKPSNILDGTVGAVKLCDFGICGQ  
LSESAKTHDAGCQYLAPEITSDKYDVRSDVMSLTYELIETAKPKPYQEWNSLF  
DOIATVSGDPPILHPSDDFHYSLPVKFIINTCLTKDRHRPKYDTLKSDFYRIYA  
VAGPEIEAKRILGVEAIDTRNHPVDHRG"  
join(complement(1308..1367),complement(1111..1227),  
complement(851..1066),complement(502..803),  
complement(268..327),complement(105),  
complement(248006.1:36284..36493),  
complement(248006.1:36093..36239),  
complement(248006.1:35772..35885),  
complement(248006.1:35359..35535),  
complement(248006.1:35174..35317))  
/gene="F19C6.4"  
/note="contains similarity to Pfam domain: PF01431  
(Peptidase family M13), Score=268.8, E-value=2.4e-77, N=1"  
/codon\_start=1  
/protein\_id="CAA88263.1"  
/db\_xref="GI:3877042"  
/db\_xref="SPTREMBL:Q09539"  
/translation="MKFGFIIVLTFTVSQSFHKSIDISKSPCNDFYDYVCAKDKTRSI  
SNLTFKMQNELETLKPNVTIENGTFTADLKVLRVMMKCTEIEVLTGFTVDY  
FGDLHSEKMHISERYTAVYSRLKEINTTNWTFYNALHANTEILOQMEPISSKNKF  
LHLFNTLKTNAINELETTTISEAAKSKMKKGEMSKVYFDFNTVYKAKLVY  
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MHVYYPGNFLMSNVTTAALQCARREVOMLDGTDAVKPISGNGKVAHEDVYVINA  
WRMIMKWTIKSNEKQLEALFTIVGLCKQSEKRELPHNPLSTLNCVAVQVVP  
LFTLYIGRIGDRMFAKHEEFCCKPFGDDVKVEDYAVKSSANKDVGCGFFDKLLATSKS  
FNFTYGI"  
join(complement(1308..1367),complement(1111..1227),  
complement(851..1066),complement(502..803),  
complement(268..327),complement(105),  
complement(248006.1:36284..36493),

complement(268...327),complement(105),  
complement(248006.1:36284...36493),  
complement(248006.1:36093...36239),  
complement(248006.1:35772...35885),  
complement(248006.1:35359...35535),  
complement(248006.1:35174...35317))  
/gene="P19C6.4"

BASE COUNT 4001 a 2110 c 2008 g 4426 t  
ORIGIN

Query Match 84.5%; Score 18.6; DB 6; Length 12545;  
Best Local Similarity 86.4%; Pred. No. 29;  
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22  
||||||| || ||||| |||||  
Db 10445 TGACTGTCAAGTTGGAGATGA 10424

RESULT 14  
AX036952 AX036952 22 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 9 from Patent FR2790955.  
ACCESSION AX036952  
VERSION AX036952.1 GI:11226380

SYNTHETIC  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
ARTIFICIAL SEQUENCE

REFERENCE 1 (bases 1 to 22)  
AUTHORS Carpentier A.  
JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;  
ASSIST PUBL HOPITAUX DE PARIS (FR)

FEATURES  
Location/Qualifiers  
source  
1..22

/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note=" oligodesoxynucleotide"  
7 a 2 c 6 g 7 t

BASE COUNT 7 a 2 c 6 g 7 t  
ORIGIN  
Query Match 80.9%; Score 17.8; DB 9; Length 22;  
Best Local Similarity 86.4%; Pred. No. 64;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22  
||||||| || ||||| |||||  
Db 1 TGACTGTGAACGTTATAGATGA 22

RESULT 15  
AL358135 49523 bp DNA PRI 02-FEB-2001  
LOCUS Human DNA sequence from clone RP11-342L7 on chromosome 6, complete  
DEFINITION sequence.  
ACCESSION AL358135  
VERSION AL358135.19 GI:12666263  
KEYWORDS HTG.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 49523)  
Donnelly, S.  
Direct Submission  
TITLE Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,  
JOURNAL CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk

On Feb 5, 2001 this sequence version replaced gi:12657153.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TrEMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RP11-342L7 is from the library RPc1-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-342L7 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.  
The true left end of clone RP11-342L7 is at 1 in this sequence. The true left end of clone RP1-166H4 is at 49424 in this sequence. The true right end of clone RP3-427I13 is at 19721 in this sequence.

## FEATURES

## Location/Qualifiers

## source

## 1..49523

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="6"

/clone="RP11-342L7"

/clone\_lib="RPC1-11.2"

553..856

repeat\_region

/note="AluSp repeat: matches 1..299 of consensus"

repeat\_region

1931..1969

repeat\_region

/note="L2 repeat: matches 2653..2691 of consensus"

2097..2579

repeat\_region

/note="L2 repeat: matches 2244..2749 of consensus"

2652..3105

repeat\_region

/note="L2 repeat: matches 1154..1657 of consensus"

3143..3311

repeat\_region

/note="FAM repeat: matches 1..169 of consensus"

4123..4178

repeat\_region

/note="L2 repeat: matches 2686..2744 of consensus"

5710..5802

repeat\_region

/note="3 copies 31 mer 77% conserved"

6442..6736

repeat\_region

/note="AluY repeat: matches 1..295 of consensus"

6797..6887

repeat\_region

/note="L2 repeat: matches 2611..2710 of consensus"

8158..8475

repeat\_region

/note="AluJb repeat: matches 1..312 of consensus"

8562..8866

repeat\_region

/note="AluSq repeat: matches 1..306 of consensus"

8890..9040

repeat\_region

/note="MIR repeat: matches 20..180 of consensus"

9448..9784

repeat\_region

/note="L2 repeat: matches 1155..1516 of consensus"

9802..10111

repeat\_region

/note="AluX repeat: matches 1..310 of consensus"

11283..11446

repeat\_region

/note="MER20 repeat: matches 1..175 of consensus"

11447..11843

repeat\_region

/note="L2 repeat: matches 2309..2750 of consensus"

13965..14267

repeat\_region

/note="AluY repeat: matches 1..309 of consensus"

15875..15916

repeat\_region

/note="7 copies 6 mer tggtg 81% conserved"

15876..15913

repeat\_region

/note="19 copies 2 mer gt 84% conserved"







SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	80.9	463	107	AU083559 AU083559
2	17.8	80.9	479	107	AU089685 AU089685
3	17.6	80.0	527	149	BF487041 AT21713.5
4	17.6	80.0	548	228	AQ397925 mgxb0008L
5	17.6	80.0	612	32	AV653619 AV653619
6	17.7	77.3	63	243	AZ431742 1M0216018
7	17.7	77.3	118	256	B79766 CIT-NSP-205
8	17.7	77.3	290	124	BB068341 BB068341
9	17.7	77.3	343	7	AA438163 ve64f06.r
10	17.7	77.3	374	226	AQ245026 HS_2056_B
11	17.7	77.3	471	113	AW270792 xp54b05.x
12	17.7	77.3	493	150	BF563081 UI-R-B01-
13	17.7	77.3	514	117	AW526035 UI-R-B01-
14	17.7	77.3	525	171	BF954072 QV2-NN004
15	17.7	77.3	592	244	AZ460464 1M0265118
16	17.7	77.3	614	244	AZ460101 1M0265118
17	17.7	77.3	665	249	AZ759002 1M0551114
18	17.7	77.3	697	174	BG138405 EST478847
19	17.7	77.3	972	222	CNS05PD9 Tetraodon
20	17.7	77.3	1043	220	CNS05J4W Tetraodon
21	16.8	76.4	398	167	BE428418 MTD006.G1
22	16.8	76.4	474	167	BE419241 WWR021.G5
23	16.8	76.4	477	149	BF475131 WHE2111_B
24	16.8	76.4	561	249	AZ755668 ev02q09.x
25	16.8	76.4	620	162	BE060267 HVSME9001
26	16.8	76.4	667	149	BF484589 WHE2317_D
27	16.8	76.4	930	146	BF257509 HVSMEF001
28	16.6	75.5	360	156	C61384 C61384.YuJ1
29	16.6	75.5	360	156	D37148 CELK041CXF
30	16.6	75.5	397	122	AH930320 EST340873
31	16.6	75.5	513	231	AQ607969 HS_2126_B
32	16.6	75.5	681	32	AV732648 AV732648
33	16.2	73.6	424	139	BE723539 193384.MA
34	16.2	73.6	533	143	BF039764 BP250014B
35	16.2	73.6	546	237	AZ058706 RPCI-23-4
36	16.2	73.6	554	241	AZ280611 RPCI-23-1
37	16.2	73.6	585	244	AZ490370 1M0323K14
38	16.2	73.6	599	237	AZ068022 RPCI-23-4
39	16.2	73.6	711	250	AZ818181 2M0088L01
40	16.2	73.6	934	220	CNS027SC Tetraodon
41	16.7	72.7	130	3	AA217796 mv54h02.r
42	16.7	72.7	202	4	AA236074 ZS05304.r
43	16.7	72.7	236	127	BB183285 BB183285
44	16.7	72.7	236	171	BF932252 IL2-NT019
45	16.7	72.7	251	161	BB565758 BB565758

ALIGNMENTS

RESULT 1					
LOCUS	AU083559	463 bp	mrna	EST	21-MAR-2000
DEFINITION	AU083559 Rice green shoot Oryza sativa cdna clone SI4862, mrna sequence.				
ACCESSION	AU083559				
VERSION	AU083559.1 GI:7274015				
KEYWORDS	EST.				
SOURCE	Oryza sativa.				
ORGANISM	Oryza sativa.				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.				
AUTHORS	1 (bases 1 to 463)				
TITLE	Sasaki, T. and Yamamoto, K.				
JOURNAL	Rice cdna from green shoot (2000) Unpublished (2000)				

COMMENT	Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program 2-1-2 Kannondai, Tsukuba Ibaraki, Japan 305 Tel: 0298-38-7441 Fax: 0298-38-7468 Email: tsasaki@abr.affrc.go.jp PROJECT = 'RGP', SI4862_62.				
FEATURES	Location/Qualifiers 1..463 /organism="Oryza sativa" /strain="Nipponbare" /db_xref="taxon:4530" /clone="SI4862" /clone_lib="Rice green shoot" /note="Green shoot (8 days old)" 2 others				
BASE COUNT	151 a	74 c	109 g	127 t	
ORIGIN					
Query Match	80.9%; Score 17.8; DB 107; Length 463;				
Best Local Similarity	86.4%; Pred. No. 1.5e+02;				
Matches	19;	Conservative	0;	Mismatches	3; Indels 0; Gaps 0;
QY	1	tgactgtgaangttbgaatga	22		
Db	151	TTGACTGTGAATGTTAGAGATGA	172		
RESULT 2					
LOCUS	AU089685 479 bp mRNA EST 27-APR-2000				
DEFINITION	AU089685 Rice callus Oryza sativa subsp. japonica CDNA clone C40060				
ACCESSION	AU089685				
VERSION	AU089685.1 GI:7652165				
KEYWORDS	EST.				
SOURCE	Oryza sativa subsp. japonica.				
ORGANISM	Oryza sativa subsp. japonica. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
REFERENCE	1 (bases 1 to 479)				
AUTHORS	Sasaki, T. and Yamamoto, K.				
TITLE	Rice CDNA from callus (2000)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program 2-1-2 Kannondai, Tsukuba Ibaraki, Japan 305 Tel: 0298-38-7441 Fax: 0298-38-7468 Email: tsasaki@abr.affrc.go.jp PROJECT = 'RGP', C40060_32.				
FEATURES	Location/Qualifiers 1..479 /organism="Oryza sativa subsp. japonica" /strain="cultivar Nipponbare, sub_species Japonica" /db_xref="taxon:39947" /clone="C40060" /clone_lib="Rice callus" /note="Vector: pBluescript II SK+; Site_1: SalI; Site_2: NotI; cDNA prepared from rice callus mRNAs by using oligo(dT) as a primer and ligating to the SalI-NotI site of pBluescript II SK+ phagemid."				
BASE COUNT	149 a	96 c	104 g	130 t	
ORIGIN					



AQ397925/c 548 bp DNA GSS 06-MAR-1999  
 LOCUS mgxb0008L06f CUGI Rice Blast BAC Library Magnaporthe grisea genomic  
 DEFINITION clone mgxb0008L06f, DNA sequence.  
 ACCESSION AQ397925  
 VERSION AQ397925  
 KEYWORDS AQ397925.1 GI:4368952  
 SOURCE GSS.  
 ORGANISM Magnaporthe grisea.  
 Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.  
 1 (bases 1 to 548)  
 Yu, Y., Zhu, H., Boyd, C. A., Gaudette, B., Gayle, A., Kingsbury, R.,  
 Phillips, K., Sasinowski, M., Wing, R. A. and Dean, R. A.  
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea  
 Genome  
 Unpublished (1998)  
 JOURNAL Contact: Dean RA  
 COMMENT Clemson University Genomics Institute  
 100 Jordan Hall, Clemson University, Clemson, SC 29634  
 Tel: 864 656 5737  
 Fax: 864 656 4293  
 Email: rdean@clemson.edu  
 Seq primer: TAATACGACTCACTATAGGG  
 Class: BAC ends  
 High quality sequence start: 56  
 High quality sequence stop: 467.  
 Location/Qualifiers  
 1..548  
 /organism="Magnaporthe grisea"  
 /strain="70-15"  
 /db\_xref="taxon:148305"  
 /clone="mgxb0008L06f"  
 /clone\_lib="CUGI Rice Blast BAC Library"  
 /tissue\_type="Protoplasts"  
 /lab\_host="E. coli DH10B"  
 /note="Vector: pBACWICH; Site: 1: HindIII; Site 2: HindIII;  
 Rice blast is one of the most devastating fungal diseases  
 of rice world wide. It is a filamentous ascomycete with  
 a haploid genome (n=7) of approximately 40 Mbp. Rice  
 blast is an important model fungal pathogen for studying  
 numerous aspects of the fungal-host interaction. In  
 order to facilitate genome wide analysis, a BAC library  
 containing 9216 clones with an average insert size of 130  
 kbp was constructed. This library represents greater  
 than 25X genome coverage. High density colony filters  
 are available upon request."  
 BASE COUNT 159 a 134 c 110 g 144 t 1 others  
 ORIGIN  
 Query Match 80.0%; Score 17.6; DB 228; Length 548;  
 Best Local Similarity 85.7%; Pred. No. 2e+02;  
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 gactgtgaangtttbgacatga 22  
 ||||| ||||| ||||| |||||  
 DB 301 GACTGTGAATTTTGACATGA 281  
 RESULT 5  
 AV653619 612 bp mRNA EST 07-SEP-2000  
 LOCUS AV653619 GLC Homo sapiens cDNA clone GLCDMG10 3', mRNA sequence.  
 DEFINITION AV653619  
 ACCESSION AV653619  
 VERSION AV653619.1 GI:9874633  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 612)





MGI:491227  
Seq primer: -28ml3 rev1 ET from Amersham  
High quality sequence stop: 336.  
Location/Qualifiers

#### FEATURES

source  
1. .343  
/organism="Mus musculus"  
/strain="C57BL6 x DBA"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:822947"  
/clone\_lib="Beddington mouse embryonic region"  
/sex="pooled"  
/tissue\_type="embryo"  
/dev\_stage="7.5dpc"  
/lab\_host="DH12S"

/note="Organ: whole embryo; Vector: pCMV-SPORT; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Gastrulating embryos were collected at 7.5dpc from C57BL6 x DBA matings, excluding embryos that had developed head folds and all extraembryonic tissues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1995)"

#### BASE COUNT

78 a 123 c 74 g 68 t

#### ORIGIN

Query Match 77.3%; Score 17; DB 7; Length 343;

Best Local Similarity 81.8%; Pred. No. 3.6e+02;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22

||||| ||||| ||||| ||||| |||||

Db 82 TCACGGTGACGGTTGGAGATGA 61

#### RESULT 10

AQ245026

LOCUS

DEFINITION

HS.2056\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone plate-2056 Col-5 Row-J, DNA sequence.

ACCESSION

AQ245026

VERSION

AQ245026.1

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

MAHAIRAS, G.G., WALLACE, J.C., SMITH, K., SWARTZELL, S., HOLZMAN, T., KELLER, A., SHAKER, R., FURLONG, J., YOUNG, J., ZHAO, S., ADAMS, M.D. and HOOD, L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL

MEDLINE

COMMENT

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
99380589  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 2056 row: J column: 5  
Class: BAC ends  
High quality sequence stop: 374.

#### FEATURES

source

1. .374  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="plate-2056 Col-5 Row-J"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBelorAC11; BAC Clones in

BASE COUNT 91 a 73 c 92 g 117 t 1 others

#### ORIGIN

Query Match 77.3%; Score 17; DB 226; Length 374;

Best Local Similarity 81.8%; Pred. No. 3.7e+02;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22

||||| ||||| ||||| ||||| |||||

Db 207 TCACGTGACGATTGAGATCA 228

#### RESULT 11

AW270792

LOCUS

DEFINITION

XP54B05.X1 NCI\_CGAP\_HN12 Homo sapiens cDNA clone IMAGE:2744145 3', mRNA sequence.

ACCESSION

AW270792

VERSION

AW270792.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITILE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: John F. Ensley, M.D., Silvio Cutkind Ph.D., Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyt not found

Seq primer: -40UP from Gibco

High quality sequence stop: 427.

#### FEATURES

source

Location/Qualifiers  
1. .471  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2744145"  
/clone\_lib="NCI\_CGAP\_HN12"  
/tissue\_type="moderate to poorly differentiated invasive carcinoma"  
/lab\_host="DH10B"  
/note="Organ: tongue; Vector: pAMP10; cDNA made by oligo-dt priming. Non-directionally cloned into the UDS sites of pAMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. CDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 127 a 100 c 124 g 120 t

#### ORIGIN

Query Match 77.3%; Score 17; DB 113; Length 471;

Best Local Similarity 81.8%; Pred. No. 3.9e+02;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22

||||| ||||| ||||| ||||| |||||

Db 183 TGACGGTGACGGTTGGAGATGA 204

```

RESULT 12
BF563081 493 bp mRNA EST 12-DEC-2000
LOCUS
DEFINITION
ACCESSION
BF563081
VERSION
BF563081.1 GI:11672811
KEYWORDS
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 493)
AUTHORS
Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (infoimage.llnl.gov). IMAGE ID= 1797843
Seq primer: M13 Forward.

FEATURES
source
Location/Qualifiers
1..493
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-e-06-0-UI"
/clone_lib="UI-R-B01"
/dev_stage="adult"
/lab_host="DHI08 (Life Technologies)"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Ronaldo, Lennon and Soares, Genome Research
6:791-806, 1996)."
BASE COUNT 112 a 122 c 144 g 115 t
ORIGIN
Query Match 77.3%; Score 17; DB 150; Length 493;
Best Local Similarity 81.8%; Pred. No. 3.9e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22
|||||
Db 469 TGACACTGAAGTTTCAGATGA 490

RESULT 13
AW526035/c 514 bp mRNA EST 06-MAR-2000
LOCUS
DEFINITION
ACCESSION
AW526035
VERSION
AW526035.1 GI:7168420
KEYWORDS
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 493)
AUTHORS
Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (infoimage.llnl.gov). IMAGE ID= 1797843
Seq primer: M13 Forward.

FEATURES
source
Location/Qualifiers
1..493
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-e-06-0-UI"
/clone_lib="UI-R-B01"
/dev_stage="adult"
/lab_host="DHI08 (Life Technologies)"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Ronaldo, Lennon and Soares, Genome Research
6:791-806, 1996)."
BASE COUNT 112 a 122 c 144 g 115 t
ORIGIN
Query Match 77.3%; Score 17; DB 150; Length 493;
Best Local Similarity 81.8%; Pred. No. 3.9e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22
|||||
Db 469 TGACACTGAAGTTTCAGATGA 490

```

```

SOURCE
ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 514)
AUTHORS
Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dt track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dt track served to identify it as a clone from the
normalized medulla library cDNA library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..514
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-e-06-0-UI"
/clone_lib="UI-R-B01"
/dev_stage="adult"
/lab_host="DHI08 (Life Technologies)"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Ronaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-B01
TAG_TISSUE=medulla
TAG_SEQ=GAACCG"
BASE COUNT 116 a 146 c 125 g 127 t
ORIGIN
Query Match 77.3%; Score 17; DB 117; Length 514;
Best Local Similarity 81.8%; Pred. No. 4e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22
|||||
Db 42 TGACACTGAAGTTTCAGATGA 21

RESULT 14
BF954072/c 525 bp mRNA EST 22-JAN-2001
LOCUS
DEFINITION
ACCESSION
BF954072
VERSION
BF954072.1 GI:12371347
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 525)

# REFERENCE AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

# JOURNAL MEDLINE COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-131100-412-g11&t3=2000-11-13&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 525.

# FEATURES source

1..525  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NN0045"  
/dev\_stage="Adult"  
/note="Organ: nervous\_normal; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
162 a 119 c 94 g 150 t

# BASE COUNT ORIGIN

Query Match 77.3%; Score 17; DB 171; Length 525;  
Best Local Similarity 81.8%; Pred. No. 4e+02;  
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22  
||||||| ||:|||||  
Db 385 TGACTGTGAANAATGGAGAGGA 364

# RESULT 15 LOCUS

AZ460464 592 bp DNA GSS 04-OCT-2000  
NM0265L18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0265L18 R, DNA sequence.

# ACCESSION VERSION KEYWORDS SOURCE

AZ460464.1 GI:10618589  
GSS.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

# REFERENCE AUTHORS

1 (bases 1 to 592)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

# COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0265 row: L column: 18  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 592.

# FEATURES source

1..592  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="UUGC1M0265L18"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWB42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
166 a 112 c 122 g 192 t

# BASE COUNT ORIGIN

Query Match 77.3%; Score 17; DB 244; Length 592;  
Best Local Similarity 81.8%; Pred. No. 4.1e+02;  
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22  
||||||| ||:|||||  
Db 425 TGACAGTGAATGATGGAGATGA 404

Search completed: October 9, 2001, 18:20:27  
Job time: 9797 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds  
(without alignments)  
26.779 Million cell updates/sec

Title: US-09-713-136-8

Perfect score: 22  
Sequence: 1 tgactgtgaangttbgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.2	91.8	22	19	AAV32080
2	20.2	91.8	22	19	AAV32079
3	20.2	91.8	22	20	AAV36624
4	20.2	91.8	22	20	AAV36625
5	20.2	91.8	22	20	AAV80097
6	20.2	91.8	22	20	AAV80102
7	20.2	91.8	22	20	AAV80103
8	20.2	91.8	22	21	AAV64051
9	20.2	91.8	22	21	AAV96253
10	20.2	91.8	22	21	AAV90458
11	20.2	91.8	22	21	AAV14467

12	20.2	91.8	22	21	AAV14468	Inactive immunostimulatory
13	20.2	91.8	22	21	AAV38065	Immunostimulatory
14	20.2	91.8	22	21	AAV38071	Immunostimulatory
15	20.2	91.8	22	21	AAV38072	Immunostimulatory
16	20.2	91.8	22	21	AAV55876	Immunomodulatory o
17	20.2	91.8	22	21	AAV55880	Immunomodulatory o
18	20.2	91.8	22	22	AAV77040	Immunomodulatory D
19	20.2	91.8	22	22	AAV77046	Immunostimulatory
20	20.2	91.8	22	22	AAV77047	Immunostimulatory
21	20.2	91.8	22	22	AAV29800	Cholera toxin immu
22	20.2	91.8	22	22	AAV82107	Oligonucleotide OD
23	20.2	91.8	22	22	AAV92377	CG motif and CFA c
24	20.2	91.8	22	21	AAV55881	Immunomodulatory o
25	19.4	88.2	22	20	AAV55797	Immunostimulatory
26	19.4	88.2	22	20	AAV55788	Immunostimulatory
27	19.4	88.2	22	20	AAV80104	Oligo used in expe
28	19.4	88.2	22	21	AAV64052	Non-CpG control ph
29	19.4	88.2	22	21	AAV6252	Sequence of a stab
30	18.6	84.5	22	20	AAV80105	Oligo used in expe
31	18.6	84.5	22	20	AAV80096	Immunomodulatory o
32	18.6	84.5	22	20	AAV80099	Immunomodulatory o
33	18.6	84.5	22	20	AAV80101	Immunomodulatory o
34	18.6	84.5	22	21	AAV6254	Sequence of a stab
35	18.6	84.5	22	21	AAV38066	Immunostimulatory
36	18.6	84.5	22	21	AAV38068	Immunostimulatory
37	18.6	84.5	22	21	AAV38070	Immunostimulatory
38	18.6	84.5	22	21	AAV55877	Immunomodulatory o
39	18.6	84.5	22	22	AAV77041	Immunostimulatory
40	18.6	84.5	22	22	AAV77043	Immunostimulatory
41	18.6	84.5	22	22	AAV77045	Immunostimulatory
42	17.8	80.9	22	20	AAV55790	Immunostimulatory
43	17.8	80.9	22	20	AAV55791	Immunostimulatory
44	17.8	80.9	22	20	AAV80106	Oligo used in expe
45	17.8	80.9	22	22	AAV92378	CG motif and CFA c

#### ALIGNMENTS

RESULT	1
AAV32080	
ID	AAV32080 standard; DNA; 22 Bp.
XX	
AC	AAV32080;
XX	
DT	09-SEP-1998 (first entry)
XX	
DE	Nucleotide sequence of DY1019.
XX	
KW	DY1019; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
KW	immunisation; anaphylaxis; IgE; retinopathies; ss.
XX	
OS	synthetic.
XX	
FH	Key
FT	modified_base 1..22
FT	/*tag= a
FT	/note= "phosphothioate backbone"
XX	
PN	WO9816247-A1.
XX	
PD	23-APR-1998.
XX	
PF	09-OCT-1997; 97WO-US19004.
XX	
PR	11-OCT-1996; 96US-0028118.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Carson DA, Raz E, Roman M;
XX	
DR	WPI; 1998-261028/23.
XX	





CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:  
CC (a) reduction in, or the absence of, a Th2 type immune response is  
CC measured; or (b) there is a reduction or absence of other clinical signs  
CC of inflammation in the host after antigen challenge. The method is used  
CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
CC and to modulate the host's immune responsiveness to an antigen,  
CC particularly where the subject suffers from asthma, nasal polyposis,  
CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
CC antigen immunisation, the method is an antigen-independent method  
CC and avoids host production of both interleukin-4 (IL-4), which carries  
CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
CC adhesion to endothelia.  
XX  
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 20; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.42;  
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagttbgagatga 22  
||||||| |||:|||||  
Db 1 tgactgtgaagttcgagatga 22

RESULT 4  
AAX36625  
ID AAX36625 standard; DNA; 22 BP.  
AC AAX36625;  
XX  
XX  
DT 09-JUL-1999 (first entry)  
XX  
XX  
DE ISS-ODN mutant DY1019 nucleotide sequence.  
XX  
KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;  
KW granulocyte-mediated tissue inflammation; Th2 type immune response;  
KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;  
KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;  
KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;  
KW eosinophilic fasciitis; therapy; ss.  
OS Synthetic.  
XX  
XX WO9911275-A2.  
XX  
XX 11-MAR-1999.  
XX  
XX 04-SEP-1998; 98WO-US18382.  
XX  
XX 05-SEP-1997; 97US-0927120.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Ray E;  
XX  
XX WPI; 1999-312404/26.  
XX  
XX Reducing antigen-stimulated granulocyte-mediated inflammation  
XX  
XX Example 2; Page 30; 69pp; English.  
XX  
XX This is the ISS-ODN mutant DY1019 nucleotide sequence.  
CC The invention relates to a method for preventing or reducing  
CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:  
CC (a) reduction in, or the absence of, a Th2 type immune response is  
CC measured; or (b) there is a reduction or absence of other clinical signs  
CC of inflammation in the host after antigen challenge. The method is used  
CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
CC and to modulate the host's immune responsiveness to an antigen,  
CC particularly where the subject suffers from asthma, nasal polyposis,  
CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
CC antigen immunisation, the method is an antigen-independent method  
CC and avoids host production of both interleukin-4 (IL-4), which carries  
CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
CC adhesion to endothelia.

CC and to modulate the host's immune responsiveness to an antigen,  
CC particularly where the subject suffers from asthma, nasal polyposis,  
CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
CC antigen immunisation, the method is an antigen-independent method,  
CC and avoids host production of both interleukin-4 (IL-4), which carries  
CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
CC adhesion to endothelia.  
XX  
SQ Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 20; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.42;  
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagttbgagatga 22  
||||||| |||:|||||  
Db 1 tgactgtgaagttcgagatga 22

RESULT 5  
AAV80097  
ID AAV80097 standard; DNA; 22 BP.  
XX  
XX  
AC AAV80097;  
XX  
XX  
DT 12-MAR-1999 (first entry)  
XX  
XX  
DE Immunomodulatory oligo comprising an ISS sequence.  
XX  
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.  
XX  
XX Synthetic.  
XX  
XX WO9855495-A2.  
XX  
XX 10-DEC-1998.  
XX  
XX 05-JUN-1998; 98WO-US11578.  
XX  
XX 06-JUN-1997; 97US-0048793.  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
XX Dina D, Roman M, Schwartz D;  
XX  
XX WPI; 1999-059898/05.  
XX  
XX Immunostimulatory oligonucleotides regulate the immune system - and  
XX contain an immune-stimulating octanucleotide sequence; for treating  
XX cancer, allergic and infectious diseases  
XX  
XX Claim 5; Page 29; 63pp; English.  
XX  
XX The invention relates to immunomodulatory oligonucleotides that comprise  
XX at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
XX sequences are selected from the group consisting of AACGTTC, AACGTTCG,  
XX GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat  
XX patients needing immune regulation, such as those suffering from cancer,  
XX an allergic disease and asthma. They are also used to prevent infectious  
XX diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
XX and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
XX Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
XX Schistosoma. The immunomodulatory sequences are used to screen for human  
XX immunostimulatory activity by incubating macrophage cells and the  
XX oligonucleotide; and determining the relative amount of Th1-biased  
XX cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
XX specific claimed examples of such immunomodulatory oligonucleotides.

```

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
Query Match 91.8%; Score 20.2; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
    ||||| ||||| ||||| |||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 6
AAV80102
ID AAV80102 standard; DNA: 22 BP.
XX
AC AAV80102;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 11
FT /*tag= a
FT /note= "5-bromocytosine"
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11578.
XX
PR 06-JUN-1997; 97US-0048793.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Dina D, Roman M, Schwartz D;
XX
DR WPI: 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases
XX
PS Claim 23; Page 30; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC GAGGTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
    ||||| ||||| ||||| |||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 7
AAV80103
ID AAV80103 standard; DNA: 22 BP.
XX
AC AAV80103;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 11
FT /*tag= a
FT /note= "5-bromocytosine"
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11578.
XX
PR 06-JUN-1997; 97US-0048793.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Dina D, Roman M, Schwartz D;
XX
DR WPI: 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases
XX
PS Claim 24; Page 30; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC GAGGTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

Oy 1 tgactgtgaangttbgagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 8  
 AAC64051  
 ID AAC64051 standard; DNA; 22 BP.  
 XX  
 AC AAC64051;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.  
 XX  
 KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;  
 KW enhanced antigen presentation; antigen-presenting cell; APC;  
 KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;  
 KW vaccine; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200062787-A1.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 11-APR-2000; 2000WO-US09664.  
 XX  
 PR 15-APR-1999; 99US-0292278.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Raz E, Martin-Orozco E;  
 XX  
 XX WPI; 2000-679548/66.  
 XX  
 PT Enhancing antigen-presentation capabilities of T-cells for cancer  
 PT immunotherapy, by contacting cells with an immunostimulatory  
 PT oligonucleotide  
 XX  
 PS Example 1; Page 18; 42pp; English.  
 XX  
 CC The invention relates to a method of inducing activation of T-cells  
 CC to respond to an antigen, comprising contacting antigen-presenting cells  
 CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs  
 CC thus treated have enhanced antigen presenting capabilities compared to  
 CC antigen-activated APCs. APCs with enhanced antigen-presentation  
 CC capabilities then present the antigen to T-cells. The method is useful  
 CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour  
 CC antigen presenting capacity of tumour cells, thereby inducing T-cell  
 CC activation, and is therefore useful for treating tumours. Additionally,  
 CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.  
 CC ISS-ODN treated APCs are induced to take up antigen through upregulation  
 CC of Fc-receptor expression, to present antigen through upregulation of  
 CC major histocompatibility complex (MHC) Class I and II expression and  
 CC CD40 expression, to produce co-stimulatory factors (B7 and CD40), to  
 CC provide cell-to-cell adhesion through upregulation of intercellular  
 CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory  
 CC cytokine production, all at levels greater than that achieved through  
 CC contact of APC with antigen alone. The present sequence represents  
 CC a phosphorothioate cpG ISS-ODN used in the exemplifications of the  
 CC invention.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 0.42;  
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 9  
 AAA96253  
 ID AAA96253 standard; DNA; 22 BP.  
 XX  
 AC AAA96253;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Sequence of a stabilised oligonucleotide with antitumour activity.  
 XX  
 KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;  
 KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2000056342-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 17-MAR-2000; 2000WO-FR00676.  
 XX  
 PR 19-MAR-1999; 99FR-0003433.  
 XX  
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
 XX  
 PI Carpentier A;  
 XX  
 XX WPI; 2000-602192/57.  
 XX  
 PT Use of stabilized oligonucleotides as antitumor agents, particularly  
 PT against nervous system tumors, have optimal activity and are not toxic  
 PT .  
 XX  
 PS Example 2; Page 16; 57pp; French.  
 XX  
 CC The present sequence represents a stabilised oligonucleotide which has  
 CC antitumour activity. The oligonucleotide comprises an octamer motif  
 CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where  
 CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are  
 CC immunostimulatory, and are not toxic. They may be adapted for use in  
 CC animals or humans. The stabilised oligonucleotides are used for  
 CC treating tumours, of any type and any degree of anaplasia, particularly  
 CC human tumours in the peripheral or central nervous systems, specifically  
 CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 0.42;  
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 10  
 AAA90458  
 ID AAA90458 standard; DNA; 22 BP.  
 XX  
 AC AAA90458;  
 XX  
 DT 10-JAN-2001 (first entry)  
 XX  
 DE CpG adjuvant oligonucleotide, SEQ ID NO:19.  
 XX  
 KW CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;  
 KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;  
 KW viral infection; bacterial infection; parasitic infection; HCV; HBV;

KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;  
 KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;  
 KW rabies virus; cholera; diphtheria; tetanus; pertussis;  
 KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.

XX Synthetic.

XX WO200050006-A2.

XX 31-AUG-2000.

XX 09-FEB-2000; 2000WO-US03331.

XX 26-FEB-1999; 99US-0121858.

XX 29-JUL-1999; 99US-0146391.

XX 28-OCT-1999; 99US-0161997.

XX (CHIR ) CHIRON CORP.

XX O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Uguzzoli M, Singh M;  
 PI Barackman J;

XX WPI: 2000-597123/55.

XX Microemulsion having an adsorbent surface comprising a microdroplet  
 PT emulsion consisting of a metabolizable oil and an emulsifying agent  
 PT which is a detergent, useful as a vaccine to treat bacterial, viral,  
 PT and parasitic infection

XX Claim 17; Page 40; 95pp; English.

XX The invention relates to a microdroplet emulsion (microemulsion) with an  
 CC adsorbent surface, and which comprises a metabolizable oil and an  
 CC emulsifying agent (a detergent). It also relates to a composition  
 CC comprising the microemulsion and a microparticle with an adsorbent  
 CC surface, where the microparticle comprises a polymer selected from a  
 CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a  
 CC polycaprolactone, a polyorthoester, a polyhydride, and a  
 CC polycyanoacrylate, and a second detergent. The surface of the  
 CC microparticle efficiently adsorb biologically active macromolecules such  
 CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,  
 CC mediators of transcription or translation, metabolic intermediates and  
 CC adjuvants. Additionally, a second biologically active molecule may be  
 CC encapsulated within the microparticle. The microemulsion can be used in  
 CC methods of immunising a host animal, particularly a human, against a  
 CC viral, bacterial or parasitic infection, and in methods of increasing a  
 CC Th1 immune response. The microemulsions (having the appropriate antigens  
 CC adsorbed) may be particularly used as vaccines for hepatitis C virus  
 CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human  
 CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and  
 CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and  
 CC pertussis; Helicobacter pylori and Haemophilus influenzae; and  
 CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1  
 CC lymphocyte stimulating oligonucleotides containing at least one CpG motif  
 CC which are claimed for use as adjuvants in the compositions of the  
 CC invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 0.42;  
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 11

AAAI4467

ID AAAI4467 standard; DNA; 22 BP.

XX

AC AAAI4467;  
 XX 21-AUG-2000 (first entry)  
 DT  
 XX Immunostimulatory oligonucleotide (ISS-ODN) DY1018.  
 DE  
 XX Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;  
 KW secretory immunoglobulin A production; sigA; Th1 phenotype; ds.  
 KW  
 XX Synthetic.

XX WO200020039-A1.

XX 13-APR-2000.

XX 15-SEP-1999; 99WO-US21203.

XX 05-OCT-1998; 98US-0167039.

XX (REGC ) UNIV CALIFORNIA.

XX Raz E, Horner AA, Carson DA;

XX WPI: 2000-303647/26.

XX Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to  
 PT an antigen in a mammalian host through production of secretory  
 PT immunoglobulin A

XX Claim 8; Page 21; 64pp; English.

XX The invention relates to a method of inducing mucosal immunity to an  
 CC antigen in a mammalian host, including the production of secretory  
 CC immunoglobulin A (sIgA). Immune protection in the mucosa (the principal  
 CC site of entry of most foreign antigens) is mediated by mucosa-associated  
 CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory  
 CC cell sub-populations. The primary immune response which characterises  
 CC the induction of mucosal immunity to an antigen is sIgA production by  
 CC activated B-cells. The method comprises introducing an immunostimulatory  
 CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the  
 CC ISS-ODN includes a core nucleotide sequence. The core nucleotide  
 CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific  
 CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID Nos 1-3). A  
 CC specific example of an ISS-ODN is DY1018 (AAAI4467). The ISS-ODN is used  
 CC as an adjuvant with an antigen for stimulating mucosal immunity. The  
 CC level of sIgA production induced in the host is at least 3 times the  
 CC magnitude of sIgA production achievable in response to introduction of  
 CC antigen alone into the mucosal tissue and is equivalent or greater than  
 CC the magnitude of sIgA production achievable in response to introduction  
 CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The  
 CC host immune response is stimulated to antigen specific IgA production,  
 CC biased towards the Th1 phenotype while antigen-induced IgE production is  
 CC avoided. The adjuvant has little or no known toxicity in mammals and its  
 CC efficacy is comparable to that of cholera toxin which is used as a  
 CC mucosal adjuvant. The present sequence represents the immunostimulatory  
 CC oligonucleotide DY1018.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 0.42;  
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 12

AAAI4468

ID AAAI4468 standard; DNA; 22 BP.

XX

```

AC AA14468;
XX
XX
DT 21-AUG-2000 (first entry)
XX
XX
DE Inactive immunostimulatory oligonucleotide DY1019.
XX
XX
KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
KW secretory immunoglobulin A production; sigA; Th1 phenotype; mutant; ds.
XX
XX
OS Synthetic.
XX
XX
PN WO200020039-A1.
XX
XX
PD 13-APR-2000.
XX
XX
PF 15-SEP-1999; 99WO-US21203.
XX
XX
PR 05-OCT-1998; 98US-0167039.
XX
XX
PA (REGC ) UNIV CALIFORNIA.
XX
XX
PI Raz E, Horner AA, Carson DA;
XX
XX
PI WPI; 2000-303647/26.
XX
XX
DR Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to
XX antigen in a mammalian host through production of secretory
XX immunoglobulin A.
XX
XX
PS Example 7; Page 63; 64pp; English.
XX
XX
CC The invention relates to a method of inducing mucosal immunity to an
XX antigen in a mammalian host, including the production of secretory
XX immunoglobulin A (sigA). Immune protection in the mucosa (the principal
XX site of entry of most foreign antigens) is mediated by mucosa-associated
XX lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory
XX cell sub-populations. The primary immune response which characterises
XX the induction of mucosal immunity to an antigen is sigA production by
XX activated B-cells. The method comprises introducing an immunostimulatory
XX oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the
XX ISS-ODN includes a core nucleotide sequence. The core nucleotide
XX sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific
XX examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A
XX specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used
XX as an adjuvant with an antigen for stimulating mucosal immunity. The
XX level of sigA production induced in the host is at least 3 times the
XX magnitude of sigA production achievable in response to introduction of
XX antigen alone into the mucosal tissue and is equivalent or greater than
XX the magnitude of sigA production achievable in response to introduction
XX of the antigen and cholera toxin adjuvant into the mucosal tissue. The
XX host immune response is stimulated to antigen specific IgA production,
XX biased towards the Th1 phenotype while antigen-induced IgE production is
XX avoided. The adjuvant has little or no known toxicity in mammals and its
XX efficacy is comparable to that of cholera toxin which is used as a
XX mucosal adjuvant. The present sequence represents an inactive ISS-ODN,
XX DY1019, used in an exemplification of the invention.
XX
XX
SQ Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttbgagatga 22
| | | | | | | | | | | | | | | |
Db 1 tgactgtgaaggttbgagatga 22

RESULT 13
AAA38065
ID AAA38065 standard; DNA; 22 BP.
XX

```

```

AC AAA38065;
XX
XX
DT 24-AUG-2000 (first entry)
XX
XX
DE Immunostimulatory sequence (ISS) #1.
XX
XX
KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW gp120; human immunodeficiency virus; HIV; immune response; infection;
KW development; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200021556-A1.
XX
XX
PD 20-APR-2000.
XX
XX
PF 08-OCT-1999; 99WO-US23677.
XX
XX
PR 09-OCT-1998; 98US-0103733.
XX
XX
PR 07-OCT-1999; 98US-0415186.
XX
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX
PI Tighe H, Raz E, Schwartz D, Takabayashi K;
XX
XX
PI WPI; 2000-317846/27.
XX
XX
DR Anti-HIV composition comprises immunostimulatory polynucleotides and
XX HIV glycoprotein gp120 useful for modulating, stimulating an immune
XX response against HIV in an HIV infected individual.
XX
XX
PS Claim 3; Page 16; 65pp; English.
XX
XX
CC The present invention relates to an immunostimulatory composition
XX comprising a human immunodeficiency virus (HIV) antigen, and an
XX immunostimulatory polynucleotide comprising an immunostimulatory sequence
XX (ISS). This sequence represents an ISS that can be used in the
XX composition. An immunostimulatory polynucleotide, or is proximately
XX conjugated to an immunomodulatory polynucleotide, is used for modulating or
XX associated to it and not conjugated, is used for modulating or
XX stimulating a specific immune response against gp120 in an individual by
XX producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
XX is also used for suppressing or delaying development of HIV infection in
XX an individual infected with HIV or an individual at risk of infection
XX with HIV, respectively. It is also used for treating an individual
XX infected with HIV in need of immune modulation.
XX
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttbgagatga 22
| | | | | | | | | | | | | | | |
Db 1 tgactgtgaaggttbgagatga 22

RESULT 14
AAA38071
ID AAA38071 standard; DNA; 22 BP.
XX
XX
AC AAA38071;
XX
XX
DT 24-AUG-2000 (first entry)
XX
XX
DE Immunostimulatory sequence (ISS) #7.
XX
XX
KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW gp120; human immunodeficiency virus; HIV; immune response; infection;
KW development; ss.
XX
XX

```



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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:47 ; Search time 10334.3 Seconds  
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Title: US-09-713-136-8  
Perfect score: 22  
Sequence: 1 tgactgtgaangttbgagatga 22

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Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 60: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.2	91.8	22	PCT-US00-18229-32	Sequence 32, Appl
2	20.2	91.8	22	PCT-US00-35084-1	Sequence 1, Appl
3	20.2	91.8	22	PCT-US00-35084-2	Sequence 2, Appl
4	20.2	91.8	22	PCT-US01-03029-1	Sequence 1, Appl
5	20.2	91.8	22	PCT-US01-03029-2	Sequence 2, Appl
6	20.2	91.8	22	PCT-US01-06034-1	Sequence 1, Appl
7	20.2	91.8	22	PCT-US01-06034-4	Sequence 4, Appl
8	20.2	91.8	22	PCT-US01-10118-1	Sequence 1, Appl
9	20.2	91.8	22	PCT-US01-10118-3	Sequence 3, Appl
10	20.2	91.8	22	PCT-US01-11290-1	Sequence 1, Appl
11	20.2	91.8	22	PCT-US01-11290-2	Sequence 2, Appl
12	20.2	91.8	22	PCT-US01-14508-1	Sequence 1, Appl
13	20.2	91.8	22	PCT-US99-21203-19	Sequence 19, Appl
14	20.2	91.8	22	PCT-US99-21203-20	Sequence 20, Appl
15	20.2	91.8	22	US-08-927-120-19	Sequence 19, Appl
16	20.2	91.8	22	US-08-927-120-20	Sequence 20, Appl
17	20.2	91.8	22	US-09-167-039-19	Sequence 19, Appl
18	20.2	91.8	22	US-09-167-039-20	Sequence 20, Appl
19	20.2	91.8	22	US-09-235-742-19	Sequence 19, Appl
20	20.2	91.8	22	US-09-235-742-20	Sequence 20, Appl
21	20.2	91.8	22	US-09-296-477-2	Sequence 2, Appl
22	20.2	91.8	22	US-09-296-477-15	Sequence 15, Appl
23	20.2	91.8	22	US-09-308-036A-1	Sequence 1, Appl
24	20.2	91.8	22	US-09-308-036A-2	Sequence 2, Appl
25	20.2	91.8	22	US-09-324-191A-1	Sequence 1, Appl
26	20.2	91.8	22	US-09-324-191A-5	Sequence 5, Appl
27	20.2	91.8	22	US-09-347-343-32	Sequence 32, Appl
28	20.2	91.8	22	US-09-397-198-1	Sequence 1, Appl
29	20.2	91.8	22	US-09-415-186-1	Sequence 1, Appl
30	20.2	91.8	22	US-09-415-186-7	Sequence 7, Appl
31	20.2	91.8	22	US-09-415-186-8	Sequence 8, Appl
32	20.2	91.8	22	US-09-470-382-69	Sequence 69, Appl
33	20.2	91.8	22	US-09-565-906-2	Sequence 2, Appl
34	20.2	91.8	22	US-09-570-325-19	Sequence 19, Appl
35	20.2	91.8	22	US-09-570-325-20	Sequence 20, Appl
36	20.2	91.8	22	US-09-570-325-20	Sequence 20, Appl
37	20.2	91.8	22	US-09-642-492-7	Sequence 7, Appl
38	20.2	91.8	22	US-09-642-492-7	Sequence 7, Appl
39	20.2	91.8	22	US-09-700-354-1	Sequence 1, Appl
40	20.2	91.8	22	US-09-700-354-2	Sequence 2, Appl
41	20.2	91.8	22	US-09-713-136-1	Sequence 1, Appl
42	20.2	91.8	22	US-09-713-136-7	Sequence 7, Appl
43	20.2	91.8	22	US-09-713-136-8	Sequence 8, Appl
44	20.2	91.8	22	US-09-746-130-1	Sequence 1, Appl
45	20.2	91.8	22	US-09-746-130-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
PCT-US00-18229-32  
; Sequence 32, Application PC/TUS0018229  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Kobayashi, Hiroko  
; TITLE OF INVENTION: Method for Enhancing an Immune Response  
; FILE REFERENCE: 6510-189W01  
; CURRENT APPLICATION NUMBER: PCT/US00/18229  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
PCT-US00-18229-32

Query Match 91.8% Score 20.2; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 7.1;  
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaangttbgagatga 22  
||||||| |||:|||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2  
PCT-US00-35064-1  
; Sequence 1, Application PC/TUS0035064  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Method for Preventing an Anaphylactic  
; FILE REFERENCE: 06510/201W01  
; CURRENT APPLICATION NUMBER: PCT/US00/35064  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/171,830  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule  
PCT-US00-35064-1

Query Match 91.8% Score 20.2; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 7.1;  
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaangttbgagatga 22  
||||||| |||:|||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3  
PCT-US00-35064-2  
; Sequence 2, Application PC/TUS0035064  
; GENERAL INFORMATION:

; APPLICANT: Raz, Eyal  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Method for Preventing an Anaphylactic  
; FILE REFERENCE: 06510/201W01  
; CURRENT APPLICATION NUMBER: PCT/US00/35064  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/171,830  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutant  
PCT-US00-35064-2

Query Match 91.8% Score 20.2; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 7.1;  
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaangttbgagatga 22  
||||||| |||:|||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 4  
PCT-US01-03029-1  
; Sequence 1, Application PC/TUS0103029  
; GENERAL INFORMATION:  
; APPLICANT: Eyal Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi  
; APPLICANT: Dennis A. Carson  
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in  
; FILE REFERENCE: 06510/166W01  
; CURRENT APPLICATION NUMBER: PCT/US01/03029  
; CURRENT FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/179,353  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory sequence  
PCT-US01-03029-1

Query Match 91.8% Score 20.2; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 7.1;  
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaangttbgagatga 22  
||||||| |||:|||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5  
PCT-US01-03029-2  
; Sequence 2, Application PC/TUS0103029  
; GENERAL INFORMATION:  
; APPLICANT: Eyal Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi



```

; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; FILE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
PCT-US01-03029-2

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgaatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttcgagatga 22

RESULT 6
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; OTHER INFORMATION: oligonucleotide primer
PCT-US01-06034-1

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgaatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttcgagatga 22

RESULT 7
PCT-US01-06034-4
; Sequence 4, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-4

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgaatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttcgagatga 22

RESULT 8
PCT-US01-10118-1
; Sequence 1, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; FILE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188W01
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
PCT-US01-10118-1

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgaatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttcgagatga 22

RESULT 9
PCT-US01-10118-3
; Sequence 3, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; FILE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188W01
; CURRENT APPLICATION NUMBER: PCT/US01/10118

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; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
PCT-US01-10118-3

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
Db 1 tgactgtgaacgttcgagatga 22
||||| ||||| ||||| |||||

RESULT 10
PCT-US01-11290-1
; Sequence 1, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; FILE OF INVENTION: Polynucleotide Vaccines
; FILE REFERENCE: 6510-203WO
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence
PCT-US01-11290-1

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
Db 1 tgactgtgaacgttcgagatga 22
||||| ||||| ||||| |||||

RESULT 11
PCT-US01-11290-2
; Sequence 2, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; FILE OF INVENTION: Polynucleotide Vaccines
; FILE REFERENCE: 6510-203WO
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; CURRENT FILING DATE: 2001-04-06

; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control nucleic acid sequence
PCT-US01-11290-2

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
Db 1 tgactgtgaacgttcgagatga 22
||||| ||||| ||||| |||||

RESULT 12
PCT-US01-14508-1
; Sequence 1, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; FILE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510/168WO1
; CURRENT APPLICATION NUMBER: PCT/US01/14508
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/262,321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
PCT-US01-14508-1

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
Db 1 tgactgtgaacgttcgagatga 22
||||| ||||| ||||| |||||

RESULT 13
PCT-US99-21203-19
; Sequence 19, Application PC/TUS9921203
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
; TITLE OF INVENTION: MUCOSAL IMMUNITY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 865 S. Figueroa Street, 29th Floor
; CITY: Los Angeles
; STATE: CA
; COUNTRY: US
; ZIP: 90017
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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/21203
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/927,120
; FILING DATE: 05 September 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-892-9200
; TELEFAX: 213-680-4518
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: non-coding oligonucleotides
; PCT-US99-21203-19
;
; Query Match 91.8%; Score 20.2; DB 1; Length 22;
; Best Local Similarity 90.9%; Pred. No. 7.1;
; Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 tgactgtgaangttbgagatga 22
; Db 1 TGACTGTGAACGTCGAGATGA 22
;
; RESULT 14
; PCT-US99-21203-20
; Sequence 20, Application PC/TUS9921203
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
; TITLE OF INVENTION: MUCOSAL IMMUNITY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 865 S. Figueroa Street, 29th Floor
; CITY: Los Angeles
; STATE: CA
; COUNTRY: US
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/21203
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/927,120
; FILING DATE: 05 September 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-892-9200
; TELEFAX: 213-680-4518
; INFORMATION FOR SEQ ID NO: 20:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: non-coding oligonucleotides
; PCT-US99-21203-20
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; Query Match 91.8%; Score 20.2; DB 1; Length 22;
; Best Local Similarity 90.9%; Pred. No. 7.1;
; Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 tgactgtgaangttbgagatga 22
; Db 1 TGACTGTGAACGTCGAGATGA 22
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; RESULT 15
; US-08-927-120-19
; Sequence 19, Application US/08927120
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: IMMUNIZATION-FREE METHODS
; TITLE OF INVENTION: FOR STIMULATING IMMUNE RESPONSIVENESS AND REDUCING
; TITLE OF INVENTION: INFLAMMATION IN A HOST
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,120
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/054001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: non-coding oligonucleotides
; US-08-927-120-19
;
; Query Match 91.8%; Score 20.2; DB 13; Length 22;
; Best Local Similarity 90.9%; Pred. No. 7.1;
; Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 tgactgtgaangttbgagatga 22
; Db 1 TGACTGTGAACGTCGAGATGA 22

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Wed Oct 10 05:59:29 2001

us-09-713-136-8.rnp

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Search completed: October 9, 2001, 21:12:47  
Job time: 20072 sec

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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:22 : Search time 1391.6 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-09-713-136-8  
Perfect score: 22  
Sequence: 1 tgactgtgaangttbgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq1:\*  
7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq2:\*  
8: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.2	91.8	22	7	US-09-802-518-1
2	20.2	91.8	22	7	US-09-802-518-7
3	20.2	91.8	22	7	US-09-802-359-1
4	20.2	91.8	22	7	US-09-802-359-7
5	20.2	91.8	22	7	US-09-802-376-1
6	20.2	91.8	22	7	US-09-802-376-7
7	20.2	91.8	22	7	US-09-802-518-8
8	20.2	90.9	22	7	US-09-802-359-8
9	20.2	90.9	22	7	US-09-802-376-8
10	19.4	88.2	22	6	US-09-770-943-1
11	19.4	88.2	22	6	US-09-770-943-2
12	19.4	88.2	22	6	US-09-770-943-10
13	19.4	88.2	22	7	US-09-802-518-10
14	19.4	88.2	22	7	US-09-802-359-9
15	19.4	88.2	22	7	US-09-802-376-9
16	18.6	84.5	22	7	US-09-802-518-2
17	18.6	84.5	22	7	US-09-802-518-4
18	18.6	84.5	22	7	US-09-802-518-6
19	18.6	84.5	22	7	US-09-802-359-2
20	18.6	84.5	22	7	US-09-802-359-4
21	18.6	84.5	22	7	US-09-802-359-6
22	18.6	84.5	22	7	US-09-802-376-2
23	18.6	84.5	22	7	US-09-802-376-4
24	18.6	84.5	22	7	US-09-802-376-6
25	17.8	80.9	22	6	US-09-770-943-3

Sequence 4, Appli  
Sequence 11, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 25987, A  
Sequence 29122, A  
Sequence 8379, Ap  
Sequence 8379, Ap  
Sequence 8379, Ap  
Sequence 5955, Ap  
Sequence 7, Appli  
Sequence 8, Appli  
Sequence 31699, A  
Sequence 2643, Ap  
Sequence 216, App  
Sequence 14097, A  
Sequence 7849, Ap  
Sequence 19415, A  
Sequence 771, App  
Sequence 4671, Ap

26 17.8 80.9 22 6 US-09-770-943-4  
27 17.8 80.9 22 7 US-09-802-518-11  
28 17.8 80.9 22 7 US-09-802-359-10  
29 17.8 80.9 22 7 US-09-802-376-10  
c 30 17 77.3 239 7 US-09-540-213-25987  
c 31 17 77.3 284 7 US-09-540-213-29122  
32 17 77.3 476 4 US-08-798-0748-8379  
33 17 77.3 476 4 US-08-798-0748-8379  
34 17 77.3 476 4 US-08-798-074C-8379  
c 35 17 77.3 480 6 US-09-904-809-5955  
36 16.2 73.6 22 6 US-09-770-943-7  
37 16.2 73.6 22 6 US-09-770-943-8  
38 16.2 73.6 445 6 US-09-909-629-31699  
39 16 72.7 403 6 US-09-688-848-2643  
40 16 72.7 442 6 US-09-836-472-216  
41 16 72.7 448 6 US-09-904-703-14097  
42 16 72.7 448 6 US-09-909-627-7849  
43 16 72.7 469 6 US-09-909-627-19415  
44 16 72.7 517 6 US-09-771-218-771  
45 16 72.7 541 5 US-09-824-130-4671

ALIGNMENTS

RESULT 1  
US-09-802-518-1  
; Sequence 1, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCES  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-1

Query Match 91.8%; Score 20.2; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.91; Mismatches 1; Indels 0; Gaps 0;  
Matches 20; Conservative 1;

QY 1 tgactgtgaangttbgagatga 22  
Db 1 tgactgtgaacgttcagatga 22  
|||||  
|||||

RESULT 2  
US-09-802-518-7  
; Sequence 7, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCES  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match          91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.91;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 3
US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match          91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.91;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 4
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match          91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.91;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 5
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match          91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.91;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 6
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7
```

us-09-713-136-8.rnpn

Wed Oct 10 05:59:30 2001

```

Query Match      91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.91;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
    |||||
Db 1 tgactgtgaangttcgagatga 22
    |||||

RESULT 7
US-09-802-518-8
; Sequence 8, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802.518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-8

Query Match      90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
    |||||
Db 1 tgactgtgaangttcgagatga 22
    |||||

RESULT 8
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-8

Query Match      90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
    |||||
Db 1 tgactgtgaangttcgagatga 22
    |||||

US-09-802-376-8
; Sequence 8, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-8

Query Match      90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
    |||||
Db 1 tgactgtgaangttcgagatga 22
    |||||

RESULT 10
US-09-770-943-1
; Sequence 1, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-1

Query Match      88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22

```

```
Db 1 tgactgtgaaggttagagatga 22
|||||
RESULT 11
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2
Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 tgactgtgaacgttagagatga 22
|||||

RESULT 12
US-09-770-943-10
; Sequence 10, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-10
Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 tgactgtgaacgttagagatga 22
|||||

RESULT 13
US-09-802-518-10
; Sequence 10, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-518-10
Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22
|||||

RESULT 14
US-09-802-359-9
; Sequence 9, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-359-9
Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22
|||||

RESULT 15
US-09-802-376-9
; Sequence 9, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
```



FILE REFERENCE: 37788201700  
CURRENT APPLICATION NUMBER: US/09/802,376  
CURRENT FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/188,557  
PRIOR FILING DATE: 2000-03-10  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polynucleotide not containing CG  
US-09-802-376-9

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 tgactgtgaangttbtagatga 22  
Db 1 tgactgtgaaggttagatga 22

Search completed: October 9, 2001, 21:36:22  
Job time: 21242 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:09 ; Search time 217.64 Seconds  
(without alignments)  
19.136 Million cell updates/sec

Title: US-09-713-136-8  
Perfect score: 22  
Sequence: 1 tgactgtgaangttbgagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	88.2	22	4	US-09-092-314-1
2	19.4	88.2	22	4	US-09-092-314-2
3	19.4	88.2	22	4	US-09-092-314-10
4	17.8	80.9	22	4	US-09-092-314-3
5	17.8	80.9	22	4	US-09-092-314-4
6	16.6	75.5	6638	2	US-08-070-301-2
7	16.2	73.6	22	4	US-09-092-314-7
8	16.2	73.6	22	4	US-09-092-314-8
9	16	72.7	2694	3	US-08-975-703-5
10	16	72.7	2694	4	US-09-515-884-5
11	15.4	70.0	1418	1	US-08-391-615-7
12	15.4	70.0	1830	4	US-09-019-931-2
13	15.4	70.0	2505	1	US-08-391-615-1
14	15.2	69.1	913	2	US-08-975-316-61
15	15	68.2	1892	2	US-08-933-750C-66
16	15	68.2	1892	3	US-09-234-613-66
17	14.6	66.4	22	4	US-09-092-314-5
18	14.6	66.4	6909	2	US-08-804-196-1
19	14.6	66.4	6909	2	US-08-658-340-1
20	14.6	66.4	6909	3	US-08-746-111-26
21	14.6	66.4	7655	1	US-08-619-554-1
22	14.4	65.5	327	4	US-09-240-274-130
23	14.4	65.5	579	1	US-07-749-446-1
24	14.4	65.5	603	4	US-08-149-101A-5
25	14.4	65.5	603	5	PCT-US94-12873-5
26	14.4	65.5	782	1	US-07-865-878A-1
27	14.4	65.5	782	2	US-08-308-736A-20

28 14.4 65.5 782 2 US-08-603-010-1 Sequence 1, Appli  
29 14.4 65.5 929 1 US-08-412-108-3 Sequence 3, Appli  
30 14.4 65.5 1093 1 US-08-525-505A-3 Sequence 3, Appli  
31 14.4 65.5 1272 4 US-09-053-702-1 Sequence 1, Appli  
32 14.4 65.5 16442 3 US-08-781-891-208 Sequence 208, App  
33 14 63.6 755 4 US-08-998-416-748 Sequence 748, App  
34 14 63.6 884 4 US-08-998-416-297 Sequence 297, App  
35 14 63.6 1146 1 US-08-487-810-1 Sequence 1, Appli  
36 14 63.6 1166 1 US-08-121-063-7 Sequence 7, Appli  
37 14 63.6 1314 1 US-07-662-005A-15 Sequence 15, Appli  
38 14 63.6 2102 3 US-08-966-318-2 Sequence 2, Appli  
39 14 63.6 2102 4 US-09-216-619-2 Sequence 2, Appli  
40 14 63.6 2231 4 US-09-008-271A-24 Sequence 24, Appli  
41 14 63.6 2572 3 US-08-976-255-1 Sequence 1, Appli  
42 14 63.6 3077 1 US-08-703-809-1 Sequence 1, Appli  
43 14 63.6 3077 1 US-08-703-808-1 Sequence 1, Appli  
44 14 63.6 3077 2 US-08-914-066-1 Sequence 1, Appli  
45 14 63.6 3077 2 US-08-703-807-1 Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-09-092-314-1  
; Sequence 1, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-1

Query Match 88.2%; Score 19.4; DB 4; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.18;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22  
||||||| ||| |||||  
Db 1 tgactgtgaagttgagatga 22

RESULT 2  
US-09-092-314-2  
; Sequence 2, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092.314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match      88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 3
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match      88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 4
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 5
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 6
US-08-070-301-2
; Sequence 2, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KANINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Ohji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
```

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; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687
; FILING DATE: 15-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933
; FILING DATE: 31-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-106412
; FILING DATE: 24-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-205475
; FILING DATE: 02-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-22830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-040
; TELEFAX: (202) 835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Horse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..3070
; US-08-070-301-2

Query Match 75.5%; Score 16.6; DB 2; Length 6638;
Best Local Similarity 85.0%; Pred. No. 14;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttbgagatg 21
||||| | | | |
Db 2380 GACTGTGATGTTGGAGATG 2399

RESULT 7
US-09-092-314-7
; Sequence 7, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; PATENT NO. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US/09/092,314
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 6638
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-092-314-7
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; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-092-314-7

Query Match 73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 7.4;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| | | | |
Db 1 tgactgtgaangttbgagatga 22

RESULT 8
US-09-092-314-8
; Sequence 8, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; PATENT NO. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-092-314-8

Query Match 73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 7.4;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| | | | |
Db 1 tgactgtgaangttbgagatga 22

RESULT 9
US-08-975-703-5
; Sequence 5, Application US/08975703
; Patent No. 6030832
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Bartel, Paul L.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESS: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
```

```
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,703
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2318-0174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2691
US-08-975-703-5

Query Match 72.7%; Score 16; DB 3; Length 2694;
Best Local Similarity 81.0%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttbgagatga 22
||||| ||| ||| ||| |||
Db 1785 GACTGAGAACTTTTATGATGA 1805

RESULT 10
US-09-515-884-5
Sequence 5, Application US/09515884
Patent No. 6235263
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
Teng, David H.-F.
Tavtigian, Sean V.
TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
Protein
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Flagg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
Tower
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,884
FILING DATE: 29-Feb-2000
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,703
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2318-0174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2691
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-515-884-5

Query Match 72.7%; Score 16; DB 4; Length 2694;
Best Local Similarity 81.0%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttbgagatga 22
||||| ||| ||| ||| |||
Db 1785 GACTGAGAACTTTTATGATGA 1805

RESULT 11
US-08-391-615-7
Sequence 7, Application US/08391615
Patent No. 5550054
GENERAL INFORMATION:
APPLICANT: Witte, Owen
APPLICANT: Tsukada, Satoshi
APPLICANT: Saffran, Douglas
APPLICANT: Rawlings, David
TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,615
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,449
FILING DATE: 21-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1
```

us-09-713-136-8.rni

Wed Oct 10 05:59:28 2001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299 FHT UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1418 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-391-615-7

Query Match 70.0%; Score 15.4; DB 1; Length 1418;  
Best Local Similarity 77.3%; Pred. No. 41;  
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22  
||||| ||||| || : ||||| ||  
Db 218 TGACTTTGAACGCTGGGAGA 239

RESULT 12  
US-09-019-931-2  
Sequence 2, Application US/09019931  
Patent No. 6194148  
GENERAL INFORMATION:  
APPLICANT: Hori, Kunio, Takahashi, Takeo, Okada, Takao  
TITLE OF INVENTION: A Method For Detecting A Hybridized  
TITLE OF INVENTION: Nucleic Acid Molecule  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Frischauf, Holtz, Goodman, Langer & Chick  
STREET: 767 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10017-2023

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3+ inch, 1.44 mb diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/019,931  
FILING DATE: 06-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 9-025291  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Barth, Richard  
REGISTRATION NUMBER: 28,180  
REFERENCE/DOCKET NUMBER: 980048/HG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 319-4900  
TELEFAX: (212) 319-5101  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
IMMEDIATE SOURCE:  
LIBRARY: PGEX-PH  
US-09-019-931-2

Query Match 70.0%; Score 15.4; DB 4; Length 1830;  
Best Local Similarity 77.3%; Pred. No. 43;  
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22  
||||| ||||| || : ||||| ||  
Db 881 TGACTTTGAACGCTGGGAGA 902

RESULT 13  
US-08-391-615-1  
Sequence 1, Application US/08391615  
Patent No. 5550054  
GENERAL INFORMATION:  
APPLICANT: Witte, Owen  
APPLICANT: Tsukada, Satoshi  
APPLICANT: Saffran, Douglas  
APPLICANT: Rawlings, David  
TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/391,615  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/006,449  
FILING DATE: 21-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299 FHT UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2505 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 137..2116  
US-08-391-615-1

Query Match 70.0%; Score 15.4; DB 1; Length 2505;  
Best Local Similarity 77.3%; Pred. No. 45;  
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22  
||||| ||||| || : ||||| ||  
Db 262 TGACTTTGAACGCTGGGAGA 283

RESULT 14  
US-08-975-316-61  
Sequence 61, Application US/08975316  
Patent No. 5952486  
GENERAL INFORMATION:  
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka

APPLICANT: and GRIERSON, Alastair W.  
TITLE OF INVENTION: MATERIALS AND METHODS FOR  
THE MODIFICATION OF PLANT LIGNIN CONTENT  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,316  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/713,000  
FILING DATE: September 11, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: SLEATH, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000/1003C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 913 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-975-316-61

Query Match 69.1%; Score 15.2; DB 2; Length 913;  
Best Local Similarity 81.0%; Pred. No. 47;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gactgtgaangttbgagatga 22  
||||||| || |||||  
Db 513 GACTGTGAATTTTACAGATGA 533

RESULT 15  
US-08-933-750C-66/c  
Sequence 66, Application US/08933750C  
Patent No. 5932442  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Bandman, Olga  
APPLICANT: Shah, Purvi  
APPLICANT: Au-Young, Janice  
APPLICANT: Yue, Henry  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933.750C  
FILING DATE: September 23, 1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ballings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0356 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1892 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BRSTNOT03  
CLONE: 641127  
US-08-933-750C-66

Query Match 68.2%; Score 15; DB 2; Length 1892;  
Best Local Similarity 80.0%; Pred. No. 68;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db 1278 TGAATGTGAAGGTTGAGCT 1259

Search completed: October 9, 2001, 15:42:10  
Job time: 300 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:20:40 ; Search time 2150.93 Seconds  
(without alignments)  
158.206 Million cell updates/sec

Title: US-09-713-136-9  
Perfect score: 22  
Sequence: 1 tgactgtgaagggttagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
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2: gb\_ba2: \*  
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4: gb\_in1: \*  
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6: gb\_in3: \*  
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20: em\_htgo\_inv: \*  
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24: em\_htg\_hum3: \*  
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43: em\_or: \*

44: em\_ov: \*  
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48: em\_ro: \*  
49: em\_sts: \*  
50: em\_sy: \*  
51: em\_un: \*  
52: em\_vi: \*  
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55: gb\_sts3: \*  
56: gb\_sy: \*  
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58: gb\_vil: \*  
59: gb\_vil2: \*  
60: gb\_htg1: \*  
61: gb\_htg2: \*  
62: gb\_htg3: \*  
63: gb\_htg4: \*  
64: gb\_htg5: \*  
65: gb\_htg6: \*  
66: gb\_htg7: \*  
67: gb\_htg8: \*  
68: gb\_htg9: \*  
69: gb\_htg10: \*  
70: gb\_htg11: \*  
71: gb\_htg12: \*  
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73: gb\_htg14: \*  
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81: gb\_htg22: \*  
82: gb\_htg23: \*  
83: gb\_htg24: \*  
84: gb\_htg25: \*  
85: gb\_pr1: \*  
86: gb\_pr2: \*  
87: gb\_pr3: \*  
88: gb\_pr4: \*  
89: gb\_pr5: \*  
90: gb\_pr6: \*  
91: gb\_pr7: \*  
92: gb\_pr8: \*  
93: gb\_pr9: \*  
94: gb\_rol: \*  
95: gb\_rol2: \*  
96: gb\_in4: \*  
97: gb\_pr10: \*  
98: em\_ba3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	100.0	22	9	AX036944 Sequence
2	20	90.9	22	10	AX083682 Sequence
3	20	90.9	183869	73	AC068700 Sequence
4	19.4	88.2	22	10	AX083681 Sequence
5	18.8	85.5	22	9	AX036945 Sequence
6	18.8	85.5	22	9	AX036952 Sequence
7	18.8	85.5	22	9	AX046993 Sequence
8	18.8	85.5	22	10	AX083675 Sequence



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9      18.8      85.5 171790 62 AC011106
c 10 18.8      85.5 173506 64 AC016323
11 18.8      85.5 195308 74 AC073525
12 18.8      85.5 201579 73 AC068773
13 18.4      83.6 50487 73 AC068211
14 18.4      83.6 121682 78 ALI39127
15 18.4      83.6 125661 89 ALI38773
16 18.4      83.6 136282 84 HSDJ368B9
c 17 18.4      83.6 231787 78 ALI38774
18 17.8      80.9 7031 94 AF320616
19 17.8      80.9 100000 85 AB020870
20 17.8      80.9 100000 85 AB020870
c 21 17.8      80.9 150803 74 AC073490
22 17.8      80.9 165337 70 AC027442
23 17.8      80.9 167237 86 AC007938
24 17.8      80.9 170056 77 AC087643
25 17.8      80.9 170056 77 AC087643
c 26 17.8      80.9 172974 68 AC024605
27 17.8      80.9 174829 76 AC079611
c 28 17.8      80.9 180223 73 AC068979
29 17.8      80.9 181371 65 AC018893
c 30 17.8      80.9 191442 63 AC015551
31 17.8      80.9 194485 76 AC084030
c 32 17.8      80.9 200203 72 AC053510
33 17.8      80.9 201214 75 AC074012
34 17.8      80.9 209777 69 AC024934
35 17.8      80.9 215434 65 AC019214
36 17.4      79.1 38247 15 SPCC1259
37 17.4      79.1 103009 34 AC087261
38 17.4      79.1 103009 88 AC087225
c 39 17.4      79.1 113803 85 AC004460
40 17.4      79.1 152141 97 HSU07000
c 41 17.4      79.1 158738 63 AC015500
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## ALIGNMENTS

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RESULT 1
LOCUS AX036944 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 1 from Patent FR2790955.
ACCESSION AX036944
VERSION AX036944.1 GI:11226372
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 1 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
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1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note=" oligodesoxynucleotide"
7 a 1 c 8 g 6 t

BASE COUNT 7 a 1 c 8 g 6 t
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1 tgactgtgaagggttagagatga 22
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Query Match 100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
|||||
Db 1 TGACTGTGAAGGTTAGAGATGA 22

RESULT 3
LOCUS AC068700/c
DEFINITION Homo sapiens chromosome 8 clone RP11-594N15 map 8, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
ACCESSION AC068700
VERSION AC068700.2 GI:8705190
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183869)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
2 (bases 1 to 183869)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepei,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeAtrellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,K., Rogov,P., Rothman,D.,

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Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (06-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jun 25, 2000 this sequence version replaced gi:7712246.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L9833  
 Center clone name: 594\_N\_15  
 ----- Summary Statistics  
 Sequencing vector: M13; M7815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 169522 bases at least Q40  
 Consensus quality: 177186 bases at least Q30  
 Consensus quality: 180474 bases at least Q20  
 Insert size: 182000; agarose-fp  
 Insert size: 182269; sum-of-contigs  
 Quality coverage: 3.8 in Q20 bases; agarose-fp  
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
 \* 1 1728: contig of 1728 bp in length  
 \* 1729 1828: gap of 100 bp  
 \* 1829 2828: contig of 1000 bp in length  
 \* 2829 2928: gap of 100 bp  
 \* 2929 4130: contig of 1202 bp in length  
 \* 4131 4230: gap of 100 bp  
 \* 4231 5550: contig of 1320 bp in length  
 \* 5551 5650: gap of 100 bp  
 \* 5651 10072: contig of 4422 bp in length  
 \* 10073 10172: gap of 100 bp  
 \* 10173 13473: contig of 3301 bp in length  
 \* 13474 13573: gap of 100 bp  
 \* 13574 20194: contig of 6621 bp in length  
 \* 20195 20294: gap of 100 bp  
 \* 20295 26102: contig of 5808 bp in length  
 \* 26103 26202: gap of 100 bp  
 \* 26203 33812: contig of 7610 bp in length  
 \* 33813 33912: gap of 100 bp  
 \* 33913 41322: contig of 7410 bp in length  
 \* 41323 41422: gap of 100 bp  
 \* 41423 48506: contig of 7084 bp in length  
 \* 48507 48606: gap of 100 bp  
 \* 48607 59193: contig of 10587 bp in length  
 \* 59194 59293: gap of 100 bp  
 \* 59294 70633: contig of 11342 bp in length  
 \* 70636 70735: gap of 100 bp  
 \* 70736 88617: contig of 17882 bp in length  
 \* 88618 88717: gap of 100 bp  
 \* 88718 112714: contig of 23997 bp in length  
 \* 112715 112814: gap of 100 bp  
 \* 112815 141242: contig of 28428 bp in length  
 \* 141243 141342: gap of 100 bp  
 \* 141343 183869: contig of 42527 bp in length.

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 /chromosome="8"  
 /map="8"  
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 1..1728  
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 1829..2828  
 /note="assembly\_fragment"  
 2929..4130  
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 5651..10072  
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 10173..13473  
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 13574..20194  
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 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 119504 TGACTGTGAAGGTTAGAGAT 119485  
 RESULT 4  
 AX083681  
 LOCUS AX083681 22 bp DNA  
 DEFINITION Sequence 7 from Patent WO0112223.  
 ACCESSION AX083681  
 VERSION AX083681.1 GI:13185413  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct.  
 synthetic construct  
 artificial sequence.  
 1 (bases 1 to 22)  
 van Nest,G.  
 METHODS of modulating an immune response using immunostimulatory s  
 Methodes and compositions for use therein  
 Patent: WO 0112223-A 7 22-FEB-2001;  
 Dynavax Technologies Corporation (US)  
 JOURNAL

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FEATURES
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 TGACTGTGAAGTTCGAGATGA 22

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DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 TGACTGTGAACGTTTCGAGATGA 22

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DEFINITION Sequence 9 from Patent FR2790955.
ACCESSION AX036952
VERSION AX036952.1 GI:11226380
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier A.
JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
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Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagatga 22
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Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 7
LOCUS AX046993 22 bp DNA PAT 15-DEC-2000
DEFINITION Sequence 2 from Patent WO0067787.
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss, R.B.
JOURNAL HIV immunogenic compositions and methods
Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
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Query Match      85.5%; Score 18.8; DB 9; Length 22;
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from Patent WO0112223.
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VERSION AX083675.1 GI:13185407
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest, G.
JOURNAL Methods of modulating an immune response using immunostimulatory s
quences and compositions for use therein
Patent: WO 0112223-A 1 22-FEB-2001;
Dynavax Technologies Corporation (US)
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9  
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LOCUS Homo sapiens chromosome 3 clone RP11-400P3 map 3, \*\*\* SEQUENCING IN  
DEFINITION PROGRESS \*\*\*, 42 unordered pieces.  
AC011106  
AC011106.2 GI:6479142  
VERSION  
KEYWORDS HTG: HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 171790)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens chromosome 3, clone RP11-400P3  
Unpublished  
2 (bases 1 to 171790)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhvalter,B.,  
Brown,A., Castler,A., Colangelo,M., Collins,S., Collymore,A.,  
Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,  
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,  
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,  
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,  
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 30, 1999 this sequence version replaced gi:6006223.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RN/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submission@genome.wi.mit.edu  
----- Project Information  
Center project name: L1839  
Center clone name: 400\_P\_3  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 42 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 1154: contig of 1154 bp in length  
\* gap of unknown length  
\* 1155 2246: contig of 1092 bp in length  
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\* 2247 3610: contig of 1364 bp in length  
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\* 3611 4929: contig of 1319 bp in length  
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\* 4930 6513: contig of 1584 bp in length  
\* gap of unknown length  
\* 6514 7865: contig of 1352 bp in length  
\* gap of unknown length

7866 9274: contig of 1409 bp in length  
gap of unknown length  
9275 10813: contig of 1539 bp in length  
gap of unknown length  
10814 12951: contig of 2138 bp in length  
gap of unknown length  
12952 14173: contig of 1222 bp in length  
gap of unknown length  
14174 16264: contig of 2091 bp in length  
gap of unknown length  
16265 17933: contig of 1669 bp in length  
gap of unknown length  
17934 19427: contig of 1494 bp in length  
gap of unknown length  
19428 20694: contig of 1267 bp in length  
gap of unknown length  
20695 23140: contig of 2446 bp in length  
gap of unknown length  
23141 25542: contig of 2402 bp in length  
gap of unknown length  
25543 29256: contig of 3714 bp in length  
gap of unknown length  
29257 31894: contig of 2638 bp in length  
gap of unknown length  
31895 35730: contig of 3836 bp in length  
gap of unknown length  
35731 37730: contig of 2000 bp in length  
gap of unknown length  
37731 40878: contig of 3148 bp in length  
gap of unknown length  
40879 43394: contig of 2516 bp in length  
gap of unknown length  
43395 46817: contig of 3423 bp in length  
gap of unknown length  
46818 50213: contig of 3396 bp in length  
gap of unknown length  
50214 53478: contig of 3265 bp in length  
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53479 58333: contig of 4855 bp in length  
gap of unknown length  
58334 61663: contig of 3330 bp in length  
gap of unknown length  
61664 64521: contig of 2858 bp in length  
gap of unknown length  
64522 69899: contig of 5378 bp in length  
gap of unknown length  
69900 75112: contig of 5213 bp in length  
gap of unknown length  
75113 79169: contig of 4057 bp in length  
gap of unknown length  
79170 84604: contig of 5435 bp in length  
gap of unknown length  
84605 88809: contig of 4205 bp in length  
gap of unknown length  
88810 92798: contig of 3989 bp in length  
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92799 100287: contig of 7489 bp in length  
gap of unknown length  
100288 106455: contig of 6168 bp in length  
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106456 114533: contig of 8078 bp in length  
gap of unknown length  
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123378 131249: contig of 7872 bp in length  
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131250 141016: contig of 9767 bp in length  
gap of unknown length  
141017 152525: contig of 11509 bp in length  
gap of unknown length  
152526 171790: contig of 19265 bp in length.  
Location/Qualifiers  
1. 171790

FEATURES  
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chr="3"
/clone="RP11-400P3"
/clone_lib="RPC1-11 Human Male BAC"
BASE COUNT 49228 a 37059 c 37358 g 48110 t 35 others
ORIGIN

Query Match      85.5%; Score 18.8; DB 62; Length 171790;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TGACTGTAAGGTTAGAGATGA 22
   ||| ||| ||| ||| ||| |||
Db 31193 TGATTGTGAAGGTGAGAGATGA 31214

RESULT 10
AC016323/c      173506 bp      DNA      HTG      21-APR-2000
LOCUS           Homo sapiens clone RP11-29G15, WORKING DRAFT SEQUENCE, 24 unordered
DEFINITION      pieces.
ACCESSION       AC016323
VERSION         AC016323.4 GI:7630675
KEYWORDS        HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173506)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-29G15
Unpublished
2 (bases 1 to 173506)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Collangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Horton,L.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 21, 2000 this sequence version replaced gi:6850421.
All repeats were identified using RepeatMasker:
Snit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4831
Center clone name: 29_G15
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 157003 bases at least Q40
Consensus quality: 164655 bases at least Q30
Consensus quality: 167889 bases at least Q20
Insert size: 183000; agarose-fp

Insert size: 171206; sum-of-contigs
Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality coverage: 3.7 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1485: contig of 1485 bp in length
* 1486 1585: gap of 100 bp
* 1586 2613: contig of 1028 bp in length
* 2614 2713: gap of 100 bp
* 2714 3169: contig of 456 bp in length
* 3170 3269: gap of 100 bp
* 3270 5955: contig of 2686 bp in length
* 5956 6055: gap of 100 bp
* 6056 7651: contig of 1596 bp in length
* 7652 7751: gap of 100 bp
* 7752 9634: contig of 1903 bp in length
* 9635 9754: gap of 100 bp
* 9755 10982: contig of 1228 bp in length
* 10983 11082: gap of 100 bp
* 11083 14021: contig of 2939 bp in length
* 14022 14121: gap of 100 bp
* 14122 17251: contig of 3130 bp in length
* 17252 17351: gap of 100 bp
* 17352 21912: contig of 4561 bp in length
* 21913 22012: gap of 100 bp
* 22013 25748: contig of 3736 bp in length
* 25749 25848: gap of 100 bp
* 25849 30769: contig of 4921 bp in length
* 30770 30869: gap of 100 bp
* 30870 35835: contig of 4966 bp in length
* 35836 35935: gap of 100 bp
* 35936 39836: contig of 3901 bp in length
* 39837 39936: gap of 100 bp
* 39937 48353: contig of 8417 bp in length
* 48354 48453: gap of 100 bp
* 48454 57952: contig of 9499 bp in length
* 57953 58052: gap of 100 bp
* 58053 68259: contig of 10207 bp in length
* 68260 68359: gap of 100 bp
* 68360 76540: contig of 8181 bp in length
* 76541 76640: gap of 100 bp
* 76641 85924: contig of 9284 bp in length
* 85925 86024: gap of 100 bp
* 86025 98936: contig of 12912 bp in length
* 98937 99036: gap of 100 bp
* 99037 110947: contig of 11911 bp in length
* 110948 111047: gap of 100 bp
* 111048 126572: contig of 15525 bp in length
* 126573 126672: gap of 100 bp
* 126673 143956: contig of 17284 bp in length
* 143957 144056: gap of 100 bp
* 144057 173506: contig of 29450 bp in length.

FEATURES
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                           /clone_lib="RPC1-11 Human Male BAC"
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            misc_feature   1586..2613
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            misc_feature   2714..3169
                           /note="assembly_fragment"
                           vector_side:right

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\* as soon as it is available and the accession number will  
\* be preserved.

\* 92251: contig of 92251 bp in length  
\* 92251: gap of unknown length  
\* 92352  
\* 115219: contig of 22868 bp in length  
\* 115220  
\* 115319: gap of unknown length  
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\* 130980: contig of 15661 bp in length  
\* 130981  
\* 131080: gap of unknown length  
\* 131081  
\* 140758: contig of 9678 bp in length  
\* 140759  
\* 140858: gap of unknown length  
\* 140859  
\* 143950: contig of 3092 bp in length  
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\* 144050: gap of unknown length  
\* 144051  
\* 146265: contig of 2215 bp in length  
\* 146266  
\* 146365: gap of unknown length  
\* 146366  
\* 149065: contig of 2700 bp in length  
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\* 149165: gap of unknown length  
\* 149166  
\* 150935: contig of 1670 bp in length  
\* 150936  
\* 150935: gap of unknown length  
\* 150936  
\* 152644: contig of 1709 bp in length  
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\* 152744: gap of unknown length  
\* 152745  
\* 154629: contig of 1885 bp in length  
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\* 154729: gap of unknown length  
\* 154730  
\* 156167: contig of 1438 bp in length  
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\* 156267: gap of unknown length  
\* 156268  
\* 157702: contig of 1435 bp in length  
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\* 164699: contig of 1322 bp in length  
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\* 164799: gap of unknown length  
\* 164800  
\* 166225: contig of 1426 bp in length  
\* 166226  
\* 166325: gap of unknown length  
\* 166326  
\* 168051: contig of 1726 bp in length  
\* 168052  
\* 168151: gap of unknown length  
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\* 169384: contig of 1213 bp in length  
\* 169385  
\* 169464: gap of unknown length  
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\* 171125: contig of 1661 bp in length  
\* 171126  
\* 171235: gap of unknown length  
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\* 172510: contig of 1285 bp in length  
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\* 174029: gap of unknown length  
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\* 175488: contig of 1459 bp in length  
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\* 177362: contig of 1774 bp in length  
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\* 177462: gap of unknown length  
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\* 178962: contig of 1500 bp in length  
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\* 180184: contig of 1122 bp in length  
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\* 181420: contig of 1136 bp in length  
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\* 184094: contig of 1121 bp in length  
\* 184095  
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\* 184195  
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\* 185436: gap of unknown length  
\* 185437  
\* 186747: contig of 1311 bp in length  
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\* 187917: contig of 1070 bp in length  
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\* 188017: gap of unknown length  
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\* 189057: contig of 1080 bp in length  
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\* 189197: gap of unknown length  
\* 189198  
\* 190398: contig of 1201 bp in length  
\* 190399  
\* 190498: gap of unknown length  
\* 190499  
\* 191607: contig of 1109 bp in length

\* 191608 191707: gap of unknown length  
\* 191708 192719: contig of 1012 bp in length  
\* 192720 192819: gap of unknown length  
\* 192820 193588: contig of 1039 bp in length  
\* 193859 193958: gap of unknown length  
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ORIGIN  
  
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Best Local Similarity 90.9%; Pred. No. 51;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 tgactgtgaaggtagagatga 22  
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Db 182471 TGAATGAGGTGAGAGATGA 182492  
  
RESULT 12  
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LOCUS  
DEFINITION Homo sapiens chromosome 3 clone RP11-875H7, WORKING DRAFT SEQUENCE,  
19 unordered pieces.  
AC068773  
AC068773.12 GI:10645231  
VERSION  
KEYWORDS HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 201579)  
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,  
Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Banks,T., Barberia,J.,  
Benton,J., Blmage,K., Blankenburg,K., Bonnin,D., Bouck,J.,  
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,  
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,  
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,  
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,  
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,  
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,  
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,  
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,  
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,  
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,  
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,  
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Haves,A.,  
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,  
Hollins,B., Homsí,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,  
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,  
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,  
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,  
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,  
Louisege,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,  
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,  
Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,  
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,  
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,  
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,  
Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,  
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,  
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,  
Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoostari,N.,  
Slisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,  
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,  
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,  
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,

Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,  
Watlington, S., Williams, G., Williamson, A., Wleczky, R., Woodson, S.,  
Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.  
and Gibbs, R.  
Direct Submission  
2 (bases 1 to 201579)  
Worley, K.C.  
Submitted (09-MAY-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Oct 5, 2000 this sequence version replaced gi:9665007.  
-----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
-----  
Project Information  
Center project name: HBHM  
Center clone name: RP11-875H7  
-----  
Summary Statistics  
Sequencing vector: M13; L08821  
Chemistry: Dye-terminator Big Dye; 7% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 179484 bases at least Q40  
Consensus quality: 189049 bases at least Q30  
Consensus quality: 194048 bases at least Q20  
Estimated insert size: 197176; sum-of-contigs estimation  
Quality coverage: 0x in Q20 bases; agarose-fp estimation  
Quality coverage: 3.7x in Q20 bases; sum-of-contigs estimation  
-----

NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 19 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.  
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1 26889: contig of 26889 bp in length  
26890: gap of unknown length  
26990: contig of 21923 bp in length  
48912: gap of unknown length  
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71859: gap of unknown length  
71959: contig of 19513 bp in length  
91473: gap of unknown length  
91573: contig of 19055 bp in length  
110627: gap of unknown length  
110828: contig of 14127 bp in length  
124834: gap of unknown length  
124954: contig of 17275 bp in length  
124955: gap of unknown length  
142229: contig of 16058 bp in length  
142330: gap of unknown length  
158387: contig of 4662 bp in length  
158488: gap of unknown length  
164949: contig of 5773 bp in length  
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170923: gap of unknown length  
174867: contig of 4800 bp in length  
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184887: contig of 4168 bp in length  
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189386: gap of unknown length  
193553: gap of unknown length  
193554: gap of unknown length

NOTE: This is a 'working draft' sequence. It currently  
consists of 19 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.  
-----  
1 26889: contig of 26889 bp in length  
26890: gap of unknown length  
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91573: contig of 19055 bp in length  
110627: gap of unknown length  
110828: contig of 14127 bp in length  
124834: gap of unknown length  
124954: contig of 17275 bp in length  
124955: gap of unknown length  
142229: contig of 16058 bp in length  
142330: gap of unknown length  
158387: contig of 4662 bp in length  
158488: gap of unknown length  
164949: contig of 5773 bp in length  
165049: gap of unknown length  
170822: contig of 3945 bp in length  
170923: gap of unknown length  
174867: contig of 4800 bp in length  
174967: gap of unknown length  
179768: contig of 4519 bp in length  
179868: gap of unknown length  
184387: contig of 4799 bp in length  
184486: gap of unknown length  
184887: contig of 4168 bp in length  
189285: gap of unknown length  
189286: contig of 4168 bp in length  
189386: gap of unknown length  
193553: gap of unknown length  
193554: gap of unknown length

\* 193654 195798: contig of 2145 bp in length  
\* 195799 195898: gap of unknown length  
\* 195899 197854: contig of 1956 bp in length  
\* 197855 197954: gap of unknown length  
\* 197955 200320: contig of 2366 bp in length  
\* 200321 200420: gap of unknown length  
\* 200421 201579: contig of 1159 bp in length.  
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Location/Qualifiers  
1..201579  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
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BASE COUNT 55675 a 43175 c 42625 g 58257 t 1847 others  
ORIGIN

Query Match 85.5%; Score 18.8; DB 73; Length 201579;  
Best Local Similarity 90.9%; Pred. No. 51;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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QY 1 tgactgtgaaggttagagatga 22  
|||||  
Db 52875 TGATTGTGAAGGTGAGAGATGA 52854  
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RESULT 13  
AC068211/c  
AC068211/c  
LOCUS  
DEFINITION  
Homo sapiens chromosome 4 clone RP11-510P6 map 4, LOW-PASS SEQUENCE  
SAMPLING.  
AC068211 DNA HTG 15-JUN-2000  
AC068211.2 GI:8567828  
HTG: HTGS\_PHASE0.  
human.  
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ACCESSION  
AC068211  
VERSION  
AC068211.2  
KEYWORDS  
HTG: HTGS\_PHASE0.  
SOURCE  
human.  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
-----  
REFERENCE  
1 (bases 1 to 50487)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 4, clone RP11-510P6  
Unpublished  
2 (bases 1 to 50487)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,  
Boguslavsky, L., Bouckigalter, B., Brown, A., Burkett, G.,  
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collamore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S.,  
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,  
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehotzky, J.,  
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,  
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,  
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neill, D., Oliver, F.M., Oliver, J., Peterson, K., Pierre, N.,  
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jun 15, 2000 this sequence version replaced gi:7671271.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
-----  
Center: Whitehead Institute/ MIT Center for Genome Research

AC068211 50487 bp DNA HTG 15-JUN-2000  
Homo sapiens chromosome 4 clone RP11-510P6 map 4, LOW-PASS SEQUENCE  
SAMPLING.  
AC068211  
AC068211.2 GI:8567828  
HTG: HTGS\_PHASE0.  
human.  
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ACCESSION  
AC068211  
VERSION  
AC068211.2  
KEYWORDS  
HTG: HTGS\_PHASE0.  
SOURCE  
human.  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
-----  
REFERENCE  
1 (bases 1 to 50487)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 4, clone RP11-510P6  
Unpublished  
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehotzky, J.,  
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,  
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,  
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neill, D., Oliver, F.M., Oliver, J., Peterson, K., Pierre, N.,  
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
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Center: Whitehead Institute/ MIT Center for Genome Research

AC068211 50487 bp DNA HTG 15-JUN-2000  
Homo sapiens chromosome 4 clone RP11-510P6 map 4, LOW-PASS SEQUENCE  
SAMPLING.  
AC068211  
AC068211.2 GI:8567828  
HTG: HTGS\_PHASE0.  
human.  
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ACCESSION  
AC068211  
VERSION  
AC068211.2  
KEYWORDS  
HTG: HTGS\_PHASE0.  
SOURCE  
human.  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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REFERENCE  
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Unpublished  
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Center: Whitehead Institute/ MIT Center for Genome Research

AC068211 50487 bp DNA HTG 15-JUN-2000  
Homo sapiens chromosome 4 clone RP11-510P6 map 4, LOW-PASS SEQUENCE  
SAMPLING.  
AC068211  
AC068211.2 GI:8567828  
HTG: HTGS\_PHASE0.  
human.  
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ACCESSION  
AC068211  
VERSION  
AC068211.2  
KEYWORDS  
HTG: HTGS\_PHASE0.  
SOURCE  
human.  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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REFERENCE  
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Homo sapiens chromosome 4, clone RP11-510P6  
Unpublished  
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Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jun 15, 2000 this sequence version replaced gi:7671271.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
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Center: Whitehead Institute/ MIT Center for Genome Research



Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project information  
 Center project name: L10078  
 Center clone name: 510\_P\_6  
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 \* NOTE: This record contains 64 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.  
 \*  
 \* 1 692: contig of 692 bp in length  
 \* 693 792: gap of 100 bp  
 \* 793 1480: contig of 688 bp in length  
 \* 1481 1580: gap of 100 bp  
 \* 1581 2274: contig of 694 bp in length  
 \* 2275 2374: gap of 100 bp  
 \* 2375 3068: contig of 694 bp in length  
 \* 3069 3168: gap of 100 bp  
 \* 3169 3868: contig of 700 bp in length  
 \* 3869 3968: gap of 100 bp  
 \* 3969 4677: contig of 709 bp in length  
 \* 4678 4777: gap of 100 bp  
 \* 4778 5497: contig of 720 bp in length  
 \* 5498 5597: gap of 100 bp  
 \* 5598 6280: contig of 683 bp in length  
 \* 6281 6380: gap of 100 bp  
 \* 6381 7062: contig of 682 bp in length  
 \* 7063 7162: gap of 100 bp  
 \* 7163 7858: contig of 696 bp in length  
 \* 7859 7958: gap of 100 bp  
 \* 7959 8643: contig of 685 bp in length  
 \* 8644 8743: gap of 100 bp  
 \* 8744 9462: contig of 719 bp in length  
 \* 9463 9562: gap of 100 bp  
 \* 9563 10243: contig of 681 bp in length  
 \* 10244 10343: gap of 100 bp  
 \* 10344 11021: contig of 678 bp in length  
 \* 11022 11121: gap of 100 bp  
 \* 11122 11832: contig of 711 bp in length  
 \* 11833 11932: gap of 100 bp  
 \* 11933 12635: contig of 703 bp in length  
 \* 12636 12735: gap of 100 bp  
 \* 12736 13454: contig of 719 bp in length  
 \* 13455 13554: gap of 100 bp  
 \* 13555 14247: contig of 693 bp in length  
 \* 14248 14347: gap of 100 bp  
 \* 14348 15042: contig of 695 bp in length  
 \* 15043 15142: gap of 100 bp  
 \* 15143 15823: contig of 681 bp in length  
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 \* 15924 16617: contig of 694 bp in length  
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 \* 16718 17386: contig of 669 bp in length  
 \* 17387 17486: gap of 100 bp  
 \* 17487 18178: contig of 692 bp in length  
 \* 18179 18278: gap of 100 bp  
 \* 18279 18979: contig of 701 bp in length  
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 \* 19781 19880: gap of 100 bp  
 \* 19881 20555: contig of 675 bp in length  
 \* 20556 20655: gap of 100 bp  
 \* 20656 21327: contig of 672 bp in length  
 \* 21328 21427: gap of 100 bp  
 \* 21428 22111: contig of 684 bp in length

22112 22211: gap of 100 bp  
 22212 22882: contig of 671 bp in length  
 22883 22982: gap of 100 bp  
 22983 23676: contig of 694 bp in length  
 23677 23776: gap of 100 bp  
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 24485 24584: gap of 100 bp  
 24585 25284: contig of 700 bp in length  
 25285 25384: gap of 100 bp  
 25385 26079: contig of 695 bp in length  
 26080 26179: gap of 100 bp  
 26180 26860: contig of 681 bp in length  
 26861 26960: gap of 100 bp  
 26961 27674: contig of 714 bp in length  
 27675 27774: gap of 100 bp  
 27775 28463: contig of 689 bp in length  
 28464 28563: gap of 100 bp  
 28564 29246: contig of 683 bp in length  
 29247 29346: gap of 100 bp  
 29347 30031: contig of 685 bp in length  
 30032 30131: gap of 100 bp  
 30132 30816: contig of 685 bp in length  
 30817 30916: gap of 100 bp  
 30917 31620: contig of 704 bp in length  
 31621 31720: gap of 100 bp  
 31721 32386: contig of 666 bp in length  
 32387 32486: gap of 100 bp  
 32487 33154: contig of 668 bp in length  
 33155 33254: gap of 100 bp  
 33255 33931: contig of 677 bp in length  
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 35505 35604: gap of 100 bp  
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 42597 42696: gap of 100 bp  
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 44202 44301: gap of 100 bp  
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 45748 45847: gap of 100 bp  
 45848 46525: contig of 678 bp in length  
 46526 46625: gap of 100 bp  
 46626 47313: contig of 688 bp in length  
 47314 47413: gap of 100 bp  
 47414 48102: contig of 689 bp in length  
 48103 48202: gap of 100 bp  
 48203 48893: contig of 691 bp in length  
 48894 48993: gap of 100 bp  
 48994 49683: contig of 690 bp in length  
 49684 49783: gap of 100 bp  
 49784 50487: contig of 704 bp in length.

Location/Qualifiers

FEATURES

\* 118077 121682: contig of 3606 bp in length.

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/db\_xref="taxon:9606"  
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clone\_end:SP6  
vector\_side:left"  
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/note="assembly\_fragment:01300  
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66408. .112097  
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fragment\_chain:1"  
112198. .117976  
/note="assembly\_fragment:00252  
fragment\_chain:1"  
118077. .121682  
/note="assembly\_fragment:00060  
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Best Local Similarity 95.0%; Pred. No. 81;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 gactgtgaaggttagatg 21  
|| ||||| ||||| |||||  
Db 79149 GAATGTGAAGGTAGAGATG 79168  
RESULT 15  
AL138773 125661 bp DNA PRI 26-SEP-2000  
LOCUS  
DEFINITION Human DNA sequence from clone RP4-660B20 on chromosome 10 Contains STSS, GSSs and a CpG island, complete sequence.  
ACCESSION AL138773  
VERSION AL138773.4 GI:7801531  
KEYWORDS HTG; CpG island.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 125661)  
AUTHORS Chapman, J.  
TITLE Direct Submission  
JOURNAL Submitted (08-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerquest@sanger.ac.uk  
COMMENT On May 14, 2000 this sequence version replaced gi:7799640. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at

source  
1. .50487  
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/db\_xref="taxon:9606"  
/chromosome="4"  
/map="4"  
/clone="rp11-510P6"  
/clone\_lib="RPC1-11 Human Male BAC"  
BASE COUNT 9358 a 12945 c 11645 g 9887 t 6652 others  
ORIGIN  
Query Match 83.6%; Score 18.4; DB 73; Length 50487;  
Best Local Similarity 95.0%; Pred. No. 78;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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||||| ||||| |||||  
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RESULT 14  
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LOCUS  
DEFINITION Homo sapiens chromosome 10 clone RP5-964H6 map p14-15.3, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 5 unordered pieces.  
ACCESSION AL139127  
VERSION AL139127.3 GI:9931359  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 121682)  
AUTHORS Sims, S.  
TITLE Direct Submission  
JOURNAL Submitted (19-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerquest@sanger.ac.uk  
COMMENT On Aug 28, 2000 this sequence version replaced gi:9863522.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: dj964H6  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 119498 bases at least Q40  
Consensus quality: 120247 bases at least Q30  
Consensus quality: 120704 bases at least Q20  
Insert size: 121282; sum-of-contigs  
Insert size: 131684; 5.8% error; agarose-fp  
Quality coverage: 4.1ix in Q20 bases; sum-of-contigs Quality coverage: 3.35x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
\* 1 59702: contig of 59702 bp in length  
\* 59703 59802: gap of 100 bp  
\* 59803 66307: contig of 6505 bp in length  
\* 66308 66407: gap of 100 bp  
\* 66408 112097: contig of 45690 bp in length  
\* 112098 112197: gap of 100 bp  
\* 112198 117976: contig of 5779 bp in length  
\* 117977 118076: gap of 100 bp



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misc_feature      /note="match: GSS: Em:AQ076707"
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complement(35050..35753)
repeat_region     /note="match: GSS: Em:AQ508227"
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misc_feature      /note="AluYb8 repeat: matches 243..304 of consensus"
35376..35492
repeat_region     /note="MSTB repeat: matches 300..422 of consensus"
complement(35725..35995)
misc_feature      /note="match: STS: Em:L30522"
35874..35971
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35885..35972
repeat_region     /note="22 copies 4 mer tcta 79% conserved"
36012..36375
repeat_region     /note="MLT1A1 repeat: matches 2..365 of consensus"
36437..36480
repeat_region     /note="11 copies 4 mer tcca 86% conserved"

Query Match      83.6%; Score 18.4; DB 89; Length 125661;
Best Local Similarity 95.0%; Pred No. 81;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 gactgtgaaggttagagatg 21
||| ||||| ||||| |||||
Db 114151 GAATGTGAAGTTAGAGATG 114170
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Search completed: October 9, 2001, 16:21:09  
Job time: 2639 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:27 ; Search time 6788.49 Seconds  
(without alignments)  
30.635 Million cell updates/sec

Title: US-09-713-136-9  
Perfect score: 22  
Sequence: 1 tgactgtgaaggtagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

COMMENT Contact: Takuji Sasaki  
National Institute of Agrobiological Resources  
Rice Genome Research Program  
2-1-2 Kannondai, Tsukuba  
Ibaraki,  
Japan 305  
Tel: 0298-38-7441  
Fax: 0298-38-7468  
Email: tsasaki@abr.affrc.go.jp  
PROJECT = "RGP".  
S14862\_62.

FEATURES Location/Qualifiers  
source  
1. 463  
/organism="Oryza sativa"  
/strain="Nipponbare"  
/db\_xref="taxon:4530"  
/clone="S14862"  
/clone\_lib="Rice green shoot"  
/note="green shoot (8 days old)" 2 others  
BASE COUNT 151 a 74 c 109 g 127 t  
ORIGIN

Query Match 85.5%; Score 18.8; DB 107; Length 463;  
Best Local Similarity 90.9%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagatga 22  
||| ||||| ||||| ||||| |||||  
Db 151 TGAGTGTGAATGTTAGAGATGA 172

RESULT 2  
AU089685 479 bp mRNA EST 27-APR-2000  
LOCUS AU089685 Rice callus Oryza sativa subsp. japonica CDNA clone C40060  
DEFINITION AU089685 mRNA sequence.  
ACCESSION AU089685  
VERSION AU089685.1 GI:7652165  
KEYWORDS EST.  
SOURCE Oryza sativa subsp. japonica.  
ORGANISM Oryza sativa subsp. japonica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 479)  
AUTHORS Sasaki, T. and Yamamoto, K.  
TITLE Rice cDNA from callus (2000)  
JOURNAL Unpublished (2000)  
COMMENT Contact: Takuji Sasaki  
National Institute of Agrobiological Resources  
Rice Genome Research Program  
2-1-2 Kannondai, Tsukuba  
Ibaraki,  
Japan 305  
Tel: 0298-38-7441  
Fax: 0298-38-7468  
Email: tsasaki@abr.affrc.go.jp  
PROJECT = "RGP".  
C40060\_32.

FEATURES Location/Qualifiers  
source  
1. 479  
/organism="Oryza sativa subsp. japonica"  
/strain="cultivar Nipponbare, sub\_species Japonica"  
/db\_xref="taxon:39947"  
/clone="C40060"  
/clone\_lib="Rice callus"  
/note="Vector: pBluescript II SK+; Site\_1: SalI; Site\_2:  
NotI; cDNA prepared from rice callus mRNAs by using  
NotI; cDNA as a primer and ligating to the SalI-NotI site  
of pBluescript II SK+ phagemid."  
BASE COUNT 149 a 96 c 104 g 130 t  
ORIGIN

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	85.5	463	107	AU083559
2	18.8	85.5	479	107	AU089685
3	17.8	80.9	267	139	BE752532
4	17.8	80.9	398	167	BE428418
5	17.8	80.9	474	167	BE419241
6	17.8	80.9	477	149	BF475131
7	17.8	80.9	541	114	AW305665
8	17.8	80.9	558	114	AW282093
9	17.8	80.9	561	249	AV755668
10	17.8	80.9	612	32	AV653619
11	17.8	80.9	620	162	BE060267
12	17.8	80.9	622	245	AZ503307
13	17.8	80.9	667	149	BF484589
14	17.8	80.9	930	146	BF257509
15	17.8	80.9	1616	81	BF631455
16	17.4	79.1	461	244	AZ447787
17	17.4	79.1	468	243	AZ431843
18	17.4	79.1	497	151	BF651333
19	17.4	79.1	627	243	AZ391922
20	17.4	79.1	711	106	AL586641
21	17.2	78.2	343	7	AA438163
22	17.2	78.2	361	32	AV695932
23	17.2	78.2	364	32	AV697012
24	17.2	78.2	367	152	BG373458
25	17.2	78.2	374	148	BF395765
26	17.2	78.2	380	163	BE116790
27	17.2	78.2	402	163	BE104970
28	17.2	78.2	405	239	AZ179136
29	17.2	78.2	411	32	AV684231
30	17.2	78.2	424	139	BE723539
31	17.2	78.2	452	238	AZ105474
32	17.2	78.2	456	240	AZ227719
33	17.2	78.2	471	21	A1555197
34	17.2	78.2	471	113	AW270792
35	17.2	78.2	510	228	AQ435695
36	17.2	78.2	513	148	BF388422
37	17.2	78.2	519	168	BF681745
38	17.2	78.2	521	230	AQ567409
39	17.2	78.2	533	143	BF039764
40	17.2	78.2	547	140	BE803661
41	17.2	78.2	573	242	AZ385615
42	17.2	78.2	588	232	AQ680793
43	17.2	78.2	616	240	AZ229260
44	17.2	78.2	624	21	A1514086
45	17.2	78.2	665	249	AZ759002

ALIGNMENTS

RESULT 1  
AU083559 463 bp mRNA EST 21-MAR-2000  
LOCUS AU083559 Rice green shoot Oryza sativa CDNA clone S14862, mRNA  
DEFINITION AU083559 sequence.  
ACCESSION AU083559  
VERSION AU083559.1 GI:7274015  
KEYWORDS EST.  
SOURCE Oryza sativa.  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 463)  
AUTHORS Sasaki, T. and Yamamoto, K.  
TITLE Rice cDNA from green shoot (2000)  
JOURNAL Unpublished (2000)

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Query Match      85.5%; Score 18.8; DB 107; Length 479;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tgactgtgaaggttagatga 22
    ||| ||||| ||||| |||||
Db 299 TGAGTGTGAATGTTAGAGATGA 320

RESULT 3
LOCUS BE752532 267 bp mRNA EST 15-SEP-2000
DEFINITION 204944 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE752532
VERSION BE752532.1 GI:10166524
SOURCE EST.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 267)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrnerkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keefe,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGAC
Plate: 53 row: M column: 1
Seq primer: ATTAGTGACACTATAG.
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    source
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        /db_xref="taxon:9913"
        /clone_lib="MARC 2B0V"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /note="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;
        Library made from pooled tissue from testis, thymus,
        semitendinosus muscle, longissimus muscle, pancreas,
        adrenal, and endometrium."
BASE COUNT 86 a 56 c 63 g 62 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 139; Length 267;
Best Local Similarity 90.5%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gactgtgaaggttagatga 22
    | ||||| ||||| |||||
Db 223 GCCTGTGAAGGTTAAGATGA 243

RESULT 4
LOCUS BE428418 398 bp mRNA EST 26-JUL-2000
DEFINITION MTD006.G10F990616 ITEC MTD Durum Wheat Root Library Triticum
turgidum subsp. durum cDNA clone MTD006.G10, mRNA sequence.

Query Match      80.9%; Score 17.8; DB 167; Length 398;
Best Local Similarity 90.3%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gactgtgaaggttagatga 22
    ||| ||||| ||||| |||||
Db 321 GACGGTGAAAGTTAGAGATGA 341

RESULT 5
LOCUS BE419241 474 bp mRNA EST 24-JUL-2000
DEFINITION WMR021.GSR000101 ITEC WMR Wheat Root Library Triticum aestivum cDNA
clone WMR021.G5, mRNA sequence.
ACCESSION BE419241
VERSION BE419241.1 GI:9417087
SOURCE EST.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 474)
Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorrrells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
Contact: Joudrier P
INRA, Unite de Biochimie et Biologie Moleculaire des Cereales
2, place VIALA, 34060 Montpellier cedex 01 FRANCE
Tel: 33 4 99 61 23 84
Fax: 33 4 99 61 23 48
Email: joudrier@enscm.inra.fr
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
FEATURES
    source
        1..398
        /organism="Triticum turgidum subsp. durum"
        /cultivar="Sillana"
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        /note="Vector: pSPORT1; T7 primers used. See pSPORT1
        polylinker site. 0.3-2.0 kbp average insert size."
BASE COUNT 99 a 77 c 104 g 118 t
ORIGIN

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COMMENT Contact: Schuch W  
zeneca Wheat Improvement Centre, Norwich Research Park  
Colney Lane, Norwich NR4 7UH UNITED KINGDOM  
Tel: 44 1603 250 2600  
Fax: 44 1603 250 699  
Email: wolfgang.schuch@zeneca.com  
International Triticeae EST Cooperative (ITPC)  
http://wheat.pw.usda.gov/genome.  
Location/Qualifiers

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/clone="WNR021.G5"  
/clone\_lib="ITPC WMR Wheat Root Library"  
/tissue\_type="root"  
/note="W13 Reverse sequencing primer used for 5' end of clone."  
119 a 87 c 127 g 141 t

## BASE COUNT

Query Match 80.9%; Score 17.8; DB 167; Length 474;  
Best Local Similarity 90.5%; Pred. No. 3.3e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gactgtgaagggttagagatga 22  
||||| ||||| ||||| ||||| |||||

Db 350 GACGGTGAAGGTAGAGATGA 370

## RESULT 6

BF475131 477 bp mRNA EST 04-DEC-2000  
LOCUS WHE2111\_B12\_D23ZS wheat salt-stressed crown cDNA library Triticum  
DEFINITION aestivum cDNA clone WHE2111\_B12\_D23, mRNA sequence.  
BF475131  
ACCESSION BF475131.1 GI:115444313  
VERSION  
KEYWORDS EST.  
SOURCE bread wheat.  
ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
; Triticeae; Triticum.  
1 (bases 1 to 477)  
AUTHORS Ahunov, E., Anderson, O.D., Chao, S., Chin, A., Choi, D.W., Close, T.J.,  
Dvorak, J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Kianian, P.,  
Lazo, G.R., Miller, R., Otto, C., Nguyen, H.T., Rausch, C.J., Seaton,  
C.L., Simons, K., Tong, J.C. and Zhang, D.  
TITLE The structure and function of the expressed  
genomes - Salt-stressed crown cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: andersn@pw.usda.gov  
Sequence have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20  
Seq primer: Stratagene SK primer.  
Location/Qualifiers

## FEATURES

1. 477  
/organism="Triticum aestivum"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="WHE2111\_B12\_D23"  
/clone\_lib="Wheat salt-stressed crown cDNA library"  
/tissue\_type="Crown"  
/dev\_stage="Adult plant"  
/lab\_host="E. coli SOLR"  
/note="Vector: Lambda Uni-2AP XR, excised phagemid;

Site\_1: ECORI; Site\_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Ahunov in J Dvorak lab). Total RNA and poly(A) RNA were prepared from crown tissue, equal portions of RNA were pooled from the two treatments, a cDNA library was made, and the cDNA clones were in vivo excised to give phaluescript phagemids in the TJ Close lab at the University of California, Riverside (Ahunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 132 a 84 c 120 g 140 t 1 others  
ORIGIN

Query Match 80.9%; Score 17.8; DB 149; Length 477;  
Best Local Similarity 90.5%; Pred. No. 3.3e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gactgtgaagggttagagatga 22  
||||| ||||| ||||| ||||| |||||

Db 197 GACGGTGAAGGTAGAGATGA 217

## RESULT 7

AW305665 541 bp mRNA EST 20-JAN-2000  
LOCUS f162b09.y1 zebrafish adult brain Danio rerio cDNA 5' similar to  
DEFINITION TR:075223 O75223 WUGSC:H\_DJ077023.1 PROTEIN.; contains Alu  
repetitive element.; mRNA sequence.  
AW305665  
ACCESSION AW305665.1 GI:6718018  
VERSION  
KEYWORDS EST.  
SOURCE zebrafish.  
ORGANISM Danio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Rasbora; Danio.  
1 (bases 1 to 541)  
AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy,  
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood,  
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,  
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,  
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.  
and Wilson, R.

TITLE WashU Zebrafish EST Project 1998  
JOURNAL Unpublished (1998)  
COMMENT Other ESTs: f162b09.x1  
Contact: Stephen L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: zbrafish@watson.wustl.edu  
CNA Library Preparation: John Ngai. cDNA Library Arrayed by:  
Matthew Clark. DNA Sequencing by: Washington University Genome  
Sequencing Center Clone distribution: Genome Systems, St. Louis,  
Missouri (web address: www.genomesystems.com) (email contact:  
info@genomesystems.com) and Research Genetics, Huntsville, Alabama  
(web address: www.resgen.com) (email contact: info@resgen.com) and  
ReSourceZentrumPrimaDatenbank, Berlin, Germany (web address:  
www.rzpd.de)  
Seq primer: T3 ET from Amersham  
High quality sequence stop: 458.  
Location/Qualifiers

## FEATURES

1. 541  
/organism="Danio rerio"  
/db\_xref="taxon:7955"  
/clone\_lib="zebrafish adult brain"  
/sex="mixed male and female"  
/tissue\_type="brain"  
/dev\_stage="adult"

```

/lab_host="E. coli DH10B"
/Note="Vector: pZiPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZiPLOX. Mass
excision of the cDNA library was performed to yield
pZiPLOX plasmids. Insert check was done in original
library."
BASE COUNT      145 a 123 c 161 g 112 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 114; Length 541;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaaggttagagatga 22
||| ||||| ||||| |||||
Db 434 GAGTGTGAAGATTAGAGATGA 454

RESULT 8
AW282093/c      558 bp mRNA EST 04-JAN-2000
LOCUS
DEFINITION      f162809.x1 zebrafish adult brain Danio rerio cDNA 3' similar to
TR:075223 O75223 WUGSC:H_DJ077023.1 PROTEIN. ; mRNA sequence.
ACCESSION      AW282093
VERSION
KEYWORDS
SOURCE
ORGANISM        Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio.
REFERENCE
AUTHORS        Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.,
and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.fzpd.de)
Seq primer: T7 ET from Amersham
High quality sequence stop: 406.
FEATURES
Source
Location/Qualifiers
1..558
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/Note="Vector: pZiPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZiPLOX. Mass
excision of the cDNA library was performed to yield
pZiPLOX plasmids. Insert check was done in original
library."
BASE COUNT      111 a 165 c 123 g 158 t 1 others
ORIGIN

/lab_host="E. coli DH10B"
/Note="Vector: pZiPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZiPLOX. Mass
excision of the cDNA library was performed to yield
pZiPLOX plasmids. Insert check was done in original
library."
BASE COUNT      145 a 123 c 161 g 112 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 114; Length 541;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaaggttagagatga 22
||| ||||| ||||| |||||
Db 434 GAGTGTGAAGATTAGAGATGA 454

RESULT 8
AW282093/c      558 bp mRNA EST 04-JAN-2000
LOCUS
DEFINITION      f162809.x1 zebrafish adult brain Danio rerio cDNA 3' similar to
TR:075223 O75223 WUGSC:H_DJ077023.1 PROTEIN. ; mRNA sequence.
ACCESSION      AW282093
VERSION
KEYWORDS
SOURCE
ORGANISM        Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio.
REFERENCE
AUTHORS        Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.,
and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.fzpd.de)
Seq primer: T7 ET from Amersham
High quality sequence stop: 406.
FEATURES
Source
Location/Qualifiers
1..558
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/Note="Vector: pZiPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZiPLOX. Mass
excision of the cDNA library was performed to yield
pZiPLOX plasmids. Insert check was done in original
library."
BASE COUNT      111 a 165 c 123 g 158 t 1 others
ORIGIN

/lab_host="E. coli DH10B"
/Note="Vector: pZiPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZiPLOX. Mass
excision of the cDNA library was performed to yield
pZiPLOX plasmids. Insert check was done in original
library."
BASE COUNT      145 a 123 c 161 g 112 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 114; Length 558;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaaggttagagatga 22
||| ||||| ||||| |||||
Db 168 GAGTGTGAAGATTAGAGATGA 148

RESULT 9
AZ755668/c      561 bp DNA GSS 01-MAR-2001
LOCUS
DEFINITION      ev02g09.x1 PAX3 CASTING Library 'ev' Homo sapiens genomic clone
ev02g09 random, DNA sequence.
ACCESSION      AZ755668
VERSION
KEYWORDS
SOURCE
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS        Barber, T.D., Barber, M.C., Tomescu, O., Barr, F., Ruben, S. and
Friedman, T.B.
Cyclic amplification and selection of target genes regulated by
Pax3 and PAX3/PKRX in embryogenesis and alveolar rhabdomyosarcoma
Unpublished (2000)
Contact: Friedman TB
Laboratory of Molecular Genetics
National Institute on Deafness and Other Communication Disorders,
National Institutes of Health
5 Research Court, Room 2A-15, Rockville, MD 20850, USA
Tel: 301 402 7580
Fax: 301 496 7882
Email: friedman@nidcd.nih.gov
Plate: 02 row: g column: 09
Seq primer: -21M13 forward primer (ABI)
Class: random plasmid subclone.
FEATURES
Source
Location/Qualifiers
1..561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ev02g09"
/clone_lib="PAX3 CASTING Library 'ev'"
/sex="Male"
/lab_host="DH10B"
/Note="Vector: pGEM-T Easy; Human genomic DNA was
partially digested with Sau3AI, ligated to ds linkers,
and enriched for binding to human PAX3d0+ protein using a
whole genome PCR-based strategy. DNA fragments containing
putative PAX3d0+ binding sites were amplified by PCR and
cloned into pGEM-T Easy (Promega). The ligation products
were transformed into DH10B electrocompetent cells (Life
Technologies)."
BASE COUNT      126 a 149 c 152 g 134 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 249; Length 561;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatg 21
||||| ||||| ||||| |||||
Db 461 TGACTGTGAAGTCAGAGATG 441

RESULT 10
AV653619
LOCUS
DEFINITION      AV653619 GLC Homo sapiens cDNA clone GLC2MG10 3', mRNA sequence.

```

```

ACCESSION      AV653619      1 GI:9874633
VERSION        AV653619.1
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 612)
              Qian,B., Wu,T., Huang,Q., Kang,B., Gao,X., Xu,Z., Xiao,H.
              Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Qu,J.,
              Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
              G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
              Homo sapiens cDNA clone
              Unpublished (2000)
JOURNAL        Chinese National Human Genome Center at Shanghai
COMMENT        351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919(ex.45)
              Fax: 86-21-50801922
              Email: hanzg@chgc.sh.cn
              This clone is available at CHGC in Shanghai.
FEATURES       Location/Qualifiers
               1..612
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="GICDMG10"
                /clone_lib="GLC"
                /tissue_type="corresponding non cancerous liver tissue"
                /dev_stage="Adult"
                /lab_host="SOLR"
                /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                XhoI"
BASE COUNT     155 a 121 c 152 g 183 t 1 others
ORIGIN
Query Match    80.9%; Score 17.8; DB 32; Length 612;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaagggttagagatg 21
    ||||| ||||| |||||
Db 10 TGACTGTGTCAGGTTGGAGATG 30

RESULT 11
BE060267       620 bp mRNA EST 27-FEB-2001
LOCUS          HVSMEG001M13f Hordeum vulgare pre-anthesis spike EST library
DEFINITION     HVCDA0008 (white to yellow anther) Hordeum vulgare cDNA clone
               HVSMEG001M13f, mRNA sequence.
ACCESSION      BE060267
VERSION        BE060267.2 GI:13154164
KEYWORDS       EST.
SOURCE         Hordeum vulgare
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
               ; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 620)
AUTHORS       Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
               Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
               T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
               Wood,T.
               Development of a genetically and physically anchored EST resource
               for barley genomics
               Unpublished (2000)
JOURNAL        On Jun 9, 2000 this sequence version replaced gi:8404917.
COMMENT        Contact: Wing RA
               Clemson University Genomics Institute
               Clemson University
               100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGG
High quality sequence stop: 471.
Location/Qualifiers
1..620
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEG001M13f"
 /clone_lib="Hordeum vulgare pre-anthesis spike EST library
 HVCDA0008 (white to yellow anther)"
 /tissue_type="pre-anthesis spike"
 /lab_host="SOLR"
 /note="Vector: lambda2AP; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT     165 a 115 c 155 g 185 t
ORIGIN
Query Match    80.9%; Score 17.8; DB 162; Length 620;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaagggttagagatga 22
    ||||| ||||| |||||
Db 302 GACGTCGAAAGTTAGAGATGA 322

RESULT 12
AZ503307/c     622 bp DNA GSS 05-OCT-2000
LOCUS          1M0343F02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION     clone UUGC1M0343F02 F, DNA sequence.
ACCESSION      AZ503307
VERSION        AZ503307.1 GI:10684623
KEYWORDS       GSS.
SOURCE         house mouse.
ORGANISM       Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 622)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
               M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
               and Wright,D., Weiss,R.
               Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               Unpublished (2000)
JOURNAL        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0343 row: F column: 02
               Seq primer: CGTTGTAACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 622.
               Location/Qualifiers
               1..622
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0343F02"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /note="Vector: pWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson

```

Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydronamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 177 a 144 c 140 g 161 t  
ORIGIN

Query Match 80.9%; Score 17.8; DB 245; Length 622;  
Best Local Similarity 90.5%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaaggttagatga 22  
||||| |||||||

DB 34 GACTGTGAGTGTAGATCA 14

## RESULT 13

BF484589 667 bp mRNA EST 06-DEC-2000  
LOCUS  
DEFINITION WHE2317\_D03\_G0525 wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2317\_D03\_G05, mRNA sequence.

ACCESSION BF484589  
VERSION  
KEYWORDS EST.  
SOURCE bread wheat.

## ORGANISM

Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 667)

AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han

P.S., Haia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,

Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat

genomes - Pre-anthesis spike cDNA library

Unpublished (2000)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific

West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

## FEATURES

source  
1..667  
/organism="Triticum aestivum"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="WHE2317\_D03\_G05"  
/clone\_lib="Wheat pre-anthesis spike cDNA library"  
/tissue\_type="Spike before anthesis"  
/dev\_stage="Adult plant"  
/lab\_host="E. coli SOLR"  
/note="vector: Lambda Uni-ZAP XR, excised phagemid;  
Site\_1: EcoRI; Site\_2: XhoI; plants were grown in the  
greenhouse. Whole spike with awns trimmed, white, green

and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the T3 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 172 a 125 c 170 g 199 t

## ORIGIN

Query Match 80.9%; Score 17.8; DB 149; Length 667;  
Best Local Similarity 90.5%; Pred. No. 3.5e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaaggttagatga 22  
||||| |||||||

DB 333 GACGGTGAAGTGTAGATGA 353

## RESULT 14

BF257509 930 bp mRNA EST 23-FEB-2001  
LOCUS  
DEFINITION HVSMEF0013B18f Hordeum vulgare seedling root EST library HVCDA0007 (etiolated and unstressed) Hordeum vulgare cDNA clone

ACCESSION BF257509

VERSION BF257509.1

KEYWORDS EST.

## SOURCE

barley.

ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 930)

AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu

, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo

, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and

Wood, T.

Development of a genetically and physically anchored EST resource

for barley genomics

Unpublished (2000)

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Seq primer: AATTAACCTCCTAAAGG

High quality sequence start: 48

High quality sequence stop: 764.

Location/Qualifiers

1..930

/organism="Hordeum vulgare"

/cultivar="Morex"

/db\_xref="taxon:4513"

/clone="HVSMEF0013B18f"

/clone\_lib="Hordeum vulgare seedling root EST library

HVCDA0007 (etiolated and unstressed)"

/tissue\_type="Seedling root"

/lab\_host="TJC121"

/note="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI"

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Best Local Similarity 90.5%; Pred. No. 3.7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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||||| |||||||

Wed Oct 10 05:59:37 2001

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Db 539 GACGGTGAAGCTTAGAGATGA 559
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XX
AC BF631455;
XX
SV BF631455.1
XX
DT 21-DEC-2000 (Rel. 66, Created)
DT 21-DEC-2000 (Rel. 66, Last updated, Version 1)
XX
DE HVSMEB0016A02f Hordeum vulgare seedling shoot EST library HVCDNA0002
DE (Dehydration stress) Hordeum vulgare cDNA clone HVSMEB0016A02f, mRNA
DE sequence.
XX
KW EST.
XX
OS Hordeum vulgare (barley)
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
XX
RN [1]
RP 1-1616
RA Wing R., Close T.J., Kleinhofs A., Wise R., Begum D., Frisch D., Yu Y.,
RA Anderson H., Dale J., Henry D., Kernodle S., Palmer M., Rambo T.,
RA Saski C., Schwartzbeck J., Simmons J., Choi D.W., Main D., Wood T.;
RT "Development of a genetically and physically anchored EST resource for
RT barley genomics";
RL Unpublished.
XX
CC Contact: Wing RA
CC Clemson University Genomics Institute
CC Clemson University
CC 100 Jordan Hall, Clemson, SC 29634, USA
CC Tel: 864 656 7288
CC Fax: 864 656 4293
CC Email: rwing@clemson.edu
CC Seq primer: AATTACCTCCTACTAAGGG
CC High quality sequence start: 6
CC High quality sequence stop: 146.
XX
FH Key
FH Location/Qualifiers
FT source
FT 1. 1616
FT /db_xref="taxon:4513"
FT /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"
FT /organism="Hordeum vulgare"
FT /cultivar="Morex"
FT /clone="HVSMEB0016A02f"
FT /clone_lib="Hordeum vulgare seedling shoot EST library
FT HVCDNA0002 (dehydration stress)"
FT /tissue_type="Seedling shoot"
FT /lab_host="TJCL21"
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SQ Sequence 1616 BP; 471 A; 350 C; 385 G; 341 T; 69 other;
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Best Local Similarity 86.4%; Pred. No. 4.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggtagagatga 22  
| | | | | | | | | | | | | | | | | |  
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Search completed: October 9, 2001, 18:20:29  
Job time: 9799 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds  
(without alignments)  
26.779 Million cell updates/sec

Title: US-09-713-136-9  
Perfect score: 22  
Sequence: 1 tgcactgtgaaggttagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AAV55788	Immunostimulatory
2	22	100.0	22	AAV80104	Oligo used in expe
3	22	100.0	22	AAC64052	Non-CpG control ph
4	22	100.0	22	AAV96252	Sequence of a stab
5	20.4	92.7	22	AAV32080	Nucleotide sequenc
6	20.4	92.7	22	AAV36625	ISS-ODN mutant DY1
7	20.4	92.7	22	AAV55791	Immunostimulatory
8	20.4	92.7	22	AAV55797	Immunostimulatory
9	20.4	92.7	22	AAV80110	Oligo used in expe
10	20.4	92.7	22	AAV14468	Inactive Immunost
11	20.4	92.7	22	AAV55878	Non-immunomodulato

12	20	90.9	22	AAV55881	Immunomodulatory o
13	19.6	89.1	22	AAV77046	Immunostimulatory
14	19.6	89.1	22	AAV77047	Immunostimulatory
15	19.4	88.2	22	AAV55880	Immunomodulatory o
16	18.8	85.5	22	AAV32079	Nucleotide sequenc
17	18.8	85.5	22	AAV36624	ISS-ODN DY1018 nuc
18	18.8	85.5	22	AAV55790	Immunostimulatory
19	18.8	85.5	22	AAV55794	Immunostimulatory
20	18.8	85.5	22	AAV80106	Oligo used in expe
21	18.8	85.5	22	AAV80097	Immunomodulatory o
22	18.8	85.5	22	AAV80102	Immunomodulatory o
23	18.8	85.5	22	AAV80103	Immunomodulatory o
24	18.8	85.5	22	AAV64051	Immunostimulatory
25	18.8	85.5	22	AAV96253	Sequence of a stab
26	18.8	85.5	22	AAV96260	Sequence of a stab
27	18.8	85.5	22	AAA90458	CpG adjuvant oligo
28	18.8	85.5	22	AAA90459	CpG adjuvant oligo
29	18.8	85.5	22	AAA14467	Immunostimulatory
30	18.8	85.5	22	AAA14469	Mutant immunostimu
31	18.8	85.5	22	AAA38065	Immunostimulatory
32	18.8	85.5	22	AAA38071	Immunostimulatory
33	18.8	85.5	22	AAA38072	Immunostimulatory
34	18.8	85.5	22	AAV55876	Immunomodulatory o
35	18.8	85.5	22	AAV77040	Immunomodulatory D
36	18.8	85.5	22	AAV29800	Cholera toxin immu
37	18.8	85.5	22	AAV31345	Immune response en
38	18.8	85.5	22	AAV82107	Oligonucleotide OD
39	18.8	85.5	22	AAV92377	CG motif and CFA c
40	18.8	85.5	22	AAV92378	CG motif and CFA c
41	18	81.8	22	AAV77045	Immunostimulatory
42	17.8	80.9	22	AAV55877	Immunomodulatory o
43	17.2	78.2	22	AAV80105	Oligo used in expe
44	17.2	78.2	22	AAV80107	Oligo used in expe
45	17.2	78.2	22	AAV92379	CG motif and CFA c

## ALIGNMENTS

## RESULT 1

AAV55788  
ID AAV55788 standard; DNA; 22 BP.  
XX AAV55788;  
AC AAV55788;  
XX 29-MAR-1999 (first entry)  
DT 29-MAR-1999 (first entry)  
XX Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1019.  
DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1019.  
XX Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;  
KW Immunostimulatory activity; gene therapy; genetic immunisation;  
KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.  
XX Synthetic.  
OS Synthetic.  
XX WO9855609-A1.  
PN WO9855609-A1.  
XX 10-DEC-1998.  
PD 10-DEC-1998.  
XX 05-JUN-1998; 98WO-US11391.  
PF 05-JUN-1998; 98WO-US11391.  
XX 06-JUN-1997; 97US-0048793.  
PR 06-JUN-1997; 97US-0048793.  
XX (REGC ) UNIV CALIFORNIA.  
XX Ray E, Roman M;  
PI Ray E, Roman M;  
XX WPI; 1999-080827/07.  
DR WPI; 1999-080827/07.  
XX New oligonucleotide that inhibits action of immunostimulatory  
PT sequence oligonucleotides - particularly those present in gene  
therapy vectors or microbial pathogens, used to prolong gene therapy  
PT expression and to treat e.g. infections or autoimmune disease

XX PS Example 1; Fig 1; 50pp; English.

XX CC This sequence represents an example of a immunostimulatory sequence

CC CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN

CC CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-2-Py-Py or

CC CC 5'-Pu-Pu-Y-2-Py-polyPy for inhibiting immunostimulation caused by

CC CC ISS-ODNs that contain a hexamer region consisting of at least one CpG

CC CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;

CC CC Y = any natural or synthetic nucleotide other than C; Z = any natural or

CC CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.

CC CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs

CC CC when this is present in (i) a recombinant expression vector (being used

CC CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly

CC CC one in a host and associated with an autoimmune disease). Particularly

CC CC the inhibitors prolong gene expression from the vector and reduce

CC CC inflammation caused by microbial infection. They also modulate activity

CC CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune

CC CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes

CC CC or monocytes by reducing the Th1-type response and stimulating the

CC CC Th2-type response to an antigen (including antigen-stimulated

CC CC immunoglobulin G1 production). Prolonged expression from the gene therapy

CC CC vector avoids the need for repeated treatments and re-engineering of the

CC CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over

CC CC the effect of ISS-ODN-based adjuvants and can be used even where the

CC CC existence, identity and location of the ISS-ODNs are unknown. The

CC CC inhibitors are effective at very low doses.

XX CC

SQ Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. NO. 0.14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1 tgactgtgaaggttagagatga 22

Db 1 tgactgtgaaggttagagatga 22

RESULT 2

AAV80104

ID AAV80104 standard; DNA; 22 BP.

XX AC AAV80104;

XX AC

XX 12-MAR-1999 (first entry)

DT

XX Oligo used in experiments for stimulation of cytokine production.

DE

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;

KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;

KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;

KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.

XX OS Synthetic.

XX

XX WO9855495-A2.

PN

XX 10-DEC-1998.

PD

XX 05-JUN-1998; 98WO-US11578.

PF

XX 06-JUN-1997; 97US-0048793.

PR

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PA Dina D, Roman M, Schwartz D;

PI WPI: 1999-059898/05.

XX

XX Immunostimulatory oligonucleotides regulate the immune system - and

PT contain an immune-stimulating octanucleotide sequence; for treating

PT cancer, allergic and infectious diseases

XX

PS Example 1; Page 29; 63pp; English.

XX

CC The invention relates to immunomodulatory oligonucleotides that comprise

CC CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,

CC CC GAGTTCC, and GAGTTCCG. The immunomodulatory sequences are used to treat

CC CC patients needing immune regulation, such as those suffering from cancer,

CC CC an allergic disease and asthma. They are also used to prevent infectious

CC CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

CC CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC CC immunostimulatory activity by incubating macrophage cells and the

CC CC oligonucleotide; and determining the relative amount of Th1-biased

CC CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent

CC CC oligonucleotides that were tested for immunostimulatory activity. These

CC CC were used in experiments for the stimulation of cytokine production and

CC CC were found to lack immunostimulatory activity. The invention provides

CC CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX

SQ Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. NO. 0.14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1 tgactgtgaaggttagagatga 22

Db 1 tgactgtgaaggttagagatga 22

RESULT 3

AAC64052

ID AAC64052 standard; DNA; 22 BP.

XX AC AAC64052;

XX AC

XX 15-FEB-2001 (first entry)

DT

XX Non-CpG control phosphorothioate oligodeoxynucleotide.

DE

XX Non-CpG control oligodeoxynucleotide; phosphorothioate;

KW immunostimulatory; CpG ISS ODN; enhanced antigen presentation;

KW antigen-presenting cell; APC; T-cell activation; tumour cell;

KW tumour antigen; cancer immunotherapy; vaccine; ss.

XX OS Synthetic.

XX

XX WO200062787-A1.

PN

XX 26-OCT-2000.

PD

XX 11-APR-2000; 2000WO-US09864.

PF

XX 15-APR-1999; 99US-0292278.

PR

XX (REGC) UNIV CALIFORNIA.

PA

XX Raz E, Martin-Orozco E;

PI WPI: 2000-679548/66.

DR

XX Enhancing antigen-presentation capabilities of T-cells for cancer

PT immunotherapy, by contacting cells with an immunostimulatory

PT oligonucleotide.

XX

XX Example 1; Page 18; 42pp; English.

XX

XX The invention relates to a method of inducing activation of T-cells

CC to respond to an antigen, comprising contacting antigen-presenting cells

CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs  
 CC thus treated have enhanced antigen presenting capabilities compared to  
 CC antigen-activated APCs. APCs with enhanced antigen-presentation  
 CC capabilities then present the antigen to T-cells. The method is useful  
 CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour  
 CC antigen presenting capacity of tumour cells, thereby inducing T-cell  
 CC activation, and is therefore useful for treating tumours. Additionally,  
 CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.  
 CC ISS-ODN treated APCs are induced to take up antigen through upregulation  
 CC of Fe-receptor expression, to present antigen through upregulation of  
 CC major histocompatibility complex (MHC) Class I and II expression and  
 CC CD1d expression, to produce co-stimulatory factors (B7 and CD40), to  
 CC provide cell-to-cell adhesion through upregulation of intercellular  
 CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory  
 CC cytokine production, all at levels greater than that achieved through  
 CC contact of APC with antigen alone. The present sequence represents  
 CC a phosphorothioate non-CpG oligodeoxynucleotide used as a control  
 CC with ISS-ODN AAC64051 in the exemplifications of the invention.  
 XX  
 SQ Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22  
 |||||  
 Db 1 tgactgtgaagggttagagatga 22

RESULT 4  
 AAA96252  
 ID AAA96252 standard; DNA; 22 BP.  
 AC AAA96252;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Sequence of a stabilised oligonucleotide with antitumour activity.  
 XX  
 KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;  
 KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200056342-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 17-MAR-2000; 2000WO-FR00676.  
 XX  
 PR 19-MAR-1999; 99FR-0003433.  
 XX  
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (INRM) INST NAT SANTE & RECH MEDICALE.  
 XX  
 PI Carpentier A;  
 XX  
 DR WPI; 2000-602192/57.

XX Use of stabilized oligonucleotides as antitumor agents, particularly  
 PT against nervous system tumors, have optimal activity and are not toxic  
 PT  
 PT  
 XX Example 2; Page 16; 57pp; French.

XX The present sequence represents a stabilised oligonucleotide which has  
 CC antitumour activity. The oligonucleotide comprises an octamer motif  
 CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where  
 CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are  
 CC immunostimulatory, and are not toxic. They may be adapted for use in  
 CC animals or humans. The stabilised oligonucleotides are used for

CC treating tumours, of any type and any degree of anaplasia, particularly  
 CC human tumours in the peripheral or central nervous systems, specifically  
 CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.  
 XX  
 SQ Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22  
 |||||  
 Db 1 tgactgtgaagggttagagatga 22

RESULT 5  
 AAV32080  
 ID AAV32080 standard; DNA; 22 BP.

XX AAV32080;

XX 09-SEP-1998 (first entry)  
 XX  
 DE Nucleotide sequence of DY1019.

XX  
 KW DY1019; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;  
 KW immunisation; anaphylaxis; IgE; retinopathies; ss.  
 XX  
 OS synthetic.

XX Key Location/Qualifiers  
 FT modified\_base 1..22  
 FT /\*tag= a  
 FT /note= "phosphothioate backbone"

XX WO9816247-A1.

XX 23-APR-1998.

XX 09-OCT-1997; 97WO-US19004.

XX 11-OCT-1996; 96US-0028118.

XX (REGC) UNIV CALIFORNIA.

XX Carson DA, Raz E, Roman M;

XX WPI; 1998-261028/23.

XX New immunomodulatory compositions - comprising an antigen conjugated  
 PT to a polynucleotide that contains an immunostimulatory sequence

XX Example 1; Page 36; 69pp; English.

XX This is the nucleotide sequence of DY1019, which is conjugated to  
 CC beta-gal in the method of the invention to form PN/IMM, comprising an  
 CC immunomodulatory molecule (IMM), which comprises an antigen conjugated  
 CC to a polynucleotide (PN) that contains at least one immunostimulatory  
 CC nucleotide sequence (ISS). The conjugate synergistically boost the  
 CC magnitude of the host immune response against an antigen to a level  
 CC greater than the host immune response to either the IMM, antigen or  
 CC ISS-PN alone. These responses to ISS-PN/IMM conjugates are  
 CC particularly acute during the important early phase of the host immune  
 CC response to an antigen. The ISS-PN/IMM conjugates boost both humoral  
 CC (antibody) and cellular (Th1 type) immune responses of the host. Thus,  
 CC use of the method to boost the immune responsiveness of a host to  
 CC subsequent challenge by a sensitising antigen without immunisation  
 CC avoids the risk of Th2-mediated, immunisation-induced anaphylaxis by  
 CC suppressing IgE production in response to the antigen challenge. The  
 CC conjugates can also be used to combat pathogenic infection and to  
 CC stimulate therapeutic angiogenesis to treat conditions in which  
 CC localised blood flow plays a significant etiological role, e.g.



CC retinopathies.  
 XX Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;  
 SQ Best Local Similarity 92.7%; Score 20.4; DB 19; Length 22;  
 Query Match  
 Best Local Similarity 95.5%; Pred. No. 0.8;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatga 22  
 |||||  
 Db 1 tgactgtgaaggttagagatga 22  
 |||||

RESULT 7  
 AAV55791  
 ID AAV55791 standard; DNA; 22 BP.  
 XX  
 AC AAV55791;  
 XX  
 DT 29-MAR-1999 (first entry)  
 XX  
 DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1041.  
 XX  
 KW Immunostimulatory sequence oligonucleotide; ISS-ODN; Inhibitor;  
 KW Immunostimulatory activity; gene therapy; genetic immunisation;  
 KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W09855609-A1.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 05-JUN-1998; 98WO-US11391.  
 XX  
 PR 06-JUN-1997; 97US-0048793.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Ray E, Roman M;  
 XX  
 DR WPI; 1999-080827/07.  
 XX  
 PT New oligonucleotide that inhibits action of immunostimulatory  
 PT sequence oligonucleotides - particularly those present in gene  
 PT therapy vectors or microbial pathogens, used to prolong gene therapy  
 PT expression and to treat e.g. infections or autoimmune disease  
 XX  
 PS Example 1; Fig 1; 50pp; English.  
 XX  
 CC This sequence represents an example of a immunostimulatory sequence  
 CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN  
 CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-Z-Py-Py or  
 CC 5'-Pu-Pu-Y-Z-Py-polyPy for inhibiting immunostimulation caused by  
 CC ISS-ODNs that contain a hexamer region consisting of at least one Cpg  
 CC motif flanked by two 5'-Pu and two 3'-py. Pu = purine; py = pyrimidine;  
 CC Y = any natural or synthetic nucleotide other than C; Z = any natural or  
 CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.  
 CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs  
 CC when this is present in (i) a recombinant expression vector (being used  
 CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly  
 CC one in a host and associated with an autoimmune disease). Particularly  
 CC the inhibitors prolong gene expression from the vector and reduce  
 CC inflammation caused by microbial infection. They also modulate activity  
 CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune  
 CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes  
 CC or monocytes by reducing the Th1-type response and stimulating the  
 CC Th2-type response to an antigen (including antigen-stimulated  
 CC immunoglobulin G1 production). Prolonged expression from the gene therapy  
 CC vector avoids the need for repeated treatments and re-engineering of the  
 CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over  
 CC the effect of ISS-ODN-based adjuvants and can be used even where the  
 CC existence, identity and location of the ISS-ODNs are unknown. The  
 CC inhibitors are effective at very low doses.  
 XX  
 SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

CC retinopathies.  
 XX Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;  
 SQ Best Local Similarity 92.7%; Score 20.4; DB 19; Length 22;  
 Query Match  
 Best Local Similarity 95.5%; Pred. No. 0.8;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatga 22  
 |||||  
 Db 1 tgactgtgaaggttagagatga 22  
 |||||

RESULT 6  
 AAX36625  
 ID AAX36625 standard; DNA; 22 BP.  
 XX  
 AC AAX36625;  
 XX  
 DT 09-JUL-1999 (first entry)  
 XX  
 DE ISS-ODN mutant DY1019 nucleotide sequence.  
 XX  
 KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;  
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;  
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;  
 KW allergic basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;  
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;  
 KW eosinophilic fasciitis; therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W09911275-A2.  
 XX  
 PD 11-MAR-1999.  
 XX  
 PF 04-SEP-1998; 98WO-US18382.  
 XX  
 PR 05-SEP-1997; 97US-0927120.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Ray E;  
 XX  
 DR WPI; 1999-312404/26.  
 XX  
 PT Reducing antigen-stimulated granulocyte-mediated inflammation  
 XX  
 PS Example 2; Page 30; 69pp; English.  
 XX  
 CC This is the ISS-ODN mutant DY1019 nucleotide sequence.  
 CC The invention relates to a method for preventing or reducing  
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:  
 CC (a) reduction in, or the absence of, a Th2 type immune response is  
 CC measured; or (b) there is a reduction or absence of other clinical signs  
 CC of inflammation in the host after antigen challenge. The method is used  
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
 CC and to modulate the host's immune responsiveness to an antigen,  
 CC particularly where the subject suffers from asthma, nasal polyposis,  
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
 CC antigen immunisation, the method is an antigen-independent method,  
 CC and avoids host production of both interleukin-4 (IL-4), which carries  
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
 CC adhesion to endothelia.  
 XX  
 SQ Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;

Query Match.  
 92.7%; Score 20.4; DB 20; Length 22;

Query Match 92.7%; Score 20.4; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.8;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatga 22  
 |||||  
 Db 1 tgactgtgaagcttagagatga 22

## RESULT 8

AAV55797  
 ID AAV55797 standard; DNA; 22 BP.

XX  
 AC AAV55797;

XX  
 DT 29-MAR-1999 (first entry)

XX  
 DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DV1061.

XX  
 KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;

KW Immunostimulatory activity; gene therapy; genetic immunisation;

KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.

OS Synthetic.

PN WO9855609-A1.

XX  
 PD 10-DEC-1998.

XX  
 PF 05-JUN-1998; 98WO-US11391.

XX  
 PR 06-JUN-1997; 97US-0048793.

XX  
 PA (REGC ) UNIV CALIFORNIA.

XX  
 PI Ray E, Roman M;

XX  
 DR WPI; 1999-080827/07.

XX  
 PT New oligonucleotide that inhibits action of immunostimulatory

PT sequence oligonucleotides - particularly those present in gene

PT therapy vectors or microbial pathogens, used to prolong gene therapy

PT expression and to treat e.g. infections or autoimmune disease

XX  
 PS Example 1; Fig 3; 50pp; English.

XX This sequence represents an example of a immunostimulatory sequence  
 CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN  
 CC sequences have a hexamer region of sequence 5'-pu-pu-y-2-py-py or  
 CC 5'-pu-pu-y-2-py-poly for inhibiting immunostimulation caused by  
 CC ISS-ODNs that contain a hexamer region consisting of at least one Cpg  
 CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;  
 CC y = any natural or synthetic nucleotide other than C; z = any natural or  
 CC synthetic nucleotide, but if y is not G or inosine (I), then z is G or I.  
 CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs  
 CC when this is present in (i) a recombinant expression vector (being used  
 CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly  
 CC one in a host and associated with an autoimmune disease). Particularly  
 CC the inhibitors prolong gene expression from the vector and reduce  
 CC inflammation caused by microbial infection. They also modulate activity  
 CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune  
 CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes  
 CC or monocytes by reducing the Th1-type response and stimulating the  
 CC Th2-type response to an antigen (including antigen-stimulated  
 CC immunoglobulin G1 production). Prolonged expression from the gene therapy  
 CC vector avoids the need for repeated treatments and re-engineering of the  
 CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over  
 CC the effect of ISS-ODN-based adjuvants and can be used even where the  
 CC existence, identity and location of the ISS-ODNs are unknown. The  
 CC inhibitors are effective at very low doses.

XX  
 SQ Sequence 22 BP; 7 A; 1 C; 7 G; 7 T; 0 Other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.8;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatga 22  
 |||||  
 Db 1 tgactgtgaatgttagagatga 22

## RESULT 9

AAV80110

ID AAV80110 standard; DNA; 22 BP.

XX  
 AC AAV80110;

XX  
 DT 12-MAR-1999 (first entry)

XX  
 DE Oligo used in experiments for stimulation of cytokine production.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;

KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;

KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;

KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX  
 OS Synthetic.

XX  
 PN WO9855495-A2.

XX  
 PD 10-DEC-1998.

XX  
 PF 05-JUN-1998; 98WO-US11578.

XX  
 PR 06-JUN-1997; 97US-0048793.

XX  
 PA (DYNA-) DYNAX TECHNOLOGIES CORP.

XX  
 PI Dina D, Roman M, Schwartz D;

XX  
 DR WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and

PT contain an immune-stimulating octanucleotide sequence; for treating

PT cancer, allergic and infectious diseases

XX  
 PS Example 2; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,  
 CC GAGGTTC, and GAGGTTCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent  
 CC oligonucleotides that were tested for immunostimulatory activity. These  
 CC were used in experiments for the stimulation of cytokine production and  
 CC were found to lack immunostimulatory activity. The invention provides  
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX  
 SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 Other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.8;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatga 22

Db 1 tgactgtgaagcttagagatga 22  
|||||

RESULT 10  
AAA14468  
ID AAA14468 standard; DNA: 22 BP.  
XX  
AC AAA14468;  
XX  
DT 21-AUG-2000 (first entry)  
XX  
DE Inactive immunostimulatory oligonucleotide DY1019.  
XX  
KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;  
KW secretory immunoglobulin A production; sigA; Th1 phenotype; mutant; ds.  
XX  
OS Synthetic.  
XX  
PN WO200020039-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 15-SEP-1999; 99WO-US21203.  
XX  
PR 05-OCT-1998; 98US-0167039.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Raz E, Horner AA, Carson DA;  
XX  
DR WPI; 2000-303647/26.  
XX  
PT Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to  
PT an antigen in a mammalian host through production of secretory  
PT immunoglobulin A -  
XX  
PS Example 7; Page 63; 64pp; English.

The invention relates to a method of inducing mucosal immunity to an antigen in a mammalian host, including the production of secretory immunoglobulin A (sigA). Immune protection in the mucosa (the principal site of entry of most foreign antigens) is mediated by mucosa-associated lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory cell sub-populations. The primary immune response which characterizes the induction of mucosal immunity to an antigen is sigA production by activated B-cells. The method comprises introducing an immunostimulatory oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the ISS-ODN includes a core nucleotide sequence. The core nucleotide sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used as an adjuvant with an antigen for stimulating mucosal immunity. The level of sigA production induced in the host is at least 3 times the magnitude of sigA production achievable in response to introduction of antigen alone into the mucosal tissue and is equivalent or greater than the magnitude of sigA production achievable in response to introduction of the antigen and cholera toxin adjuvant into the mucosal tissue. The host immune response is stimulated to antigen specific IgA production, biased towards the Th1 phenotype while antigen-induced IgE production is avoided. The adjuvant has little or no known toxicity in mammals and its efficacy is comparable to that of cholera toxin which is used as a mucosal adjuvant. The present sequence represents an inactive ISS-ODN, DY1019, used in an exemplification of the invention.

Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.8;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaagcttagagatga 22

Db 1 tgactgtgaagcttagagatga 22  
|||||

RESULT 11  
AAZ55878  
ID AAZ55878 standard; DNA: 22 BP.  
XX  
AC AAZ55878;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Non-immunomodulatory oligonucleotide SEQ ID NO: 3.  
XX  
KW Non-immunomodulatory; immunostimulatory sequence; adjuvant;  
KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
KW asthma; immunocontraception; ss.  
XX  
OS Mus musculus.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..22  
FT /\*tag= a  
FT /note= "Phosphorothioate linkages"  
XX  
PN WO9962923-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 04-JUN-1999; 99WO-US12538.  
XX  
PR 05-JUN-1998; 98US-0088310.  
PR 01-JUN-1999; 99US-0324191.  
XX  
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
PI Schwartz D;  
XX  
DR WPI; 2000-105687/09.  
XX  
PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune  
PT response, e.g. to tumor antigens -  
XX  
PS Example 1; Page 35; 54pp; English.  
XX  
CC Sequences AAZ55878-255879 represent oligonucleotides which do not  
CC contain an immunostimulatory sequence (ISS, e.g., AACGTC, AACGTT,  
CC AGCGTC, AGCGCT, AGCGTT, GACGTC, GACGTT, GCGGTT, AACGTTCC and GACGTTCC),  
CC and which did not exhibit immunomodulatory activity in an  
CC exemplification of the present invention. The invention relates to  
CC oligonucleotides comprising one or more ISSs, where the ISS comprises at  
CC least one modified cytosine with an electron-withdrawing moiety at  
CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886  
CC contain ISSs comprising at least one bromocytosine, whereas sequence  
CC AAZ55876 contains an unmodified ISS. The immunomodulatory  
CC oligonucleotides have an adjuvant-like effect: when formulated with an  
CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,  
CC and induce a Th1-type immune response (activation of cytotoxic T cells),  
CC while simultaneously downregulating the Th2-type response. The Th1  
CC response is particularly effective for control of viruses and  
CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
CC particularly when formulated with an antigen or a facilitator, for  
CC modulating immune responses. Such compositions may be used in tumour  
CC therapy, in treatment of allergy (including asthma), for inducing a  
CC vigorous cellular response (against a virus, bacterium, fungus or  
CC protozoan), and also in contraceptive vaccines based on sperm antigens.  
XX  
SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;  
Best Local Similarity 95.5%; Pred. No. 0.8;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaaggttagagatga 22  
 |||||  
 Db 1 tgactgtgaaggttagagatga 22  
 |||||

RESULT 12  
 AA255881  
 ID AA255881 standard; DNA; 22 BP.  
 AC AA255881;  
 XX  
 DT 10-APR-2000 (first entry)  
 XX  
 DE Immunomodulatory oligonucleotide SEQ ID NO: 6.  
 XX  
 KW Immunomodulation; immunostimulatory sequence; adjuvant;  
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
 KW asthma; immunosuppression; 5-bromocytosine; ss.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX

Key Location/Qualifiers  
 FT modified\_base 1..22  
 FT /tag= a  
 FT /note= "Phosphorothioate linkages"  
 FT misc\_feature 9..16  
 FT /tag= b  
 FT /note= "Immunostimulatory sequence (ISS)"  
 FT modified\_base 11  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "5-bromocytosine"  
 FT modified\_base 15  
 FT /tag= d  
 FT /mod\_base= OTHER  
 FT /note= "5-bromocytosine"  
 XX  
 PN WO962923-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 XX 04-JUN-1999; 99WO-US12538.  
 XX  
 PR 05-JUN-1998; 98US-0088310.  
 PR 01-JUN-1999; 99US-0324191.  
 XX  
 PA (DYNA-) DYNAX TECHNOLOGIES CORP.  
 XX  
 PI Schwartz D;  
 XX  
 XX WPI: 2000-105687/09.  
 XX  
 DR Novel immunomodulatory oligonucleotide used to induce a Th1-type immune  
 PT response, e.g. to tumor antigens  
 XX  
 XX Claim 31; Page 35; 54pp; English.  
 PS  
 XX Sequences AA255876-255877 and AA255880-255886 represent immunomodulatory  
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,  
 CC AACGTC, AACGTC, AGCGTC, AGCGTC, AGCGTC, GACGTC, GACGTC, GCGGTT,  
 CC AACGTC and GACGTC). The invention relates to oligonucleotides  
 CC comprising one or more ISSs, where the ISS comprises at least  
 CC one modified cytosine with an electron-withdrawing moiety at  
 CC position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886  
 CC contain ISSs comprising at least one bromocytosine, whereas sequence  
 CC AA255876 contains an unmodified ISS. The immunomodulatory  
 CC oligonucleotides have an adjuvant-like effect; when formulated with an  
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,  
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),  
 CC while simultaneously downregulating the Th2-type response. The Th1

CC response is particularly effective for control of viruses and  
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
 CC particularly when formulated with an antigen or a facilitator, for  
 CC modulating immune responses. Such compositions may be used in tumour  
 CC therapy, in treatment of allergy (including asthma), for inducing a  
 CC vigorous cellular response (against a virus, bacterium, fungus or  
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.  
 XX  
 SQ Sequence 22 BP; 6 A; 1 C; 7 G; 6 T; 2 other;

Query Match 90.9%; Score 20; DB 21; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.2;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tgactgtgaaggttagagatga 22  
 |||||  
 Db 1 tgactgtgaaggttagagatga 22  
 |||||

RESULT 13  
 AAF77046  
 ID AAF77046 standard; DNA; 22 BP.  
 XX  
 AC AAF77046;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Immunostimulatory DNA #6.  
 XX  
 KW Modulate; immune; antigen; immunostimulatory; ds.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200112223-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-US22835.  
 XX  
 PR 19-AUG-1999; 99US-0149768.  
 XX  
 PA (DYNA-) DYNAX TECHNOLOGIES CORP.  
 XX  
 PI Van Nest G;  
 XX  
 DR WPI: 2001-211136/21.  
 XX  
 PT Modulating immune response to a second antigen in humans involves  
 PT administering an immunostimulatory polynucleotide comprising an  
 PT immunostimulatory sequence and a first antigen  
 XX  
 PS Disclosure; Page 15; 63pp; English.  
 XX  
 XX The present invention relates to modulating an immune response to  
 CC a second antigen in an individual, involving  
 CC administering to the individual an immunomodulatory polynucleotide  
 CC comprising an immunostimulatory sequence (ISS) and a first antigen.  
 XX  
 SQ Sequence 22 BP; 6 A; 2 C; 7 G; 6 T; 1 other;

Query Match 89.1%; Score 19.6; DB 22; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.9;  
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaaggttagagatga 22  
 |||||  
 Db 1 tgactgtgaaggttagagatga 22  
 |||||

RESULT 14  
 AAF77047

```

ID AAF77047 standard; DNA; 22 BP.
XX AAF77047;
XX
DT 15-MAY-2001 (first entry)
XX
DE Immunostimulatory DNA #7.
XX
KW Modulate; immune; antigen; immunostimulatory; ds.
XX
OS Synthetic.
XX
PN WO200112223-A2.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US22835.
XX
PR 19-AUG-1999; 99US-0149768.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Van Nest G;
XX
DR WPI; 2001-211136/21.
XX
PT Modulating immune response to a second antigen in humans involves
PT administering an immunostimulatory polynucleotide comprising an
PT immunostimulatory sequence and a first antigen.
XX
PS Disclosure; Page 15; 63pp; English.
XX
CC The present invention relates to modulating an immune response to
CC a second antigen in an individual, involving
CC administering to the individual an immunomodulatory polynucleotide
CC comprising an immunostimulatory sequence (ISS) and a first antigen.
XX
SQ Sequence 22 BP; 6 A; 1 C; 7 G; 6 T; 2 other;

Query Match 89.1%; Score 19.6; DB 22; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.9;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0:

QY 1 tgactgtgaaggtagatga 22
   |||||
Db 1 tgactgtgaabgttagatga 22

RESULT 15
AAZ55880
ID AAZ55880 standard; DNA; 22 BP.
XX
AC AAZ55880;
XX
DT 10-APR-2000 (first entry)
XX
DE Immunomodulatory oligonucleotide SEQ ID NO: 5.
XX
KW Immunomodulation; immunostimulatory sequence; adjuvant;
KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
KW asthma; immunosuppression; 5-bromocytosine; ss.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..22
FT /*tag a
FT /*note "Phosphorothioate linkages"
FT misc_feature 9..16
FT /*tag b
FT /*note "Immunostimulatory sequence (ISS)"

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FT modified_base 11
FT /*tag c
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FT /*note "5-bromocytosine"
XX
PN WO9962923-A2.
XX
PD 09-DEC-1999.
XX
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XX
PR 05-JUN-1998; 98US-0088310.
PR 01-JUN-1999; 99US-0324191.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D;
XX
DR WPI; 2000-105687/09.
XX
PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
PT response, e.g. to tumor antigens.
XX
PS Claim 30; Page 35; 54pp; English.
XX
CC Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory
CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
CC AACGTC, AGCGTT, AGCGTC, AGCGTT, AGCGTC, GACGTC, GACGTC, GACGTT,
CC AACGTTCC and GACGTTCC). The invention relates to oligonucleotides
CC comprising one or more ISSs, where the ISS comprises at least
CC one modified cytosine with an electron-withdrawing moiety at
CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886
CC contain ISSs comprising at least one bromocytosine, whereas sequence
CC AAZ55876 contains an unmodified ISS. The immunomodulatory
CC oligonucleotides have an adjuvant-like effect: when formulated with an
CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
CC and induce a Th1-type immune response (activation of cytotoxic T cells),
CC while simultaneously downregulating the Th2-type response. The Th1
CC response is particularly effective for control of viruses and
CC intracellular parasites. The immunomodulatory oligonucleotides are used,
CC particularly when formulated with an antigen or a facilitator, for
CC modulating immune responses. Such compositions may be used in tumour
CC therapy, in treatment of allergy (including asthma), for inducing a
CC vigorous cellular response (against a virus, bacterium, fungus or
CC protozoan), and also in contraceptive vaccines based on sperm antigens.
XX
SQ Sequence 22 BP; 6 A; 2 C; 7 G; 6 T; 1 other;

Query Match 88.2%; Score 19.4; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0:

QY 1 tgactgtgaaggtagatga 22
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Db 1 tgactgtgaangtagatga 22

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22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq: \*

23: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq: \*

24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq: \*

25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq: \*

26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq: \*

27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq: \*

28: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq: \*

29: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq: \*

30: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq: \*

31: /cgn2\_6/ptodata/1/pna/US098\_COMB.seq: \*

32: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq: \*

33: /cgn2\_6/ptodata/1/pna/US098B\_COMB.seq: \*

34: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq: \*

35: /cgn2\_6/ptodata/1/pna/US098D\_COMB.seq: \*

36: /cgn2\_6/ptodata/1/pna/US098E\_COMB.seq: \*

37: /cgn2\_6/ptodata/1/pna/US098F\_COMB.seq: \*

38: /cgn2\_6/ptodata/1/pna/US098G\_COMB.seq: \*

39: /cgn2\_6/ptodata/1/pna/US098H\_COMB.seq: \*

40: /cgn2\_6/ptodata/1/pna/US098I\_COMB.seq: \*

41: /cgn2\_6/ptodata/1/pna/US098J\_COMB.seq: \*

42: /cgn2\_6/ptodata/1/pna/US098K\_COMB.seq: \*

43: /cgn2\_6/ptodata/1/pna/US098L\_COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	100.0	22	1 PCT-US01-03029-3	Sequence 3, Appl
2	22	100.0	22	1 PCT-US01-11290-4	Sequence 4, Appl
3	22	100.0	22	1 PCT-US01-14508-12	Sequence 12, Appl
4	22	100.0	22	16 US-09-296-477-3	Sequence 3, Appl
5	22	100.0	22	18 US-09-470-382-70	Sequence 70, Appl
6	22	100.0	22	28 US-09-713-136-9	Sequence 9, Appl
7	22	100.0	22	30 US-09-774-403-3	Sequence 3, Appl
8	22	100.0	22	31 US-09-828-505-4	Sequence 4, Appl
9	20.4	92.7	22	1 PCT-US00-35064-2	Sequence 2, Appl
10	20.4	92.7	22	1 PCT-US01-03029-2	Sequence 2, Appl
11	20.4	92.7	22	1 PCT-US01-06034-4	Sequence 4, Appl
12	20.4	92.7	22	1 PCT-US01-06034-5	Sequence 5, Appl
13	20.4	92.7	22	1 PCT-US01-06034-6	Sequence 6, Appl
14	20.4	92.7	22	1 PCT-US01-06034-8	Sequence 8, Appl
15	20.4	92.7	22	1 PCT-US01-11290-2	Sequence 2, Appl
16	20.4	92.7	22	1 PCT-US01-14508-10	Sequence 10, Appl
17	20.4	92.7	22	1 PCT-US01-14508-11	Sequence 11, Appl
18	20.4	92.7	22	1 PCT-US99-21203-20	Sequence 20, Appl
19	20.4	92.7	22	13 US-08-927-120-20	Sequence 20, Appl
20	20.4	92.7	22	15 US-09-167-039-20	Sequence 20, Appl
21	20.4	92.7	22	16 US-09-235-742-20	Sequence 20, Appl
22	20.4	92.7	22	16 US-09-296-477-13	Sequence 13, Appl
23	20.4	92.7	22	17 US-09-308-036A-2	Sequence 2, Appl
24	20.4	92.7	22	17 US-09-324-191A-3	Sequence 3, Appl
25	20.4	92.7	22	22 US-09-570-325-20	Sequence 20, Appl
26	20.4	92.7	22	28 US-09-700-354-2	Sequence 2, Appl
27	20.4	92.7	22	29 US-09-746-130-2	Sequence 2, Appl
28	20.4	92.7	22	30 US-09-774-403-2	Sequence 2, Appl
29	20.4	92.7	22	30 US-09-791-500-4	Sequence 4, Appl
30	20.4	92.7	22	30 US-09-791-500-5	Sequence 5, Appl
31	20.4	92.7	22	30 US-09-791-500-6	Sequence 6, Appl
32	20.4	92.7	22	30 US-09-791-500-8	Sequence 8, Appl
33	20.4	92.7	22	31 US-09-828-505-2	Sequence 2, Appl
34	20	90.9	22	16 US-09-296-477-16	Sequence 16, Appl
35	20	90.9	22	17 US-09-324-191A-6	Sequence 6, Appl
36	20	90.9	22	25 US-09-642-492-8	Sequence 7, Appl
37	19.6	89.1	22	18 US-09-415-186-7	Sequence 8, Appl
38	19.6	89.1	22	18 US-09-415-186-8	Sequence 8, Appl
39	19.4	88.2	22	16 US-09-296-477-15	Sequence 15, Appl
40	19.4	88.2	22	17 US-09-324-191A-5	Sequence 5, Appl
41	19.4	88.2	22	25 US-09-642-492-7	Sequence 7, Appl
42	19.4	88.2	22	28 US-09-713-136-7	Sequence 7, Appl
43	19.4	88.2	22	28 US-09-713-136-8	Sequence 8, Appl
44	18.8	85.5	22	1 PCT-US00-18229-32	Sequence 32, Appl
45	18.8	85.5	22	1 PCT-US00-18229-33	Sequence 33, Appl



```

RESULT 5
US-09-470-382-70
; Sequence 70, Application US/09470382
; GENERAL INFORMATION:
; APPLICANT: Eyal R. Raz
; APPLICANT: M. Teresa Magone
; TITLE OF INVENTION: METHOD FOR AMELIORATING AN ALLERGIC
; TITLE OF INVENTION: REACTION
; FILE REFERENCE: 30448.73US01
; CURRENT APPLICATION NUMBER: US/09/470.382
; CURRENT FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; US-09-470-382-70

Query Match      100.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 6
US-09-713-136-9
; Sequence 9, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713.136
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165.467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-09-713-136-9

Query Match      100.0%; Score 22; DB 28; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 7
US-09-774-403-3
; Sequence 3, Application US/09774403
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth

```

```

; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: 6510-166US1
; CURRENT APPLICATION NUMBER: US/09/774.403
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
; US-09-774-403-3

Query Match      100.0%; Score 22; DB 30; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 8
US-09-828-505-4
; Sequence 4, Application US/09828505
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; TITLE OF INVENTION: Polynucleotide Vaccines
; FILE REFERENCE: 6510-203
; CURRENT APPLICATION NUMBER: US/09/828.505
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control nucleic acid sequence
; US-09-828-505-4

Query Match      100.0%; Score 22; DB 31; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 9
PCT-US00-35064-2
; Sequence 2, Application PC/TUS0035064
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: 06510/201WO1

```



; CURRENT APPLICATION NUMBER: PCT/US00/35064  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/171,830  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutant  
PCT-US00-35064-2

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22  
||||| ||||| ||||| ||||| |||||  
DB 1 tgactgtgaagggttagagatga 22

RESULT 10  
PCT-US01-03029-2  
; Sequence 2, Application PC/TUS0103029  
; GENERAL INFORMATION:  
; APPLICANT: Eyal Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi  
; APPLICANT: Dennis A. Carson  
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in  
; FILE REFERENCE: 06510/166W01  
; CURRENT APPLICATION NUMBER: PCT/US01/03029  
; CURRENT FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/179,353  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Control sequence  
PCT-US01-03029-2

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22  
||||| ||||| ||||| ||||| |||||  
DB 1 tgactgtgaagggttagagatga 22

RESULT 11  
PCT-US01-06034-4  
; Sequence 4, Application PC/TUS0106034  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Rachmillewitz, Daniel  
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
; FILE REFERENCE: 6510-202WO  
; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
PCT-US01-06034-4

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22  
||||| ||||| ||||| ||||| |||||  
DB 1 tgactgtgaagggttagagatga 22

RESULT 12  
PCT-US01-06034-5  
; Sequence 5, Application PC/TUS0106034  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Rachmillewitz, Daniel  
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
; FILE REFERENCE: 6510-202WO  
; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
PCT-US01-06034-5

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22  
||||| ||||| ||||| ||||| |||||  
DB 1 tgactgtgaagggttagagatga 22

RESULT 13  
PCT-US01-06034-6  
; Sequence 6, Application PC/TUS0106034  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Rachmillewitz, Daniel  
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
; FILE REFERENCE: 6510-202WO  
; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
PCT-US01-06034-6

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 10;

Search completed: October 9, 2001, 21:12:48  
Job time: 20073 sec

Matches 21: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22  
|||||  
Db 1 tgactgtgaaggttagagatga 22

## RESULT 14

PCT-US01-06034-8  
; Sequence 8, Application PC/TUS0106034  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Rachmilewitz, Daniel  
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.  
; FILE REFERENCE: 6510-202WO  
; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
PCT-US01-06034-8

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 10;  
Matches 21: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22  
|||||  
Db 1 tgactgtgaaggttagagatga 22

## RESULT 15

PCT-US01-11290-2  
; Sequence 2, Application PC/TUS0111290  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Takabayashi, Kenji  
; APPLICANT: Nguyen, Minh-Duc  
; TITLE OF INVENTION: Synergistic Improvements to  
; TITLE OF INVENTION: Polynucleotide Vaccines  
; FILE REFERENCE: 6510-203WO  
; CURRENT APPLICATION NUMBER: PCT/US01/11290  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,890  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Control nucleic acid sequence  
PCT-US01-11290-2

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 10;  
Matches 21: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22  
|||||  
Db 1 tgactgtgaaggttagagatga 22

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:22 ; Search time 1391.6 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-09-713-136-9

Perfect score: 22

Sequence: 1 tgactgtgaaggttagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	6 US-09-770-943-1	Sequence 1, Appl
2	22	100.0	22	7 US-09-802-518-10	Sequence 10, Appl
3	22	100.0	22	7 US-09-802-359-9	Sequence 9, Appl
4	22	100.0	22	7 US-09-802-376-9	Sequence 9, Appl
5	20.4	92.7	22	6 US-09-770-943-2	Sequence 2, Appl
6	20.4	92.7	22	6 US-09-770-943-4	Sequence 4, Appl
7	20.4	92.7	22	6 US-09-770-943-10	Sequence 10, Appl
8	20	90.9	22	7 US-09-802-518-8	Sequence 8, Appl
9	20	90.9	22	7 US-09-802-359-8	Sequence 8, Appl
10	20	90.9	22	7 US-09-802-376-8	Sequence 8, Appl
11	19.4	88.2	22	7 US-09-802-518-7	Sequence 7, Appl
12	19.4	88.2	22	7 US-09-802-359-7	Sequence 7, Appl
13	19.4	88.2	22	7 US-09-802-376-7	Sequence 7, Appl
14	18.8	85.5	22	6 US-09-770-943-3	Sequence 3, Appl
15	18.8	85.5	22	6 US-09-770-943-7	Sequence 7, Appl
16	18.8	85.5	22	6 US-09-770-943-8	Sequence 8, Appl
17	18.8	85.5	22	7 US-09-802-518-11	Sequence 11, Appl
18	18.8	85.5	22	7 US-09-802-359-11	Sequence 11, Appl
19	18.8	85.5	22	7 US-09-802-359-10	Sequence 10, Appl
20	18.8	85.5	22	7 US-09-802-376-10	Sequence 10, Appl
21	18.8	85.5	22	7 US-09-802-376-1	Sequence 1, Appl
22	18.8	85.5	22	7 US-09-802-376-6	Sequence 6, Appl
23	17.8	80.9	22	7 US-09-802-359-6	Sequence 6, Appl
24	17.8	80.9	22	7 US-09-802-376-6	Sequence 6, Appl
25	17.8	80.9	22	7 US-09-802-376-6	Sequence 6, Appl

```

c 26 17.4 79.1 480 6 US-09-898-888-23372 Sequence 23372, A
27 17.2 78.2 22 7 US-09-802-518-2 Sequence 2, Appl
28 17.2 78.2 22 7 US-09-802-359-2 Sequence 2, Appl
29 17.2 78.2 22 7 US-09-802-359-4 Sequence 4, Appl
30 17.2 78.2 22 7 US-09-802-376-2 Sequence 2, Appl
31 17.2 78.2 22 7 US-09-802-376-2 Sequence 2, Appl
32 17.2 78.2 22 7 US-09-802-376-4 Sequence 4, Appl
33 17.2 78.2 445 6 US-09-909-629-31699 Sequence 31699, A
34 17.2 78.2 480 6 US-09-904-809-59595 Sequence 5955, A
35 17.2 78.2 786 7 US-09-861-478-5970 Sequence 5970, Ap
36 17.2 78.2 2555 8 US-60-278-258-14068 Sequence 14068, A
37 17.2 78.2 6138 7 US-09-764-905-24563 Sequence 24563, A
38 17.2 78.2 32082 6 US-09-764-891-9679 Sequence 9679, Ap
39 16.4 74.5 253 7 US-09-912-292-14215 Sequence 14215, A
40 16.4 74.5 253 7 US-09-859-662-349 Sequence 349, App
41 16.4 74.5 367 7 US-09-764-905-22190 Sequence 22190, A
42 16.2 73.6 132 7 US-09-724-750-10373 Sequence 10373, A
43 16.2 73.6 207 8 US-60-253-457-39362 Sequence 39362, A
44 16.2 73.6 212 5 US-09-920-953-4999 Sequence 4999, Ap
45 16.2 73.6 268 8 US-60-253-456-7434 Sequence 7434, Ap

```

## ALIGNMENTS

```

RESULT 1
US-09-770-943-1
; Sequence 1, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-1

```

```

Query Match 100.0% Score 22: DB 6; Length 22;
Best Local Similarity 100.0% Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 tgactgtgaaggttagagatga 22
Db 1 tgactgtgaaggttagagatga 22

```

```

RESULT 2
US-09-802-518-10
; Sequence 10, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10

```

```
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-518-10

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 3
US-09-802-359-9
; Sequence 9, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-359-9

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 4
US-09-802-376-9
; Sequence 9, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-376-9
```

```
Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 5
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match      92.7%; Score 20.4; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 6
US-09-770-943-4
; Sequence 4, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-4

Query Match      92.7%; Score 20.4; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 6
US-09-770-943-4
; Sequence 4, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-4

Query Match      92.7%; Score 20.4; DB 6; Length 22;
```

Best Local Similarity 95.5%; Pred. No. 1.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggtagagatga 22  
||||| ||||| ||||| |||||  
Db 1 tgactgtgaaggtagagatga 22

RESULT 7  
US-09-770-943-10  
; Sequence 10, Application US/09770943  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/770,943  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/092,314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-770-943-10

Query Match 92.7%; Score 20.4; DB 6; Length 22;  
Best Local Similarity 95.5%; Pred. No. 1.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggtagagatga 22  
||||| ||||| ||||| |||||  
Db 1 tgactgtgaaggtagagatga 22

RESULT 8  
US-09-802-518-8  
; Sequence 8, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-518-8

Query Match 90.9%; Score 20; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 95.5%; Pred. No. 1.5;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggtagagatga 22  
||||| ||||| ||||| |||||  
Db 1 tgactgtgaaggtagagatga 22

RESULT 9  
US-09-802-359-8  
; Sequence 8, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-359-8

Query Match 90.9%; Score 20; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggtagagatga 22  
||||| ||||| ||||| |||||  
Db 1 tgactgtgaaggtagagatga 22

RESULT 10  
US-09-802-376-8  
; Sequence 8, Application US/09802376  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201700  
; CURRENT APPLICATION NUMBER: US/09/802,376  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,557  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-376-8

Query Match 90.9%; Score 20; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 2.3;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggtagagatga 22  
||||| ||||| ||||| |||||

Db 1 tgactgtgaangttngagatga 22

RESULT 11  
US-09-802-518-7  
; Sequence 7, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-518-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 4.5;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggtagatga 22  
||||||| ||| |||||

Db 1 tgactgtgaangtcgagatga 22

RESULT 12  
US-09-802-359-7  
; Sequence 7, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-359-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 4.5;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggtagatga 22  
||||||| ||| |||||

Db 1 tgactgtgaangtcgagatga 22

RESULT 13

US-09-802-376-7  
; Sequence 7, Application US/09802376  
; GENERAL INFORMATION:  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201700  
; CURRENT APPLICATION NUMBER: US/09/802,376  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,557  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(22)  
; OTHER INFORMATION: n = 5-bromocytosine  
US-09-802-376-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 4.5;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggtagatga 22  
||||||| ||| |||||

Db 1 tgactgtgaangtcgagatga 22

RESULT 14

US-09-770-943-3  
; Sequence 3, Application US/09770943  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/770,943  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/092,314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-770-943-3

Query Match 85.5%; Score 18.8; DB 6; Length 22;  
Best Local Similarity 90.9%; Pred. No. 8.9;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggtagatga 22  
||||||| ||| |||||

Db 1 tgactgtgaacctgagatga 22

RESULT 15

US-09-770-943-7

```
; Sequence 7, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-7
```

```
Query Match      85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
   ||||||| ||| |||||||
Db 1 tgactgtgagggtcagagatga 22
```

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Search completed: October 9, 2001, 21:36:23
Job time: 21243 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:10 ; Search time 217.64 Seconds  
(without alignments)  
19.136 Million cell updates/sec

Title: US-09-713-136-9

Perfect score: 22  
Sequence: 1 tgactgtgaaggtagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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2: /cgn2.6/prodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2.6/prodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2.6/prodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2.6/prodata/1/ina/PTCUTS\_COMB.seq.\*  
6: /cgn2.6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	4	US-09-092-314-1
2	20.4	92.7	22	4	US-09-092-314-2
3	20.4	92.7	22	4	US-09-092-314-4
4	20.4	92.7	22	4	US-09-092-314-10
5	18.8	85.5	22	4	US-09-092-314-3
6	18.8	85.5	22	4	US-09-092-314-7
7	18.8	85.5	22	4	US-09-092-314-8
8	16.2	73.6	913	2	US-08-975-316-61
9	15.6	70.9	22	4	US-09-092-314-5
10	15.6	70.9	6909	2	US-08-804-196-1
11	15.6	70.9	6909	2	US-08-658-340-1
12	15.6	70.9	6909	3	US-08-746-111-26
13	15.2	69.1	1892	2	US-08-933-750C-66
14	15.2	69.1	1892	3	US-09-234-613-66
15	15.2	69.1	3655	3	US-08-878-474-6
16	15.2	69.1	4440	3	US-07-792-600-1
17	15.2	69.1	4440	3	US-09-157-021-1
18	15.2	69.1	4440	3	US-09-156-842-1
19	15.2	69.1	5433	3	US-09-157-021-35
20	15.2	69.1	5433	3	US-09-156-842-35
21	15.2	69.1	6638	2	US-08-070-301-2
22	15	68.2	6623	2	US-08-687-080-68
23	14.8	67.3	882	1	US-08-622-354-4
24	14.8	67.3	1129	3	US-08-755-587-30
25	14.6	66.4	419	4	US-08-998-416-118
26	14.6	66.4	864	1	US-08-173-510B-94
27	14.6	66.4	864	1	US-08-173-510B-96

Sequence 92, Appl  
Sequence 94, Appl  
Sequence 94, Appl  
Sequence 96, Appl  
Sequence 1, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Patent No. 5340934  
Sequence 4, Appl  
Sequence 1, Appl  
Sequence 25, Appl  
Sequence 15, Appl  
Sequence 1, Appl  
Sequence 1, Appl

28 14.6 66.4 864 1 US-08-458-218-92  
29 14.6 66.4 864 1 US-08-458-218-94  
30 14.6 66.4 864 2 US-08-450-497-94  
31 14.6 66.4 864 2 US-08-450-497-96  
32 14.6 66.4 1272 4 US-09-053-702-1  
33 14.6 66.4 2694 3 US-08-975-703-5  
34 14.6 66.4 2694 4 US-09-515-884-5  
35 14.6 66.4 3846 2 US-08-691-814B-3  
36 14.6 66.4 5687 2 US-08-380-403A-3  
37 14.6 66.4 5687 2 US-08-895-628-3  
38 14.6 65.5 1357 6 5340934-7  
39 14.4 65.5 2658 2 US-08-910-927B-4  
40 14.4 65.5 2658 4 US-09-270-270-4  
41 14.2 64.5 1261 3 US-08-530-165-1  
42 14.2 64.5 1261 3 US-08-961-083-25  
43 14.2 64.5 1314 1 US-07-662-005A-15  
44 14.2 64.5 2572 3 US-08-976-255-1  
45 14.2 64.5 2675 1 US-08-232-079-1

#### ALIGNMENTS

RESULT 1  
US-09-092-314-1  
; Sequence 1, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:

APPLICANT: Raz, Eval  
APPLICANT: Roman, Mark  
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
TITLE OF INVENTION: Sequence Activity  
Patent No. 6225292

FILE REFERENCE: 6510-173US1  
CURRENT APPLICATION NUMBER: US/09/092,314  
CURRENT FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/048,794  
PRIOR FILING DATE: 1997-06-06  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Oligonucleotide  
US-09-092-314-1

Query Match 100.0%; Score 22; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggtagagatga 22  
|||||  
Db 1 tgactgtgaaggtagagatga 22

RESULT 2  
US-09-092-314-2  
; Sequence 2, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
APPLICANT: Raz, Eval  
APPLICANT: Roman, Mark  
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
TITLE OF INVENTION: Sequence Activity  
Patent No. 6225292  
FILE REFERENCE: 6510-173US1  
CURRENT APPLICATION NUMBER: US/09/092,314  
CURRENT FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/048,794  
PRIOR FILING DATE: 1997-06-06



```
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match          92.7%  Score 20.4;  DB 4;  Length 22;
Best Local Similarity 95.5%  Pred. No. 0.1;
Matches 21;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy  1  tgactgtgaaggttagagatga 22
    ||||| ||||| ||||| |||||
Db  1  tgactgtgaacgttagagatga 22

RESULT 3
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match          92.7%  Score 20.4;  DB 4;  Length 22;
Best Local Similarity 95.5%  Pred. No. 0.1;
Matches 21;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy  1  tgactgtgaaggttagagatga 22
    ||||| ||||| ||||| |||||
Db  1  tgactgtgaacgttagagatga 22

RESULT 4
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10

Query Match          92.7%  Score 20.4;  DB 4;  Length 22;
Best Local Similarity 95.5%  Pred. No. 0.1;
Matches 21;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy  1  tgactgtgaaggttagagatga 22
    ||||| ||||| ||||| |||||
Db  1  tgactgtgaacgttagagatga 22

RESULT 5
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match          85.5%  Score 18.8;  DB 4;  Length 22;
Best Local Similarity 90.9%  Pred. No. 0.62;
Matches 20;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy  1  tgactgtgaaggttagagatga 22
    ||||| ||||| ||||| |||||
Db  1  tgactgtgaacgttagagatga 22

RESULT 6
US-09-092-314-7
; Sequence 7, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-7

Query Match      85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   ||||| ||| |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 7
US-09-092-314-8
; Sequence 8, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-8

Query Match      85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   ||||| ||| |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 8
US-08-975-316-61
; Sequence 61, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316

; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-316-61

Query Match      73.6%; Score 16.2; DB 2; Length 913;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gactgtgaagggttagagatga 22
   ||||| ||| |||||
Db 513 GACTGTGAATTTTACAGATGA 533

RESULT 9
US-09-092-314-5
; Sequence 5, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-5

Query Match      70.9%; Score 15.6; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   ||||| ||| |||||
Db 1 tgactgtgttccttagagatga 22

RESULT 10
US-08-804-196-1/c
; Sequence 1, Application US/08804196
; Patent No. 5874256
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter
```

```
; TITLE OF INVENTION: A method for diagnosing an increased
; TITLE OF INVENTION: risk for thrombosis or a genetic defect causing
; TITLE OF INVENTION: thrombosis and kit for use with the same.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5874256el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/454,353
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 948-7400
; TELEFAX: (301) 948-9751
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; US-08-804-196-1

Query Match 70.9%; Score 15.6; DB 2; Length 6909;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||| | ||| ||||
Db 793 TGACTGTGTACATTAGGGATGA 772

RESULT 11
US-08-658-340-1/c
; Sequence 1, Application US/08/58340
; Patent No. 5910576
; Patent No. 5910576 5861489
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter
; TITLE OF INVENTION: A method for diagnosing an increased
; TITLE OF INVENTION: risk for thrombosis or a genetic defect causing
; TITLE OF INVENTION: thrombosis and kit for use with the same.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5910576 5861489el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,340

Query Match 70.9%; Score 15.6; DB 2; Length 6909;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||| | ||| ||||
Db 793 TGACTGTGTACATTAGGGATGA 772

RESULT 12
US-08-746-111-26/c
; Sequence 26, Application US/08/746111
; Patent No. 6066778
; GENERAL INFORMATION:
; APPLICANT: Ginsburg, David
; APPLICANT: Cui, Jisong
; TITLE OF INVENTION: Compositions And Methods For Screening
; TITLE OF INVENTION: Compounds For Anticoagulant Activity
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,111
; FILING DATE: 06-NOV-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-746-111-26

Query Match 70.9%; Score 15.6; DB 3; Length 6909;
```

```
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/454,353
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 948-7400
; TELEFAX: (301) 948-9751
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; US-08-658-340-1

Query Match 70.9%; Score 15.6; DB 2; Length 6909;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||| | ||| ||||
Db 793 TGACTGTGTACATTAGGGATGA 772

RESULT 12
US-08-746-111-26/c
; Sequence 26, Application US/08/746111
; Patent No. 6066778
; GENERAL INFORMATION:
; APPLICANT: Ginsburg, David
; APPLICANT: Cui, Jisong
; TITLE OF INVENTION: Compositions And Methods For Screening
; TITLE OF INVENTION: Compounds For Anticoagulant Activity
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,111
; FILING DATE: 06-NOV-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-746-111-26

Query Match 70.9%; Score 15.6; DB 3; Length 6909;
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Best Local Similarity 81.8%; Pred. No. 64;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22  
||||||| | ||| |||||  
Db 793 TGAAGTGTACATTAGGATGA 772

## RESULT 13

US-08-933-750C-66/c  
; Sequence 66, Application US/08933750C  
; Patent No. 5932442  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750C  
; FILING DATE: September 23, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0356 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1892 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BRSTNOT03  
; CLONE: 641127  
US-08-933-750C-66

Query Match 69.1%; Score 15.2; DB 2; Length 1892;  
Best Local Similarity 85.0%; Pred. No. 80;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagat 20  
||| ||||| ||||| |||  
Db 1278 TGAATGTGAAGGTTCCAGCT 1259

## RESULT 14

US-09-234-613-66/c

; Sequence 66, Application US/09234613  
; Patent No. 6132973  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/234,613  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750  
; FILING DATE: September 23, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0356 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1892 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BRSTNOT03  
; CLONE: 641127  
US-09-234-613-66

Query Match 69.1%; Score 15.2; DB 3; Length 1892;  
Best Local Similarity 85.0%; Pred. No. 80;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagat 20  
||| ||||| ||||| |||  
Db 1278 TGAATGTGAAGGTTCCAGCT 1259

## RESULT 15

US-08-878-474-6  
; Sequence 6, Application US/08878474  
; Patent No. 6133232  
; GENERAL INFORMATION:  
; APPLICANT: De Robertis, Edward M.  
; APPLICANT: Bouwmeester, Tewis  
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing  
; TITLE OF INVENTION: Factors  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue

STREET: Four Embarcadero Center, Suite 1100  
CITY: San Francisco  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94111-4106  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/878,474  
FILING DATE: 18-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/020,150  
FILING DATE: 20-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Siebert, J. Suzanne  
REGISTRATION NUMBER: 28,758  
REFERENCE/DOCKET NUMBER: 3100.002US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/248-5500  
TELEFAX: 415/362-5418  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3655 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-878-474-6

Query Match 69.18; Score 15.2; DB 3; Length 3655;  
Best Local Similarity 85.08; Pred. No. 89;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 actgtgaaggttagagatga 22  
||| ||||| |||||  
Db 1467 ACAGTCAAGGTAGTAGTGA 1486

Search completed: October 9, 2001, 15:42:11  
Job time: 301 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:21:09 ; Search time 2150.93 Seconds  
(without alignments)  
158.206 Million cell updates/sec

Title: US-09-713-136-10  
Perfect score: 22  
Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba1.\*  
2: gb\_ba2.\*  
3: gb\_ba3.\*  
4: gb\_in1.\*  
5: gb\_in2.\*  
6: gb\_in3.\*  
7: gb\_om.\*  
8: gb\_ov.\*  
9: gb\_pat1.\*  
10: gb\_pat2.\*  
11: gb\_ph.\*  
12: gb\_pl1.\*  
13: gb\_pl2.\*  
14: gb\_pl3.\*  
15: gb\_pl4.\*  
16: em\_ba1.\*  
17: em\_ba2.\*  
18: em\_fun.\*  
19: em\_htgo\_hum.\*  
20: em\_htgo\_inv.\*  
21: em\_htgo\_rod.\*  
22: em\_htg\_hum1.\*  
23: em\_htg\_hum2.\*  
24: em\_htg\_hum3.\*  
25: em\_htg\_hum4.\*  
26: em\_htg\_hum5.\*  
27: em\_htg\_hum6.\*  
28: em\_htg\_hum7.\*  
29: em\_htg\_hum8.\*  
30: em\_htg\_inv1.\*  
31: em\_htg\_inv2.\*  
32: em\_htg\_other.\*  
33: em\_htg\_rod.\*  
34: em\_hum1.\*  
35: em\_hum2.\*  
36: em\_hum3.\*  
37: em\_hum4.\*  
38: em\_hum5.\*  
39: em\_hum6.\*  
40: em\_hum7.\*  
41: em\_in.\*  
42: em\_om.\*  
43: em\_or.\*

44: em\_ov.\*  
45: em\_pat.\*  
46: em\_ph.\*  
47: em\_pl.\*  
48: em\_ro.\*  
49: em\_sts.\*  
50: em\_sy.\*  
51: em\_un.\*  
52: em\_v1.\*  
53: gb\_sts1.\*  
54: gb\_sts2.\*  
55: gb\_sts3.\*  
56: gb\_sy.\*  
57: gb\_un.\*  
58: gb\_v11.\*  
59: gb\_v12.\*  
60: gb\_htg1.\*  
61: gb\_htg2.\*  
62: gb\_htg3.\*  
63: gb\_htg4.\*  
64: gb\_htg5.\*  
65: gb\_htg6.\*  
66: gb\_htg7.\*  
67: gb\_htg8.\*  
68: gb\_htg9.\*  
69: gb\_htg10.\*  
70: gb\_htg11.\*  
71: gb\_htg12.\*  
72: gb\_htg13.\*  
73: gb\_htg14.\*  
74: gb\_htg15.\*  
75: gb\_htg16.\*  
76: gb\_htg17.\*  
77: gb\_htg18.\*  
78: gb\_htg19.\*  
79: gb\_htg20.\*  
80: gb\_htg21.\*  
81: gb\_htg22.\*  
82: gb\_htg23.\*  
83: gb\_htg24.\*  
84: gb\_htg25.\*  
85: gb\_pr1.\*  
86: gb\_pr2.\*  
87: gb\_pr3.\*  
88: gb\_pr4.\*  
89: gb\_pr5.\*  
90: gb\_pr6.\*  
91: gb\_pr7.\*  
92: gb\_pr8.\*  
93: gb\_pr9.\*  
94: gb\_ro1.\*  
95: gb\_ro2.\*  
96: gb\_in4.\*  
97: gb\_pr10.\*  
98: em\_ba3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	85.5	22	9 AX036944	AX036944 Sequence
2	18.8	85.5	22	9 AX036945	AX036945 Sequence
3	18.8	85.5	22	9 AX036952	AX036952 Sequence
4	18.8	85.5	22	9 AX046993	AX046993 Sequence
5	18.8	85.5	22	10 AX083675	AX083675 Sequence
6	18.8	85.5	89163	91 HS1009H6	AL035682 Human DNA
7	18.4	83.6	22	10 AX083682	AX083682 Sequence
8	18	81.8	73938	71 AC044861	AC044861 Mus muscu

```

9      18      81.8 121332 68 AC023361
c 10      18      81.8 146306 78 AF248716
c 11      18      81.8 180558 86 AC006482
c 12      18      81.8 194026 77 AC084313
c 13      18      81.8 292420 66 AC020873
c 14      17.8 80.9 22 10 AX083681
c 15      17.8 80.9 103108 87 AC018677
c 16      17.8 80.9 118091 81 AL450407
c 17      17.8 80.9 133310 80 AL360012
c 18      17.8 80.9 149557 61 AC009111
c 19      17.8 80.9 157875 60 AC007833
c 20      17.8 80.9 167237 86 AC007938
c 21      17.8 80.9 196697 80 AL390062
c 22      17.8 80.9 201214 75 AC074012
c 23      17.8 80.9 214186 75 AC078933
c 24      17.8 80.9 309430 62 AC012209
c 25      17.4 79.1 113803 85 AC004460
c 26      17.4 79.1 151928 63 AC015688
c 27      17.4 79.1 165655 70 AC027605
c 28      17.4 79.1 165747 71 AC027807
c 29      17.4 79.1 183976 74 AC073419
c 30      17.4 79.1 187647 74 AC073220
c 31      17.4 79.1 196084 74 AC073145
c 32      17.4 79.1 221335 71 AC027654
c 33      17.4 79.1 227675 94 AF162137S2
c 34      17.2 78.2 22 9 AX036946
c 35      17.2 78.2 22 10 AX083676
c 36      17.2 78.2 22 10 AX083678
c 37      17.2 78.2 379 54 HSPF79A1
c 38      17.2 78.2 474 97 HUMF505
c 39      17.2 78.2 1587 59 HSHSUDNA
c 40      17.2 78.2 2079 5 AF025951
c 41      17.2 78.2 2495 88 AF052109
c 42      17.2 78.2 2740 94 AF220033
c 43      17.2 78.2 6652 59 HSV488A
c 44      17.2 78.2 6893 97 HUMFVA
c 45      17.2 78.2 6909 97 HUMFAV

ALIGNMENTS

RESULT 1
AX036944 AX036944 22 bp DNA PAT 16-NOV-2000
LOCUS Sequence 1 from Patent FR2790955.
DEFINITION AX036944
ACCESSION AX036944
VERSION AX036944.1 GI:11226372
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 1 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
Source Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
7 a 1 c 8 g 6 t
BASE COUNT 7 a 1 c 8 g 6 t
ORIGIN
Query Match 85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
|||||
Db 1 TGACTGTGAAGGTTAGAGATGA 22

RESULT 4
AX046993 AX046993 22 bp DNA PAT 15-DEC-2000
LOCUS Sequence 2 from Patent WO0067787.
DEFINITION AX046993
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS
SOURCE synthetic construct.

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ORGANISM      synthetic construct
REFERENCE      artificial sequence.
AUTHORS        1 (bases 1 to 22)
TITLE          HIV immunogenic compositions and methods
JOURNAL        Patent: WO 0067787-A 2 16-NOV-2000;
                THE IMMUNE RESPONSE CORPORATION (US)
FEATURES       Location/Qualifiers
source         1..22
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="phosphorothioate-modified synthetic
               oligodeoxynucleotide"
BASE COUNT    6 a 3 c 7 g 6 t
ORIGIN
Query Match   85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 tgactgtgaaccttagagatga 22
    ||||| ||||| |||||
Db 1 TGACTGTGAACGTCGAGATGA 22
    ||||| ||||| |||||

RESULT 5
AX083675
LOCUS          22 bp DNA PAT 28-FEB-2001
DEFINITION     Sequence 1 from Patent WO0112223.
ACCESSION      AX083675
VERSION        AX083675.1 GI:13185407
KEYWORDS       synthetic construct.
SOURCE          synthetic construct.
ORGANISM        artificial sequence.
REFERENCE       1 (bases 1 to 22)
AUTHORS         van Nest, G.
TITLE           Methods of modulating an immune response using immunostimulatory s
                equences and compositions for use therein
JOURNAL        Patent: WO 0112223-A 1 22-FEB-2001;
                Dynavax Technologies Corporation (US)
FEATURES       Location/Qualifiers
source         1..22
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="Synthetic construct"
BASE COUNT    6 a 3 c 7 g 6 t
ORIGIN
Query Match   85.5%; Score 18.8; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 tgactgtgaaccttagagatga 22
    ||||| ||||| |||||
Db 1 TGACTGTGAACGTCGAGATGA 22
    ||||| ||||| |||||

RESULT 6
HS1009H6
LOCUS          89163 bp DNA PRI 10-MAR-2001
DEFINITION     Human DNA sequence from clone RP5-1009H6 on chromosome 20 Contains
                parts of isoforms B and C of the NFATC2 (nuclear factor of
                activated T-cells, cytoplasmic 2) gene, ESTs, STSS and GSSs,
                complete sequence.
ACCESSION      AL035682
VERSION        AL035682.16 GI:5596686
KEYWORDS       HTG; NFATC2; nuclear factor.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 89163)
AUTHORS        Laird, G.
TITLE          Direct Submission
JOURNAL        Submitted (07-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
                CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                requests: clonerequest@sanger.ac.uk
COMMENT        On Jul 27, 1999 this sequence version replaced gi:5360968.
                During sequence assembly data is compared from overlapping clones.
                where differences are found these are annotated as variations
                together with a note of the overlapping clone name. Note that the
                variation annotation may not be found in the sequence submission
                corresponding to the overlapping clone, as we submit sequences with
                only a small overlap as described above.
                The following abbreviations are used to associate primary accession
                numbers given in the feature table with their source databases:
                Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information
                on the WormPEP database can be found at
                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                was generated from part of bacterial clone contigs of human
                chromosome 20, constructed by the Sanger Centre Chromosome 20
                Mapping Group. Further information can be found at
                http://www.sanger.ac.uk/HGP/Chr20
                This sequence is the entire insert of clone RP5-1009H6 The true
                right end of clone RP5-906P16 is at 83953 in this sequence. This
                sequence was finished as follows unless otherwise noted: all
                regions were either double-stranded or sequenced with an alternate
                chemistry or covered by high quality data (i.e., phred quality >=
                30); an attempt was made to resolve all sequencing problems, such
                as compressions and repeats; all regions were covered by at least
                one plasmid subclone or more than one M13 subclone; and the
                assembly was confirmed by restriction digest. RP5-1009H6 is from
                the library RPCI-5 constructed by the group of Pieter de Jong. For
                further details see
                http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
                Location/Qualifiers
                1..89163
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /chromosome="20"
                /clone="RP5-1009H6"
                /clone_lib="RPCI-5"
                106..496
                /note="MSTB repeat: matches 27..422 of consensus"
                646..1236
                /note="L2 repeat: matches 1760..2416 of consensus"
                1256..1338
                /note="L2 repeat: matches 2623..2700 of consensus"
                1341..1706
                /note="MSTC repeat: matches 53..404 of consensus"
                1709..2197
                /note="MLTID repeat: matches 3..484 of consensus"
                3304..3695
                /note="L2 repeat: matches 2309..2749 of consensus"
                3733..4191
                /note="L2 repeat: matches 1715..2226 of consensus"
                5322..5376
                /note="MIR repeat: matches 113..170 of consensus"
                5429..5458
                /note="15 copies 2 mer tt 86% conserved"
                6497..6590
                /note="MIR repeat: matches 78..190 of consensus"
                complement(7436..7917)
                /note="match: GSS: Em:A0429939"
                complement(7444..7910)
                /note="match: GSS: Em:A0429921"
                7612..7982
                /note="match: STS: Em:H80534"
                complement(11131..74423)
                /gene="NFATC2"
                complement(join(11131..11186,51802..52491,54923..55049,
                55441..55496,74283..74423))

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/gene="NFATC2"
/notes="continues from dJ1114A1 (AL035684) in dJ994024
(AL132866)
match: cDNAs: Em:U36575 Em:U36576 Em:U02079 Em:U43341
match: proteins: Tr:Q13469 Tr:Q60591 Tr:Q15793 Tr:Q95644
Tr:O70345 Tr:O88942 Tr:Q12865"
/codon_start=3
/evidence=not_experimental
/product="dJ1009H6.1.2 (nuclear factor of activated
T-cells, cytoplasmic 2, isoform C)"
/protein_id="CAB54871.1"
/db_xref="GI:5832399"
/db_xref="SWISS-PROT:Q13469"
/translation="ORSAHELPMVERQDTDSCLVYGGQMILTGQNFSESKVVFTEK
TTDGOIWEVMEATVDKDSQPNLVEIPEYRNKHRTPKVNFVYINGKRKRSPOH
FTYHPVPAKTEPTDEYDPTLCSTPHGLSGSQYYPQHPVAESPSCLVATMACQO
FTGLSSPDARTQONPAALVYQSRKSLSPSLGQQPALMAAPLSLADAHRSVLVHA
GSGOSSALLHPSPTNQOASPVHYSPTNQOLRCGSHQEFQHYMCENFAPGCTTRPGP
PVSGORLSPGSYPTVYQQQNTSQRANKNGPPVSDQKEVLPGVITKQEQNLDTQY
LDDVNEIRKSPSGPPARNQT"
/notes="AluJo repeat: matches 5. .287 of consensus"
complement(11933. .12426)
/gene="NFATC2"
/notes="match: GSS: Em:AQ719797"
12619. .12813
/notes="MIR repeat: matches 36. .261 of consensus"
12908. .13130
/notes="MIR repeat: matches 8. .256 of consensus"
complement(13131. .13459)
/gene="NFATC2"
/notes="match: GSS: Em:AQ076591"
complement(13131. .13463)
/gene="NFATC2"
/notes="match: GSS: Em:AQ736066"
14853. .14989
/notes="MIR repeat: matches 112. .262 of consensus"
15043. .15096
/notes="2 copies 27 mer 98% conserved"
15300. .15373
/notes="2 copies 37 mer 100% conserved"
15566. .15767
/notes="MER58A repeat: matches 2. .224 of consensus"
15770. .15829
/notes="30 copies 2 mer ta 98% conserved"
16663. .16914
/notes="AluSg repeat: matches 1. .289 of consensus"
complement(join(18422. .18485,51802. .52491,54923. .55049,
55441. .55496,74283. .74423)))
/gene="NFATC2"
/notes="continues from dJ1114A1 (AL035684) in dJ994024
(AL132866)
match: cDNAs: Em:U43341 Em:U36575 Em:U36576 Em:U02079
match: proteins: Tr:Q13469 Tr:Q60591 Tr:Q15793 Tr:Q95644
Tr:O70345 Tr:O88942 Tr:Q12865"
/codon_start=3
/evidence=not_experimental
/product="dJ1009H6.1.1 (nuclear factor of activated
T-cells, cytoplasmic 2, isoform B)"
/protein_id="CAC00529.1"
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FTGLSSPDARTQONPAALVYQSRKSLSPSLGQQPALMAAPLSLADAHRSVLVHA
GSGOSSALLHPSPTNQOASPVHYSPTNQOLRCGSHQEFQHYMCENFAPGCTTRPGP
PVSGORLSPGSYPTVYQQQNTSQRANKNGPPVSDQKEVLPGVITKQEQNLDTQY
LDELIDTHLSIQNIL"
19572. .19900
/notes="L2 repeat: matches 1632. .2028 of consensus"
20519. .20614
/notes="MIR repeat: matches 48. .143 of consensus"
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repeat_region 20740. .20822
/notes="MIR repeat: matches 113. .213 of consensus"
20823. .21087
/notes="AluSg1 repeat: matches 1. .296 of consensus"
21088. .21126
/notes="MIR repeat: matches 213. .247 of consensus"
21386. .21417
/notes="MADE1 repeat: matches 49. .80 of consensus"
complement(22146. .22630)
/gene="NFATC2"
/notes="match: GSS: Em:AQ453617"
23272. .23630
/notes="MIR1A2 repeat: matches 31. .374 of consensus"
23983. .24171
/notes="MIR repeat: matches 40. .242 of consensus"
24171. .24254
/notes="MIR repeat: matches 65. .147 of consensus"
25367. .25495
/notes="L2 repeat: matches 2582. .2748 of consensus"
25585. .25811
/notes="AluSg repeat: matches 1. .227 of consensus"
25812. .25943
/notes="MIR repeat: matches 64. .204 of consensus"
26734. .27166
/notes="L2 repeat: matches 2294. .2750 of consensus"
27967. .28266
/notes="AluX repeat: matches 1. .301 of consensus"
28331. .28522
/notes="L1M4 repeat: matches 4899. .5090 of consensus"
28537. .28676
/notes="MER3A repeat: matches 38. .180 of consensus"
28762. .29213
/notes="L1ME3A repeat: matches 5440. .5897 of consensus"
29265. .29663
/notes="L1MC5 repeat: matches 7196. .7584 of consensus"
29664. .29963
/notes="AluY repeat: matches 1. .300 of consensus"
29964. .30114
/notes="L1MC5 repeat: matches 7584. .7736 of consensus"
30280. .30353
/notes="37 copies 2 mer ag 71% conserved"
30498. .30859
/notes="L2 repeat: matches 2461. .2659 of consensus"

Query Match 85.5%; Score 18.8; DB 91; Length 89163;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagatga 22
|| ||||| ||||| |||||
DB 29289 TGGCTGTGAACCTCAGAGATGA 29310

RESULT 7
AX083682
LOCUS AX083682 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 8 from Patent WO0112223.
ACCESSION AX083682
VERSION AX083682.1 GI:13185414
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
equences and compositions for use therein
JOURNAL Patent: WO 0112223-A 8 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES
source Location/Qualifiers
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
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modified_base 11 /note="5-bromocytosine"
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modified_base 15
                /note="5-bromocytosine"
                /mod_base=OTHER
BASE COUNT    6 a 1 c 7 g 6 t 2 others
ORIGIN

Query Match      83.6%; Score 18.4; DB 10; Length 22;
Best Local Similarity 86.4%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagatga 22
    |||||  |||  |||||
Db 1 TGACTGTGAANGTNGACATGA 22

RESULT 8
AC044861/c 73938 bp DNA HTG 12-APR-2000
LOCUS Mus musculus chromosome 11 clone RP23-91F19 map 11, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
AC044861
AC044861.1 GI:7543828
VERSION HTG; HTGS_PHASE0.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 73938)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus chromosome 11, clone RP23-91F19
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 73938)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,I., Bouckhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Holland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,D., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Theodore,J., Tirrell,A., Travers,M., Triglio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L9468
Center clone name: 91_F19
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* NOTE: This record contains 87 individual

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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 722: contig of 722 bp in length
* 723 822: gap of 100 bp
* 823 1578: contig of 756 bp in length
* 1579 1678: gap of 100 bp
* 1679 2428: contig of 750 bp in length
* 2429 2528: gap of 100 bp
* 2529 3278: contig of 750 bp in length
* 3279 3378: gap of 100 bp
* 3379 4122: contig of 744 bp in length
* 4123 4222: gap of 100 bp
* 4223 4974: contig of 752 bp in length
* 4975 5074: gap of 100 bp
* 5075 5823: contig of 749 bp in length
* 5824 5923: gap of 100 bp
* 5924 6665: contig of 742 bp in length
* 6666 6765: gap of 100 bp
* 6766 7518: contig of 753 bp in length
* 7519 7618: gap of 100 bp
* 7619 8367: contig of 749 bp in length
* 8368 8467: gap of 100 bp
* 8468 9225: contig of 758 bp in length
* 9226 9325: gap of 100 bp
* 9326 10060: contig of 735 bp in length
* 10061 10160: gap of 100 bp
* 10161 10917: contig of 757 bp in length
* 10918 11017: gap of 100 bp
* 11018 11778: contig of 761 bp in length
* 11779 11878: gap of 100 bp
* 11879 12642: contig of 764 bp in length
* 12643 12742: gap of 100 bp
* 12743 13482: contig of 740 bp in length
* 13483 13582: gap of 100 bp
* 13583 14333: contig of 751 bp in length
* 14334 14433: gap of 100 bp
* 14434 15195: contig of 762 bp in length
* 15196 15295: gap of 100 bp
* 15296 16055: contig of 760 bp in length
* 16056 16155: gap of 100 bp
* 16156 16902: contig of 747 bp in length
* 16903 17002: gap of 100 bp
* 17003 17756: contig of 754 bp in length
* 17757 17856: gap of 100 bp
* 17857 18603: contig of 747 bp in length
* 18604 18703: gap of 100 bp
* 18704 19434: contig of 731 bp in length
* 19435 19534: gap of 100 bp
* 19535 20284: contig of 750 bp in length
* 20285 20384: gap of 100 bp
* 20385 21130: contig of 746 bp in length
* 21131 21230: gap of 100 bp
* 21231 21964: contig of 734 bp in length
* 21965 22064: gap of 100 bp
* 22065 22797: contig of 733 bp in length
* 22798 22897: gap of 100 bp
* 22898 23653: contig of 756 bp in length
* 23654 23753: gap of 100 bp
* 23754 24496: contig of 743 bp in length
* 24497 24596: gap of 100 bp
* 24597 25348: contig of 752 bp in length
* 25349 25448: gap of 100 bp
* 25449 26198: contig of 750 bp in length
* 26199 26298: gap of 100 bp
* 26299 27049: contig of 751 bp in length

```

```

* 27050 27149: gap of 100 bp
* 27150 27897: contig of 748 bp in length
* 27898 27997: gap of 100 bp
* 27998 28750: contig of 753 bp in length
* 28751 28850: gap of 100 bp
* 28851 29599: contig of 749 bp in length
* 29600 29699: gap of 100 bp
* 29700 30458: contig of 759 bp in length
* 30459 30558: gap of 100 bp
* 30559 31312: contig of 754 bp in length
* 31313 31412: gap of 100 bp
* 31413 32162: contig of 750 bp in length
* 32163 32262: gap of 100 bp
* 32263 32999: contig of 737 bp in length
* 33000 33099: gap of 100 bp
* 33100 33861: contig of 762 bp in length
* 33862 33961: gap of 100 bp
* 33962 34717: contig of 736 bp in length
* 34718 34817: gap of 100 bp
* 34818 35567: contig of 750 bp in length
* 35568 35667: gap of 100 bp
* 35668 36427: contig of 760 bp in length
* 36428 36527: gap of 100 bp
* 36528 37281: contig of 754 bp in length
* 37282 37381: gap of 100 bp
* 37382 38104: contig of 723 bp in length
* 38105 38204: gap of 100 bp
* 38205 38968: contig of 764 bp in length
* 38969 39068: gap of 100 bp
* 39069 39819: contig of 751 bp in length
* 39820 39919: gap of 100 bp
* 39920 40666: contig of 747 bp in length
* 40667 40766: gap of 100 bp
* 40767 41517: contig of 751 bp in length
* 41518 41617: gap of 100 bp
* 41618 42365: contig of 748 bp in length
* 42366 42465: gap of 100 bp
* 42466 43205: contig of 740 bp in length
* 43206 43305: gap of 100 bp
* 43306 44062: contig of 757 bp in length
* 44063 44162: gap of 100 bp
* 44163 44924: contig of 762 bp in length
* 44925 45024: gap of 100 bp
* 45025 45772: contig of 748 bp in length
* 45773 45872: gap of 100 bp
* 45873 46627: contig of 755 bp in length
* 46628 46727: gap of 100 bp
* 46728 47472: contig of 745 bp in length
* 47473 47572: gap of 100 bp
* 47573 48320: contig of 748 bp in length
* 48321 48420: gap of 100 bp
* 48421 49179: contig of 759 bp in length
* 49180 49279: gap of 100 bp
* 49280 50029: contig of 750 bp in length
* 50030 50129: gap of 100 bp
* 50130 50890: contig of 761 bp in length
* 50891 50990: gap of 100 bp
* 50991 51736: contig of 746 bp in length
* 51737 51836: gap of 100 bp
* 51837 52584: contig of 748 bp in length
* 52585 52684: gap of 100 bp
* 52685 53460: contig of 776 bp in length
* 53461 53560: gap of 100 bp
* 53561 54310: contig of 750 bp in length
* 54311 54410: gap of 100 bp
* 54411 55140: contig of 730 bp in length
* 55141 55240: gap of 100 bp
* 55241 55995: contig of 755 bp in length
* 55996 56095: gap of 100 bp
* 56096 56852: contig of 757 bp in length
* 56853 56952: gap of 100 bp
* 56953 57705: contig of 753 bp in length
* 57706 57805: gap of 100 bp

```

```

* 57806 58547: contig of 742 bp in length
* 58548 58647: gap of 100 bp

Query Match      81.8%; Score 18; DB 71; Length 73938;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ctgtgaaccttagagatg 21
|||||
Db 44413 CTGTGAACCTTAGAGATG 44396

RESULT
AC023361 121332 bp DNA HTG 04-NOV-2000
LOCUS Mus musculus clone RP23-316K16, *** SEQUENCING IN PROGRESS ***, 47
DEFINITION unordered pieces.
ACCESSION AC023361
VERSION AC023361.4 GI:11079344
KEYWORDS HTG; HTGS_PHASE1.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 121332)
Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Jia, Y., Kelly, J., Kelly, S.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Lozano, R.J., Martin, R.,
Kovar, C., Liu, J., Liu, W., Loulsegod, H., Lozano, R.J., Morgan, M., Morris, S.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Parish, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogih, M., Parish, S.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Worley, K. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 121332)
Worley, K.C.
Direct Submission
Submitted (14-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 3, 2000 this sequence version replaced gi:7025658.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MAAE
Center clone name: RP23-316K16
----- Summary Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy; 74% of reads
Chemistry: Dye-terminator Big Dye; 26% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 79638 bases at least Q40
Consensus quality: 100663 bases at least Q30
Consensus quality: 110213 bases at least Q20
Estimated insert size: 101687; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 1.2x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces

```

\* Is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 8407: contig of 8407 bp in length  
 \* 8408 8507: gap of unknown length  
 \* 8508 14631: contig of 6124 bp in length  
 \* 14632 14731: gap of unknown length  
 \* 14732 18775: contig of 4044 bp in length  
 \* 18776 18876: gap of unknown length  
 \* 18877 23354: contig of 4479 bp in length  
 \* 23355 23455: gap of unknown length  
 \* 23456 29014: contig of 5560 bp in length  
 \* 29015 29114: gap of unknown length  
 \* 29115 33875: contig of 4761 bp in length  
 \* 33876 33976: gap of unknown length  
 \* 33977 39221: contig of 5346 bp in length  
 \* 39222 42432: gap of unknown length  
 \* 42433 42532: contig of 3011 bp in length  
 \* 42533 45875: gap of unknown length  
 \* 45876 45975: contig of 3343 bp in length  
 \* 45976 49070: gap of unknown length  
 \* 49071 52556: contig of 3095 bp in length  
 \* 52557 52656: contig of 3386 bp in length  
 \* 52657 55765: gap of unknown length  
 \* 55766 55865: contig of 3109 bp in length  
 \* 55866 59213: gap of unknown length  
 \* 59214 59313: contig of 3347 bp in length  
 \* 59313 60922: gap of unknown length  
 \* 60923 61022: contig of 1610 bp in length  
 \* 61023 63102: gap of unknown length  
 \* 63103 63202: contig of 2080 bp in length  
 \* 63203 64446: gap of unknown length  
 \* 64447 64546: contig of 1244 bp in length  
 \* 64547 66365: gap of unknown length  
 \* 66366 69328: contig of 1819 bp in length  
 \* 69329 69428: gap of unknown length  
 \* 69429 71591: contig of 2863 bp in length  
 \* 71592 71691: gap of unknown length  
 \* 71692 73841: contig of 2163 bp in length  
 \* 73842 73941: contig of 2150 bp in length  
 \* 73942 77152: gap of unknown length  
 \* 77153 77252: contig of 3211 bp in length  
 \* 77253 79347: gap of unknown length  
 \* 79348 81097: contig of 2095 bp in length  
 \* 81098 81197: gap of unknown length  
 \* 81198 83008: contig of 1650 bp in length  
 \* 83009 83108: gap of unknown length  
 \* 83109 85686: contig of 1811 bp in length  
 \* 85687 87348: gap of unknown length  
 \* 87349 87448: gap of unknown length  
 \* 87449 88710: contig of 1562 bp in length  
 \* 88710 90252: gap of unknown length  
 \* 90253 90352: contig of 1261 bp in length  
 \* 90353 92076: gap of unknown length  
 \* 92077 92176: contig of 1443 bp in length  
 \* 92177 93952: gap of unknown length  
 \* 93953 94052: contig of 1724 bp in length  
 \* 94053 95890: contig of 1776 bp in length  
 \* 95891 95990: gap of unknown length  
 \* 95991 97702: contig of 1838 bp in length  
 \* 97703 97802: gap of unknown length  
 \* 97803 99155: contig of 1712 bp in length  
 \* 99156 99255: gap of unknown length  
 \* 99256 100824: contig of 1352 bp in length  
 \* 100825 100824: contig of 1570 bp in length

\* 100825 100924: gap of unknown length  
 \* 100925 102458: contig of 1534 bp in length  
 \* 102459 102558: gap of unknown length  
 \* 102559 104019: contig of 1461 bp in length  
 \* 104020 104119: gap of unknown length  
 \* 104120 105953: contig of 1834 bp in length  
 \* 105954 106053: gap of unknown length  
 \* 106054 108172: contig of 2119 bp in length  
 \* 108173 108272: gap of unknown length  
 \* 108273 109818: contig of 1546 bp in length  
 \* 109819 111179: gap of unknown length  
 \* 111180 111279: contig of 1261 bp in length  
 \* 111280 112976: gap of unknown length  
 \* 112977 113076: contig of 1697 bp in length  
 \* 113077 114376: gap of unknown length  
 \* 114377 114476: contig of 1300 bp in length  
 \* 114477 115792: gap of unknown length  
 \* 115793 115892: contig of 1316 bp in length  
 \* 115893 117014: gap of unknown length  
 \* 117015 117114: contig of 1122 bp in length  
 \* 117115 118392: gap of unknown length  
 \* 118393 118492: contig of 1278 bp in length  
 \* 118493 119759: gap of unknown length  
 \* 119760 119859: contig of 1267 bp in length  
 \* 119860 121332: gap of unknown length  
 \* 119861 121332: contig of 1473 bp in length.

FEATURES  
 Source  
 1. 121332  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="RP23-316K16"

BASE COUNT 30929 a 27070 c 27181 g 31494 t 4658 others  
 ORIGIN

Query Match 81.8% Score 18; DB 68; Length 121332;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ctgtgaaccttagagatg 21  
 |||||

Db 21742 CTGTGACCTTAGAGATG 21759

RESULT 10  
 AF248716/c  
 LOCUS AF248716 146306 bp DNA HTG 12-APR-2000  
 DEFINITION Mus musculus chromosome 11 clone CT7-327023, \*\*\* SEQUENCING IN  
 PROGRESS \*\*\*, in ordered pieces.  
 ACCESSION AF248716  
 VERSION AF248716.1 GI:7542829  
 KEYWORDS HTG; HTGS, PHASE2.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 146306)  
 Loois, G.G., Locksley, R.M., Blankespoor, C.M., Wang, Z.E., Miller, W.,  
 Rubin, E.M. and Frazer, K.A.  
 Identification of a coordinate regulator of interleukins 4, 13, and  
 5 by cross-species sequence comparisons  
 Science 288 (5463), 136-140 (2000)  
 JOURNAL 20217223  
 MEDLINE 10753117  
 PUBMED 10753117  
 REFERENCE 2 (bases 1 to 146306)  
 Dean, W.B., Lewis, K.D., Blankespoor, C.M., Nyugen, A., Loois, G.G.,  
 Rubin, E.M. and Frazer, K.A.  
 Direct Submission  
 Submitted (23-MAR-2000) Genome Sciences Department, Lawrence  
 Berkeley National Laboratory, 1 Cyclotron Road, Berkeley, CA  
 94720, USA

NOTE: This is a 'working draft' sequence. It consists of 8 contigs.  
 The order of contigs is believed to be correct. Gaps between the

**AUTHORS** Waterston, R. H.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (21-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

```
repeat_region 4071..4567 /rpt_family="MaLR"
repeat_region 4589..4609 /rpt_family="AT_rich"
repeat_region 4623..4769 /rpt_family="MIR"
repeat_region 6394..6531 /rpt_family="MIR"
repeat_region 7056..9142 /rpt_family="L1"
repeat_region 9146..9316 /rpt_family="Alu"
repeat_region 9352..12747 /rpt_family="L1"
repeat_region 12748..13058 /rpt_family="Alu"
repeat_region 13059..14199 /rpt_family="L1"
repeat_region 14200..14518 /rpt_family="Alu"
repeat_region 14519..14893 /rpt_family="L1"
repeat_region 15129..15514 /rpt_family="MaLR"
repeat_region 15516..15636 /rpt_family="L2"
repeat_region 15637..16028 /rpt_family="MaLR"
repeat_region 16029..16213 /rpt_family="L2"
repeat_region 16266..16699 /rpt_family="L2"
repeat_region 17832..17892 /rpt_family="MER1_type"
repeat_region 17893..18176 /rpt_family="Alu"
repeat_region 18177..18350 /rpt_family="MER1_type"
repeat_region 18351..19056 /rpt_family="L1"
repeat_region 19076..19354 /rpt_family="L1"
repeat_region 19422..20569 /rpt_family="L1"
repeat_region 20570..20651 /rpt_family="MER1_type"
repeat_region 20652..20933 /rpt_family="Alu"
repeat_region 20934..20957 /rpt_family="(TAAA)n"
repeat_region 20958..21119 /rpt_family="MER1_type"
repeat_region 21120..21423 /rpt_family="Alu"
repeat_region 21424..22042 /rpt_family="MER1_type"
repeat_region 22043..22354 /rpt_family="Alu"
repeat_region 22355..22867 /rpt_family="MER1_type"
repeat_region 22945..23016 /rpt_family="MaLR"
repeat_region 24817..24919 /rpt_family="MIR"
repeat_region 24908..25068 /rpt_family="L2"
repeat_region 25109..25253 /rpt_family="MIR"
repeat_region 26208..26565 /rpt_family="L1"
repeat_region 26896..27135 /rpt_family="L1"
repeat_region 27594..27685
```

```
repeat_region /rpt_family="MIR"
27692..27904 /rpt_family="L2"
28971..29157 /rpt_family="MER1_type"
30167..30420 /rpt_family="MIR"
30886..30945 /rpt_family="(TG)n"
32179..32291 /rpt_family="L2"
32770..32864 /rpt_family="L2"
32907..32970 /rpt_family="MIR"
33065..33123 /rpt_family="MIR"
33266..33289 /rpt_family="AT_rich"
34087..34187 /rpt_family="MER1_type"
34809..34836 /rpt_family="AT_rich"
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Query Match 81.8%; Score 18; DB 86; Length 180568;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ctgtgaaccttagagatg 21  
|||||

Db 160426 CTGTGAACCTTAGAGATG 160409

RESULT 12

AC084313

LOCUS AC084313 194026 bp DNA HTG 12-JAN-2001  
DEFINITION Homo sapiens chromosome 7 clone RP11-301D21, WORKING DRAFT  
SEQUENCE, 12 unordered pieces.

ACCESSION AC084313

VERSION AC084313.3 GI:12084094

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 194026)

AUTHORS Waterston,R.H.

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 194026)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL

Submitted (23-OCT-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA

COMMENT On Jan 12, 2001 this sequence version replaced gi:10954408.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H.NH0301D21

----- Summary Statistics -----

Sequencing vector: M13; 97%

Sequencing vector: plasmid; 0%

Chemistry: Dye-primer ET; 97% of reads

Chemistry: Dye-terminator Big Dye; 0% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 186566 bases at least Q40

Consensus quality: 188959 bases at least Q30

Consensus quality: 190127 bases at least Q20

Insert size: 193000; agarose-fp

Insert size: 192956; sum-of-contigs  
 Quality coverage: 4.67 in Q20 bases; agarose-fp  
 Quality coverage: 5.18 in Q20 bases; sum-of-contigs  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 12 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 14547: contig of 14547 bp in length  
 \* 14548 14647: gap of unknown length  
 \* 14648 31784: contig of 17137 bp in length  
 \* 31785 31884: gap of unknown length  
 \* 31885 50934: contig of 19070 bp in length  
 \* 50935 51054: gap of unknown length  
 \* 51055 76962: contig of 25908 bp in length  
 \* 76963 77062: gap of unknown length  
 \* 77063 109852: contig of 32790 bp in length  
 \* 109853 109952: gap of unknown length  
 \* 109953 148938: contig of 38986 bp in length  
 \* 148939 149038: gap of unknown length  
 \* 149039 150656: contig of 1618 bp in length  
 \* 150657 150756: gap of unknown length  
 \* 150757 155954: contig of 5198 bp in length  
 \* 155955 156034: gap of unknown length  
 \* 156035 162680: contig of 6626 bp in length  
 \* 162681 162780: gap of unknown length  
 \* 162781 170137: contig of 7357 bp in length  
 \* 170138 170237: gap of unknown length  
 \* 170238 181387: contig of 11150 bp in length  
 \* 181388 181487: gap of unknown length  
 \* 181488 194026: contig of 12539 bp in length.

## FEATURES

## Source

1. .194026  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="7"  
 /clone="RP11-301D21"

## misc\_feature

1. .14547  
 /note="assembly\_name:Contig10"  
 14648. .31784  
 /note="assembly\_name:Contig11"  
 31885. .50954  
 /note="assembly\_name:Contig12"  
 51055. .76962  
 /note="assembly\_name:Contig13"  
 77063. .109852  
 /note="assembly\_name:Contig14"  
 109953. .148938  
 /note="assembly\_name:Contig15"  
 149039. .150656  
 /note="assembly\_name:Contig14"  
 150757. .155954  
 /note="assembly\_name:Contig5"  
 156055. .162680  
 /note="assembly\_name:Contig6"  
 162781. .170137  
 /note="assembly\_name:Contig7"  
 clone\_end:T7  
 vector\_side:left  
 170238. .181387  
 /note="assembly\_name:Contig8"  
 clone\_end:SP6  
 vector\_side:left  
 181488. .194026  
 /note="assembly\_name:Contig9"

## misc\_feature

170238. .181387  
 /note="assembly\_name:Contig8"  
 clone\_end:SP6  
 vector\_side:left  
 181488. .194026  
 /note="assembly\_name:Contig9"

## misc\_feature

181488. .194026  
 /note="assembly\_name:Contig9"

## BASE COUNT

60487 a 35185 c 35984 g 61269 t 1101 others

## ORIGIN

Query Match 81.8%; Score 18; DB 77; Length 194026;  
 Best local Similarity 100.0%; Pred. No. 62;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 ctgtgaaccttagatg 21  
 |||||  
 Db 146011 CTGTGAACCTTAGAGATG 146028  
 |||||  
 RESULT 13  
 AC020873/c AC020873 292420 bp DNA HTG 29-JUN-2000  
 LOCUS Mus musculus clone RP23-327023, WORKING DRAFT SEQUENCE, 113  
 DEFINITION unorderd pieces.  
 AC020873 AC020873.2 GI:8810268  
 VERSION HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS house mouse.  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 292420)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Sequencing of Mouse  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 292420)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 On Jun 29, 2000 this sequence version replaced gi:6686435.  
 -----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: http://www.jgi.doe.gov  
 -----  
 Project Information  
 Center Project Name: 1862799  
 Center clone name: RPCI-23\_327023  
 -----  
 Summary Statistics  
 Consensus quality: 193189 bases at least Q40  
 Consensus quality: 233546 bases at least Q30  
 Consensus quality: 244455 bases at least Q20  
 Estimated insert size: 190000; pulse field gel estimation  
 Estimated insert size: 281220; sum-of-contigs estimation  
 Quality coverage: 5.6 in Q20 bases; pulse field gel estimation.  
 Quality coverage: 3.78 in Q20 bases; sum-of-contigs estimation.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 113 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 1059: contig of 1059 bp in length  
 \* 1060 1159: gap of unknown length  
 \* 1160 2247: contig of 1088 bp in length  
 \* 2248 2347: gap of unknown length  
 \* 2348 3573: contig of 1226 bp in length  
 \* 3574 3673: gap of unknown length  
 \* 3674 4728: contig of 1055 bp in length  
 \* 4729 4828: gap of unknown length  
 \* 4829 6441: contig of 1613 bp in length  
 \* 6442 6541: gap of unknown length  
 \* 6542 7697: contig of 1156 bp in length  
 \* 7698 7797: gap of unknown length  
 \* 7798 8850: contig of 1053 bp in length  
 \* 8851 8950: gap of unknown length  
 \* 8951 10178: contig of 1228 bp in length  
 \* 10179 10278: gap of unknown length  
 \* 10279 11293: contig of 1015 bp in length

\* 11294 11393: gap of unknown length  
\* 11394 13001: contig of 1608 bp in length  
\* 13002 13101: gap of unknown length  
\* 13102 14530: contig of 1429 bp in length  
\* 14531 14630: gap of unknown length  
\* 14631 15697: contig of 1067 bp in length  
\* 15698 15797: gap of unknown length  
\* 15798 16873: contig of 1076 bp in length  
\* 16874 16973: gap of unknown length  
\* 16974 18287: contig of 1314 bp in length  
\* 18288 18387: gap of unknown length  
\* 18388 19408: contig of 1021 bp in length  
\* 19409 19508: gap of unknown length  
\* 19509 20618: contig of 1110 bp in length  
\* 20619 20718: gap of unknown length  
\* 20719 22224: contig of 1506 bp in length  
\* 22225 22324: gap of unknown length  
\* 22326 23378: contig of 1054 bp in length  
\* 23379 23478: gap of unknown length  
\* 23479 24903: contig of 1425 bp in length  
\* 24904 25003: gap of unknown length  
\* 25004 26371: contig of 1368 bp in length  
\* 26372 26471: gap of unknown length  
\* 26472 27690: contig of 1219 bp in length  
\* 27691 27790: gap of unknown length  
\* 27791 28904: contig of 1114 bp in length  
\* 28905 30554: contig of 1550 bp in length  
\* 30555 30654: gap of unknown length  
\* 30656 32119: contig of 1465 bp in length  
\* 32120 32219: gap of unknown length  
\* 32220 33397: contig of 1178 bp in length  
\* 33398 33497: gap of unknown length  
\* 33498 34545: contig of 1048 bp in length  
\* 34546 34645: gap of unknown length  
\* 34646 35665: contig of 1020 bp in length  
\* 35666 37665: gap of unknown length  
\* 37666 37129: contig of 1364 bp in length  
\* 37130 37229: gap of unknown length  
\* 37230 38398: contig of 1169 bp in length  
\* 38399 38498: gap of unknown length  
\* 38499 39512: contig of 1014 bp in length  
\* 39513 39612: gap of unknown length  
\* 39613 40750: contig of 1138 bp in length  
\* 40751 40850: gap of unknown length  
\* 40851 41850: contig of 1000 bp in length  
\* 41851 41950: gap of unknown length  
\* 41951 43306: contig of 1356 bp in length  
\* 43307 43406: gap of unknown length  
\* 43407 44461: contig of 1055 bp in length  
\* 44462 44561: gap of unknown length  
\* 44562 46308: contig of 1747 bp in length  
\* 46309 46408: gap of unknown length  
\* 46409 47905: contig of 1497 bp in length  
\* 47906 48005: gap of unknown length  
\* 48006 49428: contig of 1423 bp in length  
\* 49429 49528: gap of unknown length  
\* 49529 50895: contig of 1367 bp in length  
\* 50896 50995: gap of unknown length  
\* 50996 52180: contig of 1185 bp in length  
\* 52181 52280: gap of unknown length  
\* 52281 53377: contig of 1097 bp in length  
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\* 53479 54708: contig of 1231 bp in length  
\* 54709 54808: gap of unknown length  
\* 54809 56126: contig of 1318 bp in length  
\* 56127 56226: gap of unknown length  
\* 56227 57615: contig of 1389 bp in length  
\* 57616 57715: gap of unknown length  
\* 57716 59193: contig of 1478 bp in length  
\* 59194 59293: gap of unknown length  
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\* 60442 62061: contig of 1620 bp in length  
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\* 62162 64114: contig of 1953 bp in length  
\* 64115 64214: gap of unknown length  
\* 64215 65794: contig of 1580 bp in length  
\* 65795 65894: gap of unknown length  
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\* 67376 67475: gap of unknown length  
\* 67476 68572: contig of 1097 bp in length  
\* 68573 68672: gap of unknown length  
\* 68673 69900: contig of 1228 bp in length  
\* 69901 70000: gap of unknown length  
\* 70001 71201: contig of 1201 bp in length  
\* 71202 71301: gap of unknown length  
\* 71302 73060: contig of 1759 bp in length  
\* 73061 73160: gap of unknown length  
\* 73161 74410: contig of 1250 bp in length  
\* 74411 74510: gap of unknown length  
\* 74511 76795: contig of 2285 bp in length  
\* 76796 76895: gap of unknown length  
\* 76896 78854: contig of 1959 bp in length  
\* 78855 78954: gap of unknown length  
\* 78955 80435: contig of 1481 bp in length  
\* 80436 80535: gap of unknown length  
\* 80536 81758: contig of 1223 bp in length  
\* 81759 81858: gap of unknown length  
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\* 82959 84058: contig of 1100 bp in length  
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\* 84159 86426: contig of 2268 bp in length  
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\* 86527 88314: contig of 1788 bp in length  
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\* 94561 96081: contig of 1521 bp in length  
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\* 96182 97318: contig of 1137 bp in length  
\* 97319 97418: gap of unknown length  
\* 97419 99350: contig of 1932 bp in length  
\* 99351 99450: gap of unknown length  
\* 99451 100979: contig of 1529 bp in length  
\* 100980 102079: gap of unknown length  
\* 101080 102260: contig of 1181 bp in length  
\* 102261 102360: gap of unknown length  
\* 102361 103407: contig of 1047 bp in length  
\* 103408 103507: gap of unknown length  
\* 103508 105016: contig of 1509 bp in length  
\* 105017 105116: gap of unknown length  
\* 105117 106848: contig of 1732 bp in length  
\* 106849 106948: gap of unknown length  
\* 106949 109545: contig of 2597 bp in length  
\* 109546 109645: gap of unknown length  
\* 109646 111495: contig of 1850 bp in length  
\* 111496 111595: gap of unknown length  
\* 111596 113429: contig of 1834 bp in length  
\* 113430 113529: gap of unknown length  
\* 113530 114998: contig of 1469 bp in length

Query Match 81.8%; Score 18; DB 66; Length 292420;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ctgtgaaccttagagatg 21  
|||||

Db 280795 CTGTGAACCTTAGAGATG 280778



JOURNAL  
COMMENT

RESULT 14  
 AX083681  
 LOCUS 22 bp DNA PAT 28-FEB-2001  
 DEFINITION Sequence 7 from Patent WO0112223.  
 ACCESSION AX083681  
 VERSION AX083681.1 GI:13185413  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE 1 (bases 1 to 22)  
 AUTHORS van Nest, G.  
 TITLE Methods of modulating an immune response using immunostimulatory s  
 sequences and compositions for use therein  
 JOURNAL Patent: WO 0112223-A 7 22-FEB-2001;  
 Dynavax Technologies Corporation (US)  
 FEATURES  
 source 1..22  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 modified\_base 11  
 /note="5-bromocytosine"  
 /mod\_base=OTHER

BASE COUNT 6 a 2 c 7 g 6 t 1 others  
 ORIGIN  
 Query Match 80.9%; Score 17.8; DB 10; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 40;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
 ||||| |||||  
 Db 1 TGACTGTGAAGTTCGAGATGA 22

RESULT 15  
 AC018677  
 LOCUS 103108 bp DNA PRI 30-SEP-2000  
 DEFINITION Homo sapiens BAC clone RP11-264A13 from Y, complete sequence.  
 ACCESSION AC018677  
 VERSION AC018677.3 GI:9581959  
 KEYWORDS HTG.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 103108)  
 AUTHORS Sulston, J.E. and Waterston, R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 MEDLINE 99063792  
 REFERENCE 2 (bases 1 to 103108)  
 AUTHORS Ozersky, P., Drone, K. and Wedgeworth, P.  
 TITLE The sequence of Homo sapiens BAC clone RP11-264A13  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 103108)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-DEC-1999) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE 4 (bases 1 to 103108)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-JUL-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE 5 (bases 1 to 103108)  
 AUTHORS Waterston, R.  
 TITLE Direct Submission

Submitted (30-SEP-2000) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Jul 29, 2000 this sequence version replaced gi:7630919.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc  
 Contact: saplens@wustl.edu  
 ----- Summary Statistics  
 -----  
 Center project name: H\_NH0264A13  
 -----

NOTICE: This sequence may not represent the entire insert of this  
 clone. It may be shorter because we only sequence overlapping  
 clone sections once, or longer because we provide a small overlap  
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

MAPPING INFORMATION:  
 The position of this clone was established as part of a  
 collaboration between the Human Chromosome Y Mapping Project  
 (Tomoko Kawaguchi, Helen Skaletsky, Laura G. Brown, Steve Rosen,  
 and David C. Page at the Whitehead Institute for Biomedical  
 Research, Cambridge MA) and the Washington University Genome  
 Sequencing Center, St. Louis MO.

SOURCE INFORMATION:  
 The RPCI-11 human BAC library was made from the blood of one male  
 donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,  
 Tatenoe, M., Catanese, J.J. and de Jong, P.J. (1998) An improved  
 approach for construction of bacterial artificial chromosome  
 libraries. Genomics 51:1-8. The clone may be obtained either from  
 Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong  
 and coworkers at the Roswell Park Cancer Institute  
 (http://bacpac.med.buffalo.edu)  
 VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RP11-292P9, 200 bp overlap; the  
 clone sequenced to the right is RP11-53K10. Actual start of this  
 clone is at base position 99669 of RP11-292P9; actual end is at  
 base position 103108 of RP11-264A13.

A well-conserved inverted repeat extends from RP11-292P9 to 39737  
 of RP11-264A13 with the intervening unique sequence from base 1084  
 to 4503. Due to the large size of the inverted repeat PCR and  
 digest data could not confirm the orientation of the loop.

FEATURES  
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 1..103108  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="Y"  
 /map="Y"  
 /clone="RP11-264A13"  
 /clone\_lib="RPCI-11"  
 497..807  
 /rpt\_family="Alu"  
 repeat\_region  
 1760..1824  
 /rpt\_family="ERV1"  
 repeat\_region  
 2054..2604  
 /rpt\_family="ERV1"  
 repeat\_region  
 3189..3298  
 /rpt\_family="L2"  
 repeat\_region  
 3563..3873  
 /rpt\_family="Alu"  
 repeat\_region  
 3975..4063  
 /rpt\_family="Alu"

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repeat_region 4772..5084 /rpt_family="Alu"
repeat_region 11636..11799 /rpt_family="L1"
repeat_region 11824..12039 /rpt_family="L1"
repeat_region 12083..12119 /rpt_family="MaLR"
repeat_region 12366..12445 /rpt_family="MaLR"
repeat_region 13243..13307 /rpt_family="ERV1"
repeat_region 13408..13545 /rpt_family="MER1_type"
repeat_region 13547..13635 /rpt_family="Alu"
repeat_region 13856..14014 /rpt_family="MIR"
misc_feature 14536..14929 /note="similar to EST AI807575 (NID:g5394141) wx43a10.x1"
misc_feature 14536..14900 /note="similar to EST AW448974 (NID:g6989750)"
misc_feature 14538..14980 /note="similar to EST AW339341 (NID:g6835888) x289a01.x1"
repeat_region 14596..14747 /rpt_family="MER1_type"
misc_feature 16533..16805 /note="similar to EST AA827461 (NID:g28999902) of28g01.s1"
repeat_region 16668..16765 /rpt_family="L1"
repeat_region 16766..17053 /rpt_family="Alu"
repeat_region 17054..17655 /rpt_family="L1"
repeat_region 17727..18038 /rpt_family="Alu"
repeat_region 18054..18345 /rpt_family="Alu"
repeat_region 19063..19266 /rpt_family="MER1_type"
repeat_region 20519..20812 /rpt_family="Alu"
repeat_region 22275..22455 /rpt_family="MER1_type"
repeat_region 22552..23757 /rpt_family="SVA"
repeat_region 24382..24671 /rpt_family="L1"
repeat_region 24685..24858 /rpt_family="L1"
repeat_region 25148..25516 /rpt_family="L1"
repeat_region 25518..25903 /rpt_family="MaLR"
repeat_region 25909..25975 /rpt_family="L1"
repeat_region 26444..26521 /rpt_family="L2"
repeat_region 26903..26972 /rpt_family="Mariner"
repeat_region 28311..28496 /rpt_family="Alu"
repeat_region 28497..28590 /rpt_family="Alu"
repeat_region 29127..29379 /rpt_family="Alu"
repeat_region 29831..30017 /rpt_family="ERV1"
repeat_region 30255..30636 /rpt_family="ERV1"
repeat_region 31048..31292 /rpt_family="ERV1"
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repeat_region /rpt_family="L1"
repeat_region /rpt_family="MER2_type"
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repeat_region /rpt_family="L1"
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Query Match      80.9%; Score 17.8; DB 87; Length 103108;
Best Local Similarity 90.5%; Pred. No. 76;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatg 21
   ||||| | ||||| |||||
Db 47135 TGACTGTGAGCCTTAGAGATG 47155
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Search completed: October 9, 2001, 16:21:38  
Job time: 2668 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:29 ; Search time 6788.49 Seconds  
(without alignments)  
30.635 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22  
Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
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46: gb\_est46:\*  
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44: em\_esthum10:\*  
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113: gb\_est36:\*  
114: gb\_est37:\*  
115: gb\_est38:\*  
116: gb\_est39:\*



Unpublished (1999)  
Other\_GSSs: RPCI-24-97J15.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end plate: http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html  
Plate: 97 row: J column: 15  
Seq primer: SP6  
Class: BAC ends.

Location/Qualifiers  
1. 489  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db.xref="taxon:10090"  
/clone="RPCI-24-97J15"  
/clone\_lib="RPCI-24"  
/sex="Male"  
/cell\_type="Spleen/Brain"  
/note="Vector: pTARBAC1; Site\_1: BamHI; Site\_2: BamHI; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

BASE COUNT 131 a 96 c 93 g 169 t  
ORIGIN

Query Match 83.6%; Score 18.4; DB 248; Length 489;  
Best Local Similarity 95.0%; Pred. NO. 85;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 gactgtgaaccttagatg 21  
||||| ||||||| |||||||  
Db 157 GACTTTGACCTTAGAGATG 138

RESULT 2  
AZ881693 570 bp DNA GSS 05-MAR-2001  
LOCUS  
DEFINITION RPCI-23-204F1.TV RPCI-23 Mus musculus genomic clone RPCI-23-204F1,  
DNA sequence.  
ACCESSION AZ881693  
VERSION  
KEYWORDS GSS,  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 570)  
AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.  
TITLE Mouse BAC End Sequences from Library RPCI-23  
JOURNAL Unpublished (1999)  
COMMENT Other\_GSSs: RPCI-23-204F1.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	18.4	83.6	489	248	AZ749943	AZ749943 RPCI-24-9
C 2	18.4	83.6	570	251	AZ881693	AZ881693 RPCI-23-2
C 3	17.8	80.9	431	237	AZ052737	AZ052737 RPCI-23-3
C 4	17.8	80.9	507	155	BG552950	BG552950 dab81h04
C 5	17.8	80.9	535	244	AZ479424	AZ479424 IM0300H03
C 6	17.8	80.9	561	249	AZ755668	AZ755668 ev02909.x
C 7	17.4	79.1	422	226	AQ245899	AQ245899 HS_2056.B
C 8	17.2	78.2	142	135	BB484411	BB484411 BB484411
C 9	17.2	78.2	236	107	AU053757	AU053757 AU053757
C 10	17.2	78.2	254	107	AU053032	AU053032 AU053032
C 11	17.2	78.2	265	107	AU054169	AU054169 AU054169
C 12	17.2	78.2	270	107	AU053754	AU053754 AU053754
C 13	17.2	78.2	340	107	AU040059	AU040059 AU040059
C 14	17.2	78.2	371	107	AU039239	AU039239 AU039239
C 15	17.2	78.2	398	143	BF010530	BF010530 NXCI_085
C 16	17.2	78.2	424	139	BE723539	BE723539 193384.NA
C 17	17.2	78.2	429	150	BF523228	BF523228 UT-R-C3-t
C 18	17.2	78.2	449	224	AQ114479	AQ114479 CIT-HSP-2
C 19	17.2	78.2	457	107	AU034234	AU034234 AU034234
C 20	17.2	78.2	463	107	AU083559	AU083559 AU083559
C 21	17.2	78.2	474	107	AU052381	AU052381 AU052381
C 22	17.2	78.2	474	171	BF963693	BF963693 PM4-NN120
C 23	17.2	78.2	479	107	AU089685	AU089685 AU089685
C 24	17.2	78.2	509	107	AU039788	AU039788 AU039788
C 25	17.2	78.2	513	107	AU034515	AU034515 AU034515
C 26	17.2	78.2	515	11	AA769863	AA769863 z118b04.s
C 27	17.2	78.2	520	107	AU039823	AU039823 AU039823
C 28	17.2	78.2	521	230	AQ567409	AQ567409 HS_2111.B
C 29	17.2	78.2	535	233	AQ804943	AQ804943 HS_3150.A
C 30	17.2	78.2	549	139	BE755006	BE755006 208706.NA
C 31	17.2	78.2	574	136	BE496465	BE496465 NXCI_018
C 32	17.2	78.2	669	156	C22959	C22959 C22959 Dict
C 33	17.2	78.2	681	108	AU140713	AU140713 AU140713
C 34	17.2	78.2	681	115	AW349092	AW349092 GM210003B
C 35	17.2	78.2	699	107	AU034932	AU034932 AU034932
C 36	17.2	78.2	714	107	AU033417	AU033417 AU033417
C 37	17.2	78.2	936	220	CNS03417	AL227305 Tetraodon
C 38	17.2	78.2	996	220	CNS02760	AL184630 Tetraodon
C 39	17.2	78.2	1106	222	CNS05GCO	AL336129 Tetraodon
C 40	16.8	76.4	105	2	AA094019	AA094019 cl1619.se
C 41	16.8	76.4	224	127	BB185712	BB185712 BB185712
C 42	16.8	76.4	256	189	W04058	W04058 T2023.MVAT4
C 43	16.8	76.4	368	231	AQ646701	AQ646701 RPCI93-EC
C 44	16.8	76.4	390	191	W88250	W88250 T1546.MVAT4
C 45	16.8	76.4	435	4	AA230196	AA230196 nc13b11.s

## ALIGNMENTS

RESULT 1  
AZ749943/3  
LOCUS  
DEFINITION RPCI-24-97J15.TJ RPCI-24 Mus musculus genomic clone RPCI-24-97J15,  
DNA sequence.  
ACCESSION AZ749943  
VERSION  
KEYWORDS GSS,  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 489)  
AUTHORS Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E., Russell, D., de Jong, P. and Fraser, C.M.  
TITLE Mouse BAC End Sequences from Library RPCI-24

Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end  
 page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 204 row: F column: 1  
 Seq primer: T7  
 Class: BAC ends.

## FEATURES

source

Location/Qualifiers  
 1. .570  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-204F1"  
 /clone\_lib="RPCI-23"  
 /sex="Female"  
 /lab\_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site\_1:  
 EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or  
 brain genomic DNA was isolated and partially digested  
 with a combination of EcoRI and EcoRI Methylase. Size  
 selected DNA was cloned into the pBACE3.6 vector at the  
 EcoRI sites. The ligation products were transformed into  
 DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT  
 ORIGIN

159 a 125 c 117 g 169 t

Query Match 83.6%; Score 18.4; DB 251; Length 570;  
 Best Local Similarity 95.0%; Pred. No. 87;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 gactgtgaaccttagatg 21  
 |||||  
 DB 124 GACTTTCACCTTAGATG 143

## RESULT 3

AZ052737/c  
 LOCUS  
 DEFINITION RPI-23-336P2.TVB RPI-23 Mus musculus genomic clone RPI-23-336P2,  
 DNA sequence.  
 AZ052737  
 VERSION  
 AZ052737.1 GI:7343904  
 GSS.  
 SOURCE  
 house mouse.  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 431)  
 Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret  
 ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.  
 and Fraser,C.M.  
 Mouse BAC End Sequences from Library RPI-23  
 Unpublished (1999)  
 Other\_GSSs: RPI-23-336P2.TJ  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPI-23. For BAC  
 library availability, please contact Pieter de Jong  
 (pieterdejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)  
 or from Resea ch Genetics (info@resgen.com). BAC end page:  
[http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 336 row: P column: 2  
 Seq primer: T7  
 Class: BAC ends.

FEATURES  
 source

Location/Qualifiers  
 1. .431  
 /organism="Mus musculus"  
 /strain="C57BL/6J"

/db\_xref="taxon:10090"  
 /clone="RPCI-23-336P2"  
 /clone\_lib="RPCI-23"  
 /sex="Female"  
 /lab\_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site\_1:  
 EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or  
 brain genomic DNA was isolated and partially digested  
 with a combination of EcoRI and EcoRI Methylase. Size  
 selected DNA was cloned into the pBACE3.6 vector at the  
 EcoRI sites. The ligation products were transformed into  
 DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 107 a 107 c 93 g 124 t  
 ORIGIN

Query Match 80.9%; Score 17.8; DB 237; Length 431;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaaccttagatga 22  
 |||||  
 DB 386 GACTGTGACCATAGAGATTA 366

## RESULT 4

BG552950  
 LOCUS  
 DEFINITION dab81h04.y1 NICHD XGC Emb4 Xenopus laevis cDNA clone IMAGE:4203511  
 5', mRNA sequence.  
 BG552950  
 VERSION  
 BG552950.1 GI:13564730  
 EST.  
 KEYWORDS  
 EST.  
 SOURCE  
 African clawed frog.  
 ORGANISM  
 Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 Xenopodinae; Xenopus.  
 1 (bases 1 to 507)  
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps@mail.nih.gov  
 Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: Xenopus clones from this library are available  
 through the I.M.A.G.E. Consortium/LLNL at: [info@image.llnl.gov](mailto:info@image.llnl.gov)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 380.

## FEATURES

source

Location/Qualifiers  
 1. .507  
 /organism="Xenopus laevis"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:4203511"  
 /clone\_lib="NICHD XGC Emb4"  
 /dev\_stage="embryo, stage 31-32"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site\_1:  
 NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo  
 dT. Average insert size 2.1 kb. Constructed by Life  
 Technologies. Note: This is a Xenopus Gene Collection (XGC  
 ) library."

BASE COUNT 149 a 90 c 112 g 155 t  
 ORIGIN

Query Match 80.9%; Score 17.8; DB 155; Length 507;  
 Best Local Similarity 90.5%; Pred. No. 1.7e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches	19;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	2	gactgtgaaccttagagatg	21						
Db	438	TCACTGTGAACCTTAGCGATG	458						
RESULT	5								
AZ479424									
LOCUS		535 bp	DNA		GSS		04-OCT-2000		
DEFINITION		1M0300H03F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0300H03 F, DNA sequence.							
ACCESSION		AZ479424							
VERSION		AZ479424.1		GI:10638899					
KEYWORDS		GSS.							
SOURCE		house mouse.							
ORGANISM		Mus musculus							
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
AUTHORS		1 (bases 1 to 535)							
		Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.							
TITLE		Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts							
JOURNAL		Unpublished (2000)							
COMMENT		Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0300 row: H column: 03 Seq primer: CTTGTAAACGACGCGCAGT Class: plasmid ends High quality sequence stop: 535.							
FEATURES									
source									
		1..535							
		Location/Qualifiers							
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		/strain="C57BL/6J"							
		/db_xref="taxon:10090"							
		/clone="UUGCLM0300H03"							
		/clone_lib="Mouse 10kb plasmid UUGCLM library"							
		/sex="Male"							
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"							
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114[gblAF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."							
BASE COUNT		144 a	118 c	123 g	150 t				
ORIGIN									
Query Match		80.9%		Score 17.8;	DB 244;	Length 535;			
Best Local Similarity		90.5%		Pred. No. 1.7e+02;					
Matches		19;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps
QY	1	tgactgtgaaccttagagatg	21						
Db	438	TCACTGTGAACCTTAGCGATG	458						
RESULT	5								
AZ479424									
LOCUS		535 bp	DNA		GSS		04-OCT-2000		
DEFINITION		1M0300H03F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0300H03 F, DNA sequence.							
ACCESSION		AZ479424							
VERSION		AZ479424.1		GI:10638899					
KEYWORDS		GSS.							
SOURCE		house mouse.							
ORGANISM		Mus musculus							
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
AUTHORS		1 (bases 1 to 535)							
		Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.							
TITLE		Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts							
JOURNAL		Unpublished (2000)							
COMMENT		Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0300 row: H column: 03 Seq primer: CTTGTAAACGACGCGCAGT Class: plasmid ends High quality sequence stop: 535.							
FEATURES									
source									
		1..535							
		Location/Qualifiers							
		/organism="Mus musculus"							
		/							

**SOURCE** human.  
**ORGANISM** Homo sapiens  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
**AUTHORS** 1 (bases 1 to 422)  
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
**TITLE** Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
**JOURNAL** Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
**MEDLINE** 99380589  
**COMMENT** Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 2056 row: L column: 24  
 Class: BAC ends  
 High quality sequence stop: 422.  
**FEATURES**  
 Location/Qualifiers  
 1..422  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="plate=2056 Col=24 Row=L"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /sex="male"  
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"  
**BASE COUNT** 119 a 79 c 89 g 132 t 3 others  
**ORIGIN**  
 79.1%; Score 17.4; DB 226; Length 422;  
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 ctgtgaaccttagatga 22  
 ||||| ||||| ||||| |||||  
 Db 219 CTGTGCACCTTAGAGATGA 201  
**RESULT** 8  
 BB484411/c 142 bp mRNA EST 23-JUL-2000  
**LOCUS** BB484411 RIKEN full-length enriched, 13 days embryo lung Mus  
**DEFINITION** musculus cDNA clone D430025H02 3', mRNA sequence.  
**ACCESSION** BB484411  
**VERSION** BB484411.1 GI:9402020  
**KEYWORDS** EST.  
**SOURCE** house mouse.  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 142)  
**AUTHORS** Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki.Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata.Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino M., Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Konno,H., et al.)  
 Unpublished (2000)  
 Contact: Yoshihide Hayashizaki

**FEATURES**  
 Location/Qualifiers  
 1..142  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="D430025H02"  
 /clone\_lib="RIKEN full-length enriched, 13 days embryo lung"  
 /tissue\_type="lung"  
 /dev\_stage="13 days embryo"  
 /lab\_host="DH10B"  
 /note="Site\_1: Sali; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
 GAGAGAGAGCGCGCAACCTGACGCTTTTCTTTTCTTTT 3']. cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'  
 GAGAGAGATTCTCGAGTTAATAATTAATCCGCCCCGCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."  
**BASE COUNT** 35 a 47 c 20 g 40 t  
**ORIGIN**  
 78.2%; Score 17.2; DB 135; Length 142;  
 Best Local Similarity 86.4%; Pred. No. 2.6e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 tgactgtgaaccttagatga 22  
 ||||| ||||| ||||| |||||  
 Db 121 TGAGGGTGAACCTTAGAGATGA 100  
**RESULT** 9  
 AU053757/c 236 bp mRNA EST 28-APR-1999  
**LOCUS** AU053757 Dictyostellium discoidesum SL (H.Urushihiro) Dictyostellium  
**DEFINITION** discoidesum cDNA clone SLJ623, mRNA sequence.  
**ACCESSION** AU053757  
**VERSION** AU053757.1 GI:4702239  
**KEYWORDS** EST.  
**SOURCE** Dictyostellium discoidesum.  
**ORGANISM** Dictyostellium discoidesum  
 Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

**SOURCE** human.  
**ORGANISM** Homo sapiens  
**REFERENCE** Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory  
 The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: +81-298-36-9013  
 Fax: +81-298-36-9098  
 Email: genome-res@rtc.riken.go.jp/  
 URL:http://genome.rtc.riken.go.jp/  
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Thrombostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki Y. and Hayashizaki,Y.  
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.  
**FEATURES**  
 Location/Qualifiers  
 1..142  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="D430025H02"  
 /clone\_lib="RIKEN full-length enriched, 13 days embryo lung"  
 /tissue\_type="lung"  
 /dev\_stage="13 days embryo"  
 /lab\_host="DH10B"  
 /note="Site\_1: Sali; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
 GAGAGAGAGCGCGCAACCTGACGCTTTTCTTTTCTTTT 3']. cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'  
 GAGAGAGATTCTCGAGTTAATAATTAATCCGCCCCGCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."  
**BASE COUNT** 35 a 47 c 20 g 40 t  
**ORIGIN**  
 78.2%; Score 17.2; DB 135; Length 142;  
 Best Local Similarity 86.4%; Pred. No. 2.6e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 tgactgtgaaccttagatga 22  
 ||||| ||||| ||||| |||||  
 Db 121 TGAGGGTGAACCTTAGAGATGA 100  
**RESULT** 9  
 AU053757/c 236 bp mRNA EST 28-APR-1999  
**LOCUS** AU053757 Dictyostellium discoidesum SL (H.Urushihiro) Dictyostellium  
**DEFINITION** discoidesum cDNA clone SLJ623, mRNA sequence.  
**ACCESSION** AU053757  
**VERSION** AU053757.1 GI:4702239  
**KEYWORDS** EST.  
**SOURCE** Dictyostellium discoidesum.  
**ORGANISM** Dictyostellium discoidesum  
 Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.



```

RESULT 11
AU054169/c
LOCUS
DEFINITION AU054169 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoidium cDNA clone SLK852, mRNA sequence.
ACCESSION AU054169
VERSION AU054169.1 GI:4702650
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
REFERENCE
AUTHORS 1 (bases 1 to 265)
TITLE Yoshino,R.; Morio,T. and Tanaka,Y.
JOURNAL Developmental cDNA in Dictyostelium discoideum
COMMENT Unpublished (1997)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.

FEATURES
source
1..265
/organism="Dictyostelium discoideum"
/strain="AX4"
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/clone="SLK852"
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/dev_stage="slug"
BASE COUNT 108 a 48 c 42 g 67 t
ORIGIN

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Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps

Oy 1 tgactgtgaaccttagagatga 22
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Db 134 TGACCGTAACCTTTAGAGATGA 113

RESULT 12
AU053754/c
LOCUS
DEFINITION AU053754 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoidium cDNA clone SLJ617, mRNA sequence.
ACCESSION AU053754
VERSION AU053754.1 GI:4702236
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
REFERENCE
AUTHORS 1 (bases 1 to 270)
TITLE Yoshino,R.; Morio,T. and Tanaka,Y.
JOURNAL Developmental cDNA in Dictyostelium discoideum
COMMENT Unpublished (1997)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.

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ORIGIN

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TITLE The Dictyostellium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development  
JOURNAL DNA Res. 5 (6), 335-340 (1998)  
MEDLINE 99156227  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan  
Email: d402huesakura.cc.tsukuba.ac.jp  
PROJECT = 'Dictyostellium discoideum cDNA project in Japan'.  
FEATURES  
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/dev\_stage="slug"  
BASE COUNT 153 a 68 c 61 g 89 t  
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Best Local Similarity 86.4%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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||||| ||||| ||||| |||||  
Db 239 TGACCGTAAACTTTAGAGATGA 218  
RESULT 15  
BF010530/c  
LOCUS  
DEFINITION  
BXCI\_085\_E04\_F BXCI (Nsf Xylem Compression wood Inclined) Pinus  
taeda cDNA clone NXCI\_085\_E04 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
Sederoff, R.  
Molecular Basis of Wood Formation in the Pine Megagenome  
Unpublished (2000)  
Contact: Johnson, Arthur  
North Carolina State University  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ajohnson@unity.ncsu.edu  
Seq primer: T3.  
FEATURES  
source Location/Qualifiers  
1..398  
/organism="Pinus taeda"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3357"  
/clone="NXCI\_085\_E04"  
/clone\_lib="NXCI (Nsf Xylem Compression wood Inclined)"  
/tissue\_type="Xylem"  
/cell\_type="Compression"  
/dev\_stage="Juvenile"  
/lab\_host="X11-Blue"  
/note="vector: Bluescript SK; Site\_1: Eco RI; Site\_2: XhoI  
; The library is from early (spring) wood, taken from  
three six-year old trees (three different genotypes), in  
the juvenile phase. These trees were induced to form  
compression wood by bending to a 45 degree angle and tying  
them to the ground. Differentiating xylem was harvested  
from the bottoms of the inclined stems, and a mixture of  
all three genotypes was used for the library oligo-dr.

primed cDNA was directionally cloned into the EcoRI-XhoI  
BlueScript SK vector arms. NOTE: The sequences contain a  
'cDNA adapter' between the EcoRI site and the start of the  
EST. The adapter sequence is 'AATTCGGCAGAG'.

97 a 124 c 101 g 76 t

BASE COUNT  
ORIGIN

Query Match 78.2%; Score 17.2; DB 143; Length 398;  
Best Local Similarity 86.4%; Pred. No 3.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22  
|||||  
Db 220 TGACTGTGAACCTTGATGATGA 199

Search completed: October 9, 2001, 18:20:30  
Job time: 9800 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds  
(without alignments)  
26.779 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22  
Sequence: 1 tgactgtgaaccttagatga 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_0601:\*

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2: /SIDS8/gcgdata/geneseq/geneseq/NA1981.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AAV55790	Immunostimulatory
2	22	100.0	22	AAV55790	Mutant immunostimulatory
3	22	100.0	22	AAV55790	Immunostimulatory
4	20.4	92.7	22	AAV55791	Immunostimulatory
5	20.4	92.7	22	AAV55791	Immunostimulatory
6	20.4	92.7	22	AAV55791	Immunostimulatory
7	18.8	85.5	22	AAV55791	Immunostimulatory
8	18.8	85.5	22	AAV55791	Immunostimulatory
9	18.8	85.5	22	AAV55791	Immunostimulatory
10	18.8	85.5	22	AAV55791	Immunostimulatory
11	18.8	85.5	22	AAV55791	Immunostimulatory

12	18.8	85.5	22	20	AAV80106	Oligo used in expe
13	18.8	85.5	22	20	AAV80097	Immunomodulatory o
14	18.8	85.5	22	20	AAV80102	Immunomodulatory o
15	18.8	85.5	22	20	AAV80103	Immunomodulatory o
16	18.8	85.5	22	20	AAV80104	Oligo used in expe
17	18.8	85.5	22	21	AAV80105	Immunostimulatory
18	18.8	85.5	22	21	AAV80106	Non-cpg control ph
19	18.8	85.5	22	21	AAV80107	Sequence of a stab
20	18.8	85.5	22	21	AAV80108	Sequence of a stab
21	18.8	85.5	22	21	AAV80109	Sequence of a stab
22	18.8	85.5	22	21	AAV80110	CpG adjuvant oligo
23	18.8	85.5	22	21	AAV80111	CpG adjuvant oligo
24	18.8	85.5	22	21	AAV80112	Immunostimulatory
25	18.8	85.5	22	21	AAV80113	Immunostimulatory
26	18.8	85.5	22	21	AAV80114	Immunostimulatory
27	18.8	85.5	22	21	AAV80115	Immunostimulatory
28	18.8	85.5	22	21	AAV80116	Immunostimulatory
29	18.8	85.5	22	21	AAV80117	Immunostimulatory
30	18.8	85.5	22	22	AAV80118	Immunostimulatory
31	18.8	85.5	22	22	AAV80119	Immunostimulatory
32	18.8	85.5	22	22	AAV80120	Immunostimulatory
33	18.8	85.5	22	22	AAV80121	Immunostimulatory
34	18.8	85.5	22	22	AAV80122	Immunostimulatory
35	18.8	85.5	22	22	AAV80123	Immunostimulatory
36	18.8	85.5	22	22	AAV80124	Immunostimulatory
37	18.8	85.5	22	22	AAV80125	Immunostimulatory
38	18.8	85.5	22	22	AAV80126	Immunostimulatory
39	18.8	85.5	22	22	AAV80127	Immunostimulatory
40	18.8	85.5	22	22	AAV80128	Immunostimulatory
41	18.8	85.5	22	22	AAV80129	Immunostimulatory
42	18.8	85.5	22	22	AAV80130	Immunostimulatory
43	18.8	85.5	22	22	AAV80131	Immunostimulatory
44	18.8	85.5	22	22	AAV80132	Immunostimulatory
45	18.8	85.5	22	22	AAV80133	Immunostimulatory

#### ALIGNMENTS

##### RESULT 1

AAV55790

ID AAV55790 standard; DNA; 22 BP.

XX AAV55790;

XX 29-MAR-1999 (first entry)

XX Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1040.

XX Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;

XX Immunostimulatory activity; gene therapy; genetic immunisation;

XX autoimmune disease; inflammation; microbial infection; immunotherapy; ss.

XX Synthetic.

XX WO9855609-A1.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11391.

XX 06-JUN-1997; 97US-0048793.

XX (REGC ) UNIV CALIFORNIA.

XX Ray E, Roman M;

XX WPI; 1999-080827/07.

XX New oligonucleotide that inhibits action of immunostimulatory sequence oligonucleotides - particularly those present in gene therapy vectors or microbial pathogens, used to prolong gene therapy expression and to treat e.g. infections or autoimmune disease

XX PS Example 1; Fig 1; 50pp; English.

XX CC This sequence represents an example of an immunostimulatory sequence

CC CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN

CC CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-Z-Py-Py or

CC CC 5'-Pu-Pu-Y-Z-Py-Py for inhibiting immunostimulation caused by

CC CC ISS-ODNs that contain a hexamer region consisting of at least one CpG

CC CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;

CC CC Y = any natural or synthetic nucleotide other than C; Z = any natural or

CC CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.

CC CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs

CC CC when this is present in (i) a recombinant expression vector (being used

CC CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly

CC CC one in a host and associated with an autoimmune disease). Particularly

CC CC the inhibitors prolong gene expression from the vector and reduce

CC CC inflammation caused by microbial infection. They also modulate activity

CC CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune

CC CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes

CC CC or monocytes by reducing the Th1-type response and stimulating the

CC CC Th2-type response to an antigen (including antigen-stimulated

CC CC immunoglobulin G1 production). Prolonged expression from the gene therapy

CC CC vector avoids the need for repeated treatments and re-engineering of the

CC CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over

CC CC the effect of ISS-ODN-based adjuvants and can be used even where the

CC CC existence, identity and location of the ISS-ODNs are unknown. The

CC CC inhibitors are effective at very low doses.

XX CC

XX CC Sequence 22 BP; 7 A; 3 C; 6 G; 6 T; 0 other;

XX CC

Query Match 100.0%; Score 22; DB 20; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.044;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagatga 22  
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 DB 1 tgactgtgaaccttagatga 22

RESULT 2

AAAI4469

ID AAAI4469 standard; DNA; 22 BP.

XX AC AAAI4469;

XX DT 21-AUG-2000 (first entry)

XX DE Mutant immunostimulatory oligonucleotide, M-ODN.

XX KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;

XX KW secretory immunoglobulin A production; sigA; Th1 phenotype; mutant; ds.

XX OS Synthetic.

XX OS WO200020039-A1.

XX PN 13-APR-2000.

XX PD 15-SEP-1999; 99WO-US21203.

XX PF 05-OCT-1998; 98US-0167039.

XX PR (REGC ) UNIV CALIFORNIA.

XX PA Raz E, Horner AA, Carson DA;

XX PI WPI; 2000-303647/26.

XX DR Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to

XX PT an antigen in a mammalian host through production of secretory

XX PT immunoglobulin A -

XX PT

PS Example 1; Page 21; 64pp; English.

XX CC The invention relates to a method of inducing mucosal immunity to an

CC CC antigen in a mammalian host, including the production of secretory

CC CC immunoglobulin A (sigA). Immune protection in the mucosa (the principal

CC CC site of entry of most foreign antigens) is mediated by mucosa-associated

CC CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory

CC CC cell sub-populations. The primary immune response which characterises

CC CC the induction of mucosal immunity to an antigen is sigA production by

CC CC activated B-cells. The method comprises introducing an immunostimulatory

CC CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the

CC CC ISS-ODN includes a core nucleotide sequence. The core nucleotide

CC CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific

CC CC examples of which are AACGTT, AGCGTC and GAGCTT (SEQ ID Nos 1-3). A

CC CC specific example of an ISS-ODN is DY1018 (AAAI4467). The ISS-ODN is used

CC CC as an adjuvant with an antigen for stimulating mucosal immunity. The

CC CC level of sigA production induced in the host is at least 3 times the

CC CC magnitude of sigA production achievable in response to introduction of

CC CC antigen alone into the mucosal tissue and is equivalent or greater than

CC CC the magnitude of sigA production achievable in response to introduction

CC CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The

CC CC host immune response is stimulated to antigen specific IgA production,

CC CC biased towards the Th1 phenotype while antigen-induced IgE production is

CC CC avoided. The adjuvant has little or no known toxicity in mammals and its

CC CC efficacy is comparable to that of cholera toxin which is used as a

CC CC mucosal adjuvant. The present sequence represents a mutant ISS-ODN,

XX CC M-ODN, used in an exemplification of the invention.

XX CC

XX CC Sequence 22 BP; 7 A; 3 C; 6 G; 6 T; 0 other;

XX CC

Query Match 100.0%; Score 22; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.044;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagatga 22  
 |||||  
 DB 1 tgactgtgaaccttagatga 22

RESULT 3

AAFI31345

ID AAFI31345 standard; DNA; 22 BP.

XX AC AAFI31345;

XX DT 12-APR-2001 (first entry)

XX DE Immune response enhancement method related sequence.

XX KW Immunostimulatory nucleotide sequence; immune response; cancer;

XX KW antibody production; IFNgamma release; CTL activity; Th1 response;

XX KW infection; allergy; ds.

XX OS Synthetic.

XX OS WO200102007-A1.

XX PN 11-JAN-2001.

XX PD 30-JUN-2000; 2000WO-US18229.

XX PF 02-JUL-1999; 99US-0347343.

XX PR (REGC ) UNIV CALIFORNIA.

XX PA Raz E, Kobayashi H;

XX PI WPI; 2001-138056/14.

XX DR Enhancing immune response against pathogen or antigen associated with

XX PT infectious diseases, an allergen or cancer, involves administering

XX PT immunostimulatory nucleotide sequence prior to antigen exposure -

XX PT

XX  
PS  
XX

Example 1: Page 14; 47pp; English.

The present invention describes a method for enhancing an immune response to a substance, comprising administering an immunostimulatory nucleotide sequence to a subject prior to exposure to the substance. This can be used to enhance antibody production, IFN $\gamma$  release, CTL activity and Th1 related effects. The method can be used in the prevention and treatment of allergies, cancer and infections.

XX Sequence 22 BP; 7 A; 3 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 22; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.044; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22

Db 1 tgactgtgaaccttagagatga 22

RESULT 4

AAV55791  
ID AAV55791 standard; DNA; 22 BP.

XX  
AC AAV55791;

XX  
DT 29-MAR-1999 (first entry)

XX Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1041.

XX Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;  
KW Immunostimulatory activity; gene therapy; genetic immunisation;  
KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.  
XX Synthetic.

XX WO9855609-A1.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11391.

XX 06-JUN-1997; 97US-0048793.

XX (REGC ) UNIV CALIFORNIA.

XX Ray E, Roman M;

XX WPI; 1999-080827/07.

XX New oligonucleotide that inhibits action of immunostimulatory  
PT sequence oligonucleotides - particularly those present in gene  
PT therapy vectors or microbial pathogens, used to prolong gene therapy  
PT expression and to treat e.g. infections or autoimmune disease

XX Example 1: Fig 1: 50pp; English.

XX This sequence represents an example of a immunostimulatory sequence  
CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN  
CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-Z-Py-Py or  
CC 5'-Pu-Pu-Y-Z-Py-polyPy for inhibiting immunostimulation caused by  
CC ISS-ODNs that contain a hexamer region consisting of at least one CpG  
CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;  
CC Y = any natural or synthetic nucleotide other than C; Z = any natural or  
CC synthetic nucleotide, but if Y is not G or inosine (I), then Z is G or I.  
CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs  
CC when this is present in (i) a recombinant expression vector (being used  
CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly  
CC one in a host and associated with an autoimmune disease). Particularly  
CC the inhibitors prolong gene expression from the vector and reduce  
CC inflammation caused by microbial infection. They also modulate activity

CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune  
CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes  
CC or monocytes by reducing the Th1-type response and stimulating the  
CC Th2-type response to an antigen (including antigen-stimulated  
CC immunoglobulin G1 production). Prolonged expression from the gene therapy  
CC vector avoids the need for repeated treatments and re-engineering of the  
CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over  
CC the effect of ISS-ODN-based adjuvants and can be used even where the  
CC existence, identity and location of the ISS-ODNs are unknown. The  
CC inhibitors are effective at very low doses.

XX Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.28; Mismatches 21; Conservative 0; Indels 1; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22

Db 1 tgactgtgaaccttagagatga 22

RESULT 5

AAV80110  
ID AAV80110 standard; DNA; 22 BP.

XX  
AC AAV80110;

XX  
DT 12-MAR-1999 (first entry)

XX Oligo used in experiments for stimulation of cytokine production.

XX Immunomodulatory; Immunostimulatory; octanucleotide; immune regulation;  
KW cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
PT contain an immune-stimulating octanucleotide sequence; for treating  
PT cancer, allergic and infectious diseases

XX Example 2: Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,  
CC GAGTTC, and GAGTTCG. The immunomodulatory sequences are used to treat  
CC patients needing immune regulation, such as those suffering from cancer,  
CC an allergic disease and asthma. They are also used to prevent infectious  
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
CC Schistosoma. The immunomodulatory sequences are used to screen for human  
CC immunostimulatory activity by incubating macrophage cells and the  
CC oligonucleotide; and determining the relative amount of Th1-biased  
CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent

CC oligonucleotides that were tested for immunostimulatory activity. These  
 CC were used in experiments for the stimulation of cytokine production and  
 CC were found to lack immunostimulatory activity. The invention provides  
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.  
 XX  
 SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.28;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 1 tgactgtgaagcttagagatga 22

RESULT 6  
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 ID AA255878 standard; DNA; 22 BP.  
 AC AA255878;  
 DT 10-APR-2000 (first entry)  
 DE Non-immunomodulatory oligonucleotide SEQ ID NO: 3.  
 XX Non-immunomodulatory; immunostimulatory sequence; adjuvant;  
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
 KW asthma; immunosuppression; ss.  
 XX Mus musculus.  
 OS Synthetic.

Key Location/Qualifiers  
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WO9962923-A2.  
 09-DEC-1999.  
 04-JUN-1999; 99WO-US12538.  
 05-JUN-1998; 98US-0088310.  
 01-JUN-1999; 99US-0324191.  
 (DYNA-) DYNAX TECHNOLOGIES CORP.  
 Schwartz D;  
 WPI; 2000-105687/09.  
 Novel immunomodulatory oligonucleotide used to induce a Th1-type immune response, e.g. to tumor antigens -  
 Example 1; Page 35; 54pp; English.

Sequences AA255878-255879 represent oligonucleotides which do not contain an immunostimulatory sequence (ISS, e.g., AACGTC, AACGTT, AGCGTC, AGCGCT, AGCGTT, GACGTC, GACGTT, GCGGTT, AACGTTC and GACGTTC), and which did not exhibit immunomodulatory activity in an exemplification of the present invention. The invention relates to oligonucleotides comprising one or more ISSs, where the ISS comprises at least one modified cytosine with an electron-withdrawing moiety at position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886 contain ISSs comprising at least one bromocytosine, whereas sequence AA255876 contains an unmodified ISS. The immunomodulatory oligonucleotides have an adjuvant-like effect: when formulated with an antigen, the oligonucleotides stimulate production of Th1-type cytokines, and induce a Th1-type immune response (activation of cytotoxic T cells), while simultaneously downregulating the Th2-type response. The Th1

CC response is particularly effective for control of viruses and  
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
 CC particularly when formulated with an antigen or a facilitator, for  
 CC modulating immune responses. Such compositions may be used in tumour  
 CC therapy, in treatment of allergy (including asthma), for inducing a  
 CC vigorous cellular response (against a virus, bacterium, fungus or  
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.  
 XX  
 SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;  
 Best Local Similarity 95.5%; Pred. No. 0.28;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaagcttagagatga 22

RESULT 7  
 AAV32079  
 ID AAV32079 standard; DNA; 22 BP.  
 XX AAV32079;  
 AC AAV32079;  
 DT 09-SEP-1998 (first entry)  
 DE Nucleotide sequence of DY1018.  
 XX  
 KW DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;  
 KW immunisation; anaphylaxis; IgE; retinopathies; ss.  
 XX Synthetic.

Key Location/Qualifiers  
 modified\_base 1..22  
 /\*tag= a  
 /note= "phosphothioate backbone"

WO9816247-A1.  
 23-APR-1998.  
 09-OCT-1997; 97WO-US19004.  
 11-OCT-1996; 96US-0028118.  
 (REGC ) UNIV CALIFORNIA.  
 Carson DA, Raz E, Roman M;  
 WPI; 1998-261028/23.  
 New immunomodulatory compositions - comprising an antigen conjugated to a polynucleotide that contains an immunostimulatory sequence  
 Example 1; Page 36; 69pp; English.

This is the nucleotide sequence of DY1018, which is conjugated to beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule (IMM), which comprises an antigen conjugated to a polynucleotide (PN) that contains at least one immunostimulatory nucleotide sequence (ISS). The conjugate synergistically boost the magnitude of the host immune response against an antigen to a level greater than the host immune response to either the IMM, antigen or ISS-PN alone. These responses to ISS-PN/IMM conjugates are particularly acute during the important early phase of the host immune response to an antigen. The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular (Th1 type) immune responses of the host. Thus, use of the method to boost the immune responsiveness of a host to subsequent challenge by a sensitising antigen without immunisation avoids the risk of Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE

CC production in response to the antigen challenge. The conjugates can  
 CC also be used to combat pathogenic infection and to stimulate  
 CC therapeutic angiogenesis to treat conditions in which localised blood  
 CC flow plays a significant etiological role, e.g. retinopathies.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 Other;

Query Match 85.5%; Score 18.8; DB 19; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.8;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatga 22  
 |||||  
 Db 1 tgactgtgaaccttagagatga 22

RESULT 8  
 AAX36624  
 ID AAX36624 standard; DNA; 22 BP.

AC AAX36624;

DT 09-JUL-1999 (first entry)

DE ISS-ODN DY1018 nucleotide sequence.

KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;  
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;  
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;  
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;  
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;  
 KW eosinophilic fasciitis; therapy; ss.

OS Synthetic.

XX WO9911275-A2.

XX 11-MAR-1999.

PF 04-SEP-1998; 98WO-US18382.

PR 05-SEP-1997; 97US-0927120.

PA (REGC ) UNIV CALIFORNIA.

PI Ray E;

XX WPI; 1999-312404/26.

DR Reducing antigen-stimulated granulocyte-mediated inflammation

PS Example 2; Page 30; 69pp; English.

XX This is the ISS-ODN DY1018 nucleotide sequence.

CC The invention relates to a method for preventing or reducing  
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:  
 CC (a) reduction in, or the absence of, a Th2 type immune response is  
 CC measured; or (b) there is a reduction or absence of other clinical signs  
 CC of inflammation in the host after antigen challenge. The method is used  
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
 CC and to modulate the host's immune responsiveness to an antigen,  
 CC particularly where the subject suffers from asthma, nasal polyposis,  
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or  
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by  
 CC antigen immunisation, the method is an antigen-independent method,  
 CC and avoids host production of both interleukin-4 (IL-4), which carries  
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte  
 CC adhesion to endothelia.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 85.5%; Score 18.8; DB 20; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.8;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatga 22  
 |||||  
 Db 1 tgactgtgaaccttagagatga 22

RESULT 9

AAV55792

ID AAV55792 standard; DNA; 22 BP.

XX AAV55792;

XX 29-MAR-1999 (first entry)

XX Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1042.

KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;  
 KW immunostimulatory activity; gene therapy; genetic immunisation;  
 KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.  
 OS Synthetic.

XX WO9855609-A1.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11391.

XX 06-JUN-1997; 97US-0048793.

XX (REGC ) UNIV CALIFORNIA.

XX Ray E, Roman M;

XX WPI; 1999-080827/07.

XX New oligonucleotide that inhibits action of immunostimulatory  
 PT sequence oligonucleotides - particularly those present in gene  
 PT therapy vectors or microbial pathogens, used to prolong gene therapy  
 PT expression and to treat e.g. infections or autoimmune disease

XX Example 1; Fig 1; 50pp; English.

XX This sequence represents an example of a immunostimulatory sequence  
 CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN  
 CC sequences have a hexamer region of sequence 5'-pu-pu-y-2-py-py or  
 CC 5'-pu-pu-y-2-py-poly for inhibiting immunostimulation caused by  
 CC ISS-ODNs that contain a hexamer region consisting of at least one CpG  
 CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;  
 CC y = any natural or synthetic nucleotide other than C; z = any natural or  
 CC synthetic nucleotide, but if y is not G or Inosine (I), then z is G or I.  
 CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs  
 CC when this is present in (i) a recombinant expression vector (being used  
 CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly  
 CC one in a host and associated with an autoimmune disease). Particularly  
 CC the inhibitors prolong gene expression from the vector and reduce  
 CC inflammation caused by microbial infection. They also modulate activity  
 CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune  
 CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes  
 CC or monocytes by reducing the Th1-type response and stimulating the  
 CC Th2-type response to an antigen (including antigen-stimulated  
 CC immunoglobulin G1 production). Prolonged expression from the gene therapy  
 CC vector avoids the need for repeated treatments and re-engineering of the  
 CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over  
 CC the effect of ISS-ODN-based adjuvants and can be used even where the  
 CC existence, identity and location of the ISS-ODNs are unknown. The  
 CC inhibitors are effective at very low doses.



```

SQ Sequence 22 BP: 5 A; 3 C; 6 G; 8 T; 0 other:
      Query Match      85.5%; Score 18.8; DB 20; Length 22;
      Best Local Similarity 90.9%; Pred. No. 1.8;
      Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
      QY 1 tgactgtgaaccttagatga 22
          ||||| ||||| |||||
      Db 1 tgactgtgttccttagatga 22

RESULT 10
AAV55797
ID AAV55797 standard; DNA; 22 BP.
XX
AC AAV55797;
XX
DT 29-MAR-1999 (first entry)
XX
DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1061.
XX
KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
KW immunostimulatory activity; gene therapy; genetic immunisation;
KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
XX
OS Synthetic.
XX
PN WO9855609-A1.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11391.
XX
PR 06-JUN-1997; 97US-0048793.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Ray E, Roman M;
XX
DR WPI; 1999-080827/07.
XX
PT New oligonucleotide that inhibits action of immunostimulatory
PT sequence oligonucleotides - particularly those present in gene
PT therapy vectors or microbial pathogens, used to prolong gene therapy
PT expression and to treat e.g. infections or autoimmune disease
XX
PS Example 1; Fig 3; 50pp; English.
XX
CC This sequence represents an example of a immunostimulatory sequence
CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN
CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-2-Py-Py or
CC 5'-Pu-Pu-Y-2-Py-polyPy for inhibiting immunostimulation caused by
CC ISS-ODNs that contain a hexamer region consisting of at least one CpG
CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;
CC Y = any natural or synthetic nucleotide other than C; Z = any natural or
CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.
CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs
CC when this is present in (i) a recombinant expression vector (being used
CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly
CC one in a host and associated with an autoimmune disease). Particularly
CC the inhibitors prolong gene expression from the vector and reduce
CC inflammation caused by microbial infection. They also modulate activity
CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune
CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes
CC or monocytes by reducing the Th1-type response and stimulating the
CC Th2-type response to an antigen (including antigen-stimulated
CC immunoglobulin G1 production). Prolonged expression from the gene therapy
CC vector avoids the need for repeated treatments and re-engineering of the
CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over
CC the effect of ISS-ODN-based adjuvants and can be used even where the
CC existence, identity and location of the ISS-ODNs are unknown. The
CC inhibitors are effective at very low doses.
XX
SQ Sequence 22 BP: 7 A; 1 C; 7 G; 7 T; 0 other:
      Query Match      85.5%; Score 18.8; DB 20; Length 22;
      Best Local Similarity 90.9%; Pred. No. 1.8;
      Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
      QY 1 tgactgtgaaccttagatga 22
          ||||| ||||| |||||
      Db 1 tgactgtgaatgttagatga 22

RESULT 11
AAV55788
ID AAV55788 standard; DNA; 22 BP.
XX
AC AAV55788;
XX
DT 29-MAR-1999 (first entry)
XX
DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1019.
XX
KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
KW immunostimulatory activity; gene therapy; genetic immunisation;
KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
XX
OS Synthetic.
XX
PN WO9855609-A1.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11391.
XX
PR 06-JUN-1997; 97US-0048793.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Ray E, Roman M;
XX
DR WPI; 1999-080827/07.
XX
PT New oligonucleotide that inhibits action of immunostimulatory
PT sequence oligonucleotides - particularly those present in gene
PT therapy vectors or microbial pathogens, used to prolong gene therapy
PT expression and to treat e.g. infections or autoimmune disease
XX
PS Example 1; Fig 1; 50pp; English.
XX
CC This sequence represents an example of a immunostimulatory sequence
CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN
CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-2-Py-Py or
CC 5'-Pu-Pu-Y-2-Py-polyPy for inhibiting immunostimulation caused by
CC ISS-ODNs that contain a hexamer region consisting of at least one CpG
CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;
CC Y = any natural or synthetic nucleotide other than C; Z = any natural or
CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.
CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs
CC when this is present in (i) a recombinant expression vector (being used
CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly
CC one in a host and associated with an autoimmune disease). Particularly
CC the inhibitors prolong gene expression from the vector and reduce
CC inflammation caused by microbial infection. They also modulate activity
CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune
CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes
CC or monocytes by reducing the Th1-type response and stimulating the
CC Th2-type response to an antigen (including antigen-stimulated
CC immunoglobulin G1 production). Prolonged expression from the gene therapy
CC vector avoids the need for repeated treatments and re-engineering of the
CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over
CC the effect of ISS-ODN-based adjuvants and can be used even where the
CC existence, identity and location of the ISS-ODNs are unknown. The
CC inhibitors are effective at very low doses.
```

CC Inhibitors are effective at very low doses.  
 XX Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;  
 SQ

Query Match 85.5%; Score 18.8; DB 20; Length 22;

Best Local Similarity 90.9%; Pred. No. 1.8;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatga 22  
 ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaaggttagagatga 22

## RESULT 12

AAV80106  
 ID AAV80106 standard; DNA; 22 BP.

XX AAV80106;

XX 12-MAR-1999 (first entry)

XX Oligo used in experiments for stimulation of cytokine production.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

PN 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

PS Example 1; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,  
 CC GACGTCC, and GACGTTCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent  
 CC oligonucleotides that were tested for immunostimulatory activity. These  
 CC were used in experiments for the stimulation of cytokine production and  
 CC were found to lack immunostimulatory activity. The invention provides  
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

## Query Match

85.5%; Score 18.8; DB 20; Length 22;

Best Local Similarity 90.9%; Pred. No. 1.8;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatga 22  
 ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttagcgatga 22

## RESULT 13

AAV80097  
 ID AAV80097 standard; DNA; 22 BP.

XX AAV80097;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

PS Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,  
 CC GACGTCC, and GACGTTCG. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

## Query Match

85.5%; Score 18.8; DB 20; Length 22;

Best Local Similarity 90.9%; Pred. No. 1.8;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatga 22  
 ||||| ||||| ||||| |||||  
 Db 1 tgactgtgaacgttagcgatga 22

## RESULT 14

```

AAV80102
ID AAV80102 standard; DNA; 22 BP.
XX AC AAV80102;
XX
XX 12-MAR-1999 (first entry)
XX
XX Immunomodulatory oligo comprising an ISS sequence.
XX
XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 11
FT /*tag= a
FT /*note= "5-bromocytosine"
XX
XX W09855495-A2.
XX
XX 10-DEC-1998.
XX
XX 05-JUN-1998; 98WO-US11578.
XX
XX 06-JUN-1997; 97US-0048793.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Dina D, Roman M, Schwartz D;
XX WPI; 1999-059898/05.
XX
XX Immunostimulatory oligonucleotides regulate the immune system - and
XX contain an immune-stimulating octanucleotide sequence; for treating
XX cancer, allergic and infectious diseases
XX
XX Claim 23; Page 30; 63pp; English.
XX
XX The invention relates to immunomodulatory oligonucleotides that comprise
XX at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX sequences are selected from the group consisting of AAGTTCC, AACGTTCC,
XX GAGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat
XX patients needing immune regulation, such as those suffering from cancer,
XX an allergic disease and asthma. They are also used to prevent infectious
XX diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX and papillomavirus. Hemophilus influenza, Mycobacterium tuberculosis and
XX Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
XX Schistosoma. The immunomodulatory sequences are used to screen for human
XX immunostimulatory activity by incubating macrophage cells and the
XX oligonucleotide; and determining the relative amount of Th1-biased
XX cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
XX specific claimed examples of such immunomodulatory oligonucleotides.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 85.5%; Score 18.8; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagatga 22
| | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

Search completed: October 9, 2001, 16:26:52
Job time: 2982 sec

AAV80102
ID AAV80102 standard; DNA; 22 BP.
XX AC AAV80102;
XX
XX 12-MAR-1999 (first entry)
XX
XX Immunomodulatory oligo comprising an ISS sequence.
XX
XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
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FT /*note= "5-bromocytosine"
XX
XX W09855495-A2.
XX
XX 10-DEC-1998.
XX
XX 05-JUN-1998; 98WO-US11578.
XX
XX 06-JUN-1997; 97US-0048793.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Dina D, Roman M, Schwartz D;
XX WPI; 1999-059898/05.
XX
XX Immunostimulatory oligonucleotides regulate the immune system - and
XX contain an immune-stimulating octanucleotide sequence; for treating
XX cancer, allergic and infectious diseases
XX
XX Claim 23; Page 30; 63pp; English.
XX
XX The invention relates to immunomodulatory oligonucleotides that comprise
XX at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX sequences are selected from the group consisting of AAGTTCC, AACGTTCC,
XX GAGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat
XX patients needing immune regulation, such as those suffering from cancer,
XX an allergic disease and asthma. They are also used to prevent infectious
XX diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX and papillomavirus. Hemophilus influenza, Mycobacterium tuberculosis and
XX Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
XX Schistosoma. The immunomodulatory sequences are used to screen for human
XX immunostimulatory activity by incubating macrophage cells and the
XX oligonucleotide; and determining the relative amount of Th1-biased
XX cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
XX specific claimed examples of such immunomodulatory oligonucleotides.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 85.5%; Score 18.8; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagatga 22
| | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

RESULT 15
AAV80102
ID AAV80102 standard; DNA; 22 BP.
XX AC AAV80102;

```

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:48 ; Search time 10334.3 Seconds  
(without alignments)  
31.457 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22  
Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq:\*
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- 8: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pna/US092\_COMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pna/US093\_COMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq:\*
- 23: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq:\*
- 25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq:\*
- 26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq:\*
- 27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq:\*
- 28: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq:\*
- 29: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq:\*
- 30: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq:\*
- 31: /cgn2\_6/ptodata/1/pna/US098\_COMB.seq:\*
- 32: /cgn2\_6/ptodata/1/pna/US099\_COMB.seq:\*
- 33: /cgn2\_6/ptodata/1/pna/US099A\_COMB.seq:\*
- 34: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq:\*
- 35: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq:\*
- 36: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq:\*
- 37: /cgn2\_6/ptodata/1/pna/US099E\_COMB.seq:\*
- 38: /cgn2\_6/ptodata/1/pna/US099F\_COMB.seq:\*
- 39: /cgn2\_6/ptodata/1/pna/US099G\_COMB.seq:\*
- 40: /cgn2\_6/ptodata/1/pna/US099H\_COMB.seq:\*
- 41: /cgn2\_6/ptodata/1/pna/US099I\_COMB.seq:\*
- 42: /cgn2\_6/ptodata/1/pna/US099J\_COMB.seq:\*
- 43: /cgn2\_6/ptodata/1/pna/US099K\_COMB.seq:\*

- 44: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq:\*
- 45: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq:\*
- 46: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq:\*
- 47: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq:\*
- 48: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq:\*
- 49: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq:\*
- 50: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq:\*
- 51: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq:\*
- 52: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq:\*
- 53: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq:\*
- 54: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq:\*
- 55: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq:\*
- 56: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq:\*
- 57: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq:\*
- 58: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq:\*
- 59: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq:\*
- 60: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	22	100.0	22	1	PCT-US00-18229-33
2	22	100.0	22	1	PCT-US01-06034-3
3	22	100.0	22	1	PCT-US01-10118-7
4	22	100.0	22	1	PCT-US01-14508-9
5	22	100.0	22	17	US-09-347-343-33
6	22	100.0	22	22	US-09-570-325-21
7	22	100.0	22	28	US-09-713-136-10
8	22	100.0	22	30	US-09-791-500-3
9	22	100.0	22	31	US-09-820-484-7
10	20.4	92.7	22	1	PCT-US01-06034-5
11	20.4	92.7	22	1	PCT-US01-06034-6
12	20.4	92.7	22	1	PCT-US01-10118-2
13	20.4	92.7	22	1	PCT-US01-10118-6
14	20.4	92.7	22	1	PCT-US01-14508-10
15	20.4	92.7	22	1	PCT-US01-14508-11
16	20.4	92.7	22	16	US-09-296-477-13
17	20.4	92.7	22	17	US-09-324-191A-3
18	20.4	92.7	22	30	US-09-791-500-5
19	20.4	92.7	22	30	US-09-791-500-6
20	20.4	92.7	22	31	US-09-820-484-2
21	20.4	92.7	22	31	US-09-820-484-6
22	19	86.4	20	1	PCT-US01-14508-2
23	18.8	85.5	22	1	PCT-US00-18229-32
24	18.8	85.5	22	1	PCT-US00-35064-1
25	18.8	85.5	22	1	PCT-US01-03029-1
26	18.8	85.5	22	1	PCT-US01-03029-3
27	18.8	85.5	22	1	PCT-US01-06034-1
28	18.8	85.5	22	1	PCT-US01-06034-2
29	18.8	85.5	22	1	PCT-US01-06034-8
30	18.8	85.5	22	1	PCT-US01-10118-1
31	18.8	85.5	22	1	PCT-US01-10118-3
32	18.8	85.5	22	1	PCT-US01-11290-1
33	18.8	85.5	22	1	PCT-US01-11290-4
34	18.8	85.5	22	1	PCT-US01-14508-1
35	18.8	85.5	22	1	PCT-US01-14508-12
36	18.8	85.5	22	1	PCT-US01-14508-13
37	18.8	85.5	22	1	PCT-US01-14508-14
38	18.8	85.5	22	1	PCT-US99-21203-19
39	18.8	85.5	22	13	US-08-927-120-19
40	18.8	85.5	22	15	US-09-167-039-19
41	18.8	85.5	22	16	US-09-235-742-19
42	18.8	85.5	22	16	US-09-296-477-2
43	18.8	85.5	22	16	US-09-296-477-3
44	18.8	85.5	22	16	US-09-296-477-8
45	18.8	85.5	22	31	US-09-828-505-4

## ALIGNMENTS

```
RESULT 1
PCT-US00-18229-33
; Sequence 33, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Kobayashi, Hiroko
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 6510-189W01
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-33

Query Match      100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 2
PCT-US01-06034-3
; Sequence 3, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-3

Query Match      100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 3
PCT-US01-10118-7
; Sequence 7, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
```

```
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188W01
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modN
PCT-US01-10118-7

Query Match      100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 4
PCT-US01-14508-9
; Sequence 9, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510/168W01
; CURRENT APPLICATION NUMBER: PCT/US01/14508
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/262,321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M-ODN
PCT-US01-14508-9

Query Match      100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 5
US-09-347-343-33
; Sequence 33, Application US/09347343A
; GENERAL INFORMATION:
```

```
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-33
```

```
Query Match 100.0%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22
```

```
RESULT 6
US-09-570-325-21
; Sequence 21, Application US/09570325
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Anthony A. Horner
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
; TITLE OF INVENTION: MUCOSAL IMMUNITY TO HIV
; FILE REFERENCE: 30448.92US11
; CURRENT APPLICATION NUMBER: US/09/570,325
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 09/167,039
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: 08/927,120
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 08/593,554
; PRIOR FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-570-325-21
```

```
Query Match 100.0%; Score 22; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22
```

```
RESULT 7
US-09-713-136-10
; Sequence 10, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713,136
```

```
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-10
```

```
Query Match 100.0%; Score 22; DB 28; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22
```

```
RESULT 8
US-09-791-500-3
; Sequence 3, Application US/09791500
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-3
```

```
Query Match 100.0%; Score 22; DB 30; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22
```

```
RESULT 9
US-09-820-484-7
; Sequence 7, Application US/09820484
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
```

; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mODN  
US-09-820-484-7

Query Match 100.0%; Score 22; DB 31; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagagatga 22  
|||||  
DB 1 tgactgtgaaccttagagatga 22

RESULT 10  
PCT-US01-06034-5  
; Sequence 5, Application PC/TUS0106034  
; GENERAL INFORMATION:  
; APPLICANT: Rachmilewitz, Daniel  
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.  
; FILE REFERENCE: 6510-202WO  
; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
PCT-US01-06034-5

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 7.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagagatga 22  
|||||  
DB 1 tgactgtgaaccttagagatga 22

RESULT 11  
PCT-US01-06034-6  
; Sequence 6, Application PC/TUS0106034  
; GENERAL INFORMATION:  
; APPLICANT: Rachmilewitz, Daniel  
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel  
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.  
; FILE REFERENCE: 6510-202WO  
; CURRENT APPLICATION NUMBER: PCT/US01/06034  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polynucleotide sequence  
PCT-US01-06034-6

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 7.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagagatga 22  
|||||  
DB 1 tgactgtgaaccttagagatga 22

RESULT 12  
PCT-US01-10118-2  
; Sequence 2, Application PC/TUS0110118  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Cho, Hearn Jay  
; APPLICANT: Richman, Douglas  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T  
; TITLE OF INVENTION: Lymphocyte Response in vivo.  
; FILE REFERENCE: 06510-188WO1  
; CURRENT APPLICATION NUMBER: PCT/US01/10118  
; CURRENT FILING DATE: 2001-03-17  
; PRIOR APPLICATION NUMBER: US 60/192,537  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/203,567  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/215,895  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutated ODN  
; NAME/KEY: modified\_base  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: disulfide thymine  
PCT-US01-10118-2

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 7.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagagatga 22  
|||||  
DB 1 tgactgtgaaccttagagatga 22

RESULT 13  
PCT-US01-10118-6  
; Sequence 6, Application PC/TUS0110118  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Cho, Hearn Jay  
; APPLICANT: Richman, Douglas  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T  
; TITLE OF INVENTION: Lymphocyte Response in vivo.  
; FILE REFERENCE: 06510-188WO1  
; CURRENT APPLICATION NUMBER: PCT/US01/10118  
; CURRENT FILING DATE: 2001-03-17  
; PRIOR APPLICATION NUMBER: US 60/192,537  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/203,567  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/215,895  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6

; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutated control ODN  
PCT-US01-10118-6

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 7.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaaccttagagatga 22  
||||| ||||| |||||  
Db 1 tgactgtgaaccttagagatga 22

RESULT 14  
PCT-US01-14508-10  
; Sequence 10, Application PC/TUS0114508  
; GENERAL INFORMATION:  
; APPLICANT: Rez, Eyal  
; APPLICANT: Lois, Augusto F.  
; APPLICANT: Takabayashi, Kenji  
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and  
; TITLE OF INVENTION: Methods of Use Thereof  
; FILE REFERENCE: 06510/168W01  
; CURRENT APPLICATION NUMBER: PCT/US01/14508  
; CURRENT FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/262,321  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/202,274  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ISS-ODN  
PCT-US01-14508-10

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 7.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaaccttagagatga 22  
||||| ||||| |||||  
Db 1 tgactgtgaaccttagagatga 22

RESULT 15  
PCT-US01-14508-11  
; Sequence 11, Application PC/TUS0114508  
; GENERAL INFORMATION:  
; APPLICANT: Rez, Eyal  
; APPLICANT: Lois, Augusto F.  
; APPLICANT: Takabayashi, Kenji  
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and  
; TITLE OF INVENTION: Methods of Use Thereof  
; FILE REFERENCE: 06510/168W01  
; CURRENT APPLICATION NUMBER: PCT/US01/14508  
; CURRENT FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/262,321  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/202,274  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 22

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: methylated ISS-ODN  
; NAME/KEY: modified\_base  
; LOCATION: (11)...(11)  
; OTHER INFORMATION: m5C  
PCT-US01-14508-11

Query Match 92.7%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 7.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 tgactgtgaaccttagagatga 22  
||||| ||||| |||||  
Db 1 tgactgtgaaccttagagatga 22

Search completed: October 9, 2001, 21:12:48  
Job time: 20073 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:23 ; Search time 1391.6 Seconds  
(without alignments)  
36.081 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22  
Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 204985 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4093770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2.6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2.6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2.6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2.6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2.6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2.6/ptodata/1/pna/US09\_NEW\_COMB.seq.1
- 7: /cgn2.6/ptodata/1/pna/US09\_NEW\_COMB.seq.2
- 8: /cgn2.6/ptodata/1/pna/US09\_NEW\_COMB.seq.3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	6	US-09-770-943-3
2	22	100.0	22	7	US-09-802-359-4
3	22	100.0	22	7	US-09-802-359-10
4	22	100.0	22	7	US-09-802-376-10
5	20.4	92.7	22	6	US-09-770-943-2
6	20.4	92.7	22	6	US-09-770-943-4
7	18.8	85.5	22	6	US-09-770-943-1
8	18.8	85.5	22	6	US-09-770-943-5
9	18.8	85.5	22	6	US-09-770-943-10
10	18.8	85.5	22	7	US-09-802-518-1
11	18.8	85.5	22	7	US-09-802-518-10
12	18.8	85.5	22	7	US-09-802-359-1
13	18.8	85.5	22	7	US-09-802-359-9
14	18.8	85.5	22	7	US-09-802-376-1
15	18.8	85.5	22	7	US-09-802-376-9
16	18.8	85.5	533	8	US-60-253-652-3007
17	18.4	83.6	22	7	US-09-802-518-8
18	18.4	83.6	22	7	US-09-802-359-8
19	18.4	83.6	22	7	US-09-802-376-8
20	17.8	80.9	22	7	US-09-802-518-7
21	17.8	80.9	22	7	US-09-802-359-7
22	17.8	80.9	22	7	US-09-802-376-7
23	17.8	80.9	352	8	US-60-253-378-36285
24	17.2	78.2	22	7	US-09-802-518-2
25	17.2	78.2	22	7	US-09-802-518-4

Sequence 2, Appl1  
Sequence 4, Appl1  
Sequence 2, Appl1  
Sequence 4, Appl1  
Sequence 31699, A  
Sequence 2488, Ap  
Sequence 2489, Ap  
Sequence 2446, Ap  
Sequence 1, Appl1  
Sequence 2275, Ap  
Sequence 9, Appl1  
Sequence 168, App  
Sequence 427, App  
Sequence 586, App  
Sequence 426, App  
Sequence 500, App  
Sequence 28028, A  
Sequence 47271, A  
Sequence 172, App  
Sequence 702, App

26 17.2 78.2 22 7 US-09-802-359-2  
27 17.2 78.2 22 7 US-09-802-359-4  
28 17.2 78.2 22 7 US-09-802-376-2  
29 17.2 78.2 22 7 US-09-802-376-4  
30 17.2 78.2 445 6 US-09-909-629-31699  
31 17.2 78.2 601 5 US-09-948-933-2488  
32 17.2 78.2 601 5 US-09-948-933-2489  
33 17.2 78.2 2318 1 PCT-US01-08656-2446  
34 17.2 78.2 6909 5 US-09-880-107-2275  
35 17.2 78.2 6909 7 US-09-948-933-9  
36 17.2 78.2 6987 5 US-09-948-933-168  
37 17.2 78.2 76321 5 US-09-948-933-427  
38 17.2 78.2 76338 5 US-09-948-933-586  
39 17.2 78.2 179904 5 US-09-948-933-426  
40 17.2 78.2 179905 5 US-09-948-933-500  
41 17.2 78.2 252 7 US-09-540-213-28028  
42 16.8 76.4 285 7 US-09-540-213-47271  
43 16.8 76.4 43982 6 US-09-803-736-172  
44 16.8 76.4 78172 6 US-09-803-736-702  
45 16.8 78172 6

## ALIGNMENTS

RESULT 1  
US-09-770-943-3  
; Sequence 3, Application US/09770943  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; FILE OF INVENTION: Sequence Activity  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/770,943  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/092,314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-770-943-3

Query Match 100.0%; Score 22; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
|||||  
Db 1 tgactgtgaaccttagagatga 22

## RESULT 2

US-09-802-518-11  
; Sequence 11, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; FILE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10

```
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-518-11

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 3
US-09-802-359-10
; Sequence 10, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-359-10

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 4
US-09-802-376-10
; Sequence 10, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-376-10
```

```
Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 5
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match      92.7%; Score 20.4; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 6
US-09-770-943-4
; Sequence 4, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-4

Query Match      92.7%; Score 20.4; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22
```

Best Local Similarity 95.5%; Pred. No. 0.87;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgaagcttagagatga 22

## RESULT 7

US-09-770-943-1  
; Sequence 1, Application US/09770943  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/770,943  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/092,314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-770-943-1

Query Match 85.5%; Score 18.8; DB 6; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgaagcttagagatga 22

## RESULT 8

US-09-770-943-5  
; Sequence 5, Application US/09770943  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/770,943  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/092,314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-770-943-5

Query Match 85.5%; Score 18.8; DB 6; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgtcccttagagatga 22

## RESULT 9

US-09-770-943-10  
; Sequence 10, Application US/09770943  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/770,943  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/092,314  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-770-943-10

Query Match 85.5%; Score 18.8; DB 6; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgaatgttagagatga 22

## RESULT 10

US-09-802-518-1  
; Sequence 1, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-518-1

Query Match 85.5%; Score 18.8; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgaagcttagagatga 22

RESULT 11  
US-09-802-518-10  
; Sequence 10, Application US/09802518  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF  
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCES  
; FILE REFERENCE: 377882001100  
; CURRENT APPLICATION NUMBER: US/09/802,518  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,556  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide not containing CG  
US-09-802-518-10

Query Match 85.5%; Score 18.8; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgaaggttagagatga 22

RESULT 12  
US-09-802-359-1  
; Sequence 1, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400  
; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-359-1

Query Match 85.5%; Score 18.8; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13  
US-09-802-359-9  
; Sequence 9, Application US/09802359  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201400

; CURRENT APPLICATION NUMBER: US/09/802,359  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,303  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide not containing CG  
US-09-802-359-9

Query Match 85.5%; Score 18.8; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgaaggttagagatga 22

RESULT 14  
US-09-802-376-1  
; Sequence 1, Application US/09802376  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201700  
; CURRENT APPLICATION NUMBER: US/09/802,376  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,557  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-376-1

Query Match 85.5%; Score 18.8; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22  
||||||| |||||||  
Db 1 tgactgtgaacgttcgagatga 22

RESULT 15  
US-09-802-376-9  
; Sequence 9, Application US/09802376  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201700  
; CURRENT APPLICATION NUMBER: US/09/802,376  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,557  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 22  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide not containing CG  
US-09-802-376-9

Query Match 85.5%; Score 18.8; DB 7; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.6;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
|||||  
Db 1 tgactgtgaaggtagagatga 22  
|||||

Search completed: October 9, 2001, 21:36:24  
Job time: 21244 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:11 ; Search time 217.64 Seconds  
(without alignments)  
19.136 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22  
Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.NA.\*

1: /cgn2\_6/ptodata/1/lna/5A-COMB.seq.\*  
2: /cgn2\_6/ptodata/1/lna/5B-COMB.seq.\*  
3: /cgn2\_6/ptodata/1/lna/5A-COMB.seq.\*  
4: /cgn2\_6/ptodata/1/lna/6B-COMB.seq.\*  
5: /cgn2\_6/ptodata/1/lna/PCTUS-COMB.seq.\*  
6: /cgn2\_6/ptodata/1/lna/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	4 US-09-092-314-3	Sequence 3, Appli
2	20.4	92.7	22	4 US-09-092-314-2	Sequence 2, Appli
3	20.4	92.7	22	4 US-09-092-314-4	Sequence 4, Appli
4	18.8	85.5	22	4 US-09-092-314-1	Sequence 1, Appli
5	18.8	85.5	22	4 US-09-092-314-5	Sequence 5, Appli
6	18.8	85.5	22	4 US-09-092-314-10	Sequence 10, Appli
7	17.2	78.2	6909	2 US-08-804-196-1	Sequence 1, Appli
8	17.2	78.2	6909	2 US-08-558-340-1	Sequence 1, Appli
9	17.2	78.2	6909	3 US-08-746-111-26	Sequence 26, Appli
10	16.2	73.6	913	2 US-08-975-316-61	Sequence 61, Appli
11	15.8	71.8	2088	1 US-08-331-394-1	Sequence 1, Appli
12	15.8	71.8	2088	1 US-08-250-858-1	Sequence 1, Appli
13	15.8	71.8	2088	1 US-08-446-915-1	Sequence 1, Appli
14	15.8	71.8	2088	2 US-08-744-139-1	Sequence 1, Appli
15	15.8	71.8	2088	5 PCR-US95-06639-1	Sequence 1, Appli
16	15.6	70.9	22	4 US-09-092-314-7	Sequence 7, Appli
17	15.6	70.9	22	4 US-09-092-314-8	Sequence 8, Appli
18	15.6	70.9	1653	1 US-08-218-026-3	Sequence 3, Appli
19	15.6	70.9	1653	2 US-08-653-632-3	Sequence 3, Appli
20	15.6	70.9	1813	1 US-08-030-644-1	Sequence 1, Appli
21	15.6	70.9	1813	1 US-08-013-801-1	Sequence 1, Appli
22	15.6	70.9	1813	1 US-08-072-063-1	Sequence 1, Appli
23	15.6	70.9	1813	1 US-08-212-132-1	Sequence 1, Appli
24	15.6	70.9	1813	1 US-08-414-924-1	Sequence 1, Appli
25	15.6	70.9	1813	1 US-08-311-611A-145	Sequence 145, App
26	15.6	70.9	1813	1 US-08-232-527-1	Sequence 1, Appli
27	15.6	70.9	1813	1 US-08-372-783-145	Sequence 145, App

#### ALIGNMENTS

##### RESULT 1

US-09-092-314-3  
; Sequence 3, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-092-314-3

Query Match 100.0%; Score 22; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22  
Db 1 tgactgtgaaccttagagatga 22  
|||||

##### RESULT 2

US-09-092-314-2  
; Sequence 2, Application US/09092314  
; Patent No. 6225292  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Roman, Mark  
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory  
; TITLE OF INVENTION: Sequence Activity  
; Patent No. 6225292  
; FILE REFERENCE: 6510-173US1  
; CURRENT APPLICATION NUMBER: US/09/092,314  
; CURRENT FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/048,794  
; PRIOR FILING DATE: 1997-06-06

Sequence 145, App  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 145, App  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 11, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 14, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 264, App

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match      92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.084;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgcttagagatga 22

RESULT 3
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.084;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgcttagagatga 22

RESULT 4
US-09-092-314-1
; Sequence 1, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1.

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

Query Match      85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.52;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaaggcttagagatga 22

RESULT 5
US-09-092-314-5
; Sequence 5, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-5

Query Match      85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.52;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgttccttagagatga 22

RESULT 6
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

FEATURE:  
OTHER INFORMATION: Oligonucleotide  
US-09-092-314-10

Query Match 85.5%; Score 18.8; DB 4; Length 22;  
Best Local Similarity 90.9%; Pred. No. 0.52; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccccttagagatga 22  
Db 1 tgactgtgaatgttagagatga 22

RESULT 7  
US-08-804-196-1/c  
Sequence 1, Application US/08804196  
Patent No. 5874256  
GENERAL INFORMATION:  
APPLICANT: Bertina, Rogier  
TITLE OF INVENTION: A method for diagnosing an increased risk of thrombosis or a genetic defect causing thrombosis and kit for use with the same.  
TITLE OF INVENTION: risk for thrombosis or a genetic defect causing thrombosis and kit for use with the same.  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Akzo No. 5874256el Patent Department  
STREET: 1300 Piccard Drive, Suite 206  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/804,196  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/454,353  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gormley, Mary E.  
REGISTRATION NUMBER: 34,409  
TELEPHONE: (301) 948-7400  
TELEFAX: (301) 948-9751  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6909 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
US-08-804-196-1

Query Match 78.2%; Score 17.2; DB 2; Length 6909;  
Best Local Similarity 86.4%; Pred. No. 6.8; Indels 3; Gaps 0;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccccttagagatga 22  
Db 793 TGACTGTGTACATTAGGGATGA 772

RESULT 8  
US-08-658-340-1/c  
Sequence 1, Application US/08658340  
Patent No. 5910576  
CURRENT APPLICATION DATA:

GENERAL INFORMATION:  
APPLICANT: Bertina, Rogier  
TITLE OF INVENTION: A method for diagnosing an increased risk of thrombosis or a genetic defect causing thrombosis and kit for use with the same.  
TITLE OF INVENTION: risk for thrombosis or a genetic defect causing thrombosis and kit for use with the same.  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Akzo No. 5910576 5861489el Patent Department  
STREET: 1300 Piccard Drive, Suite 206  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,340  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/454,353  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gormley, Mary E.  
REGISTRATION NUMBER: 34,409  
TELEPHONE: (301) 948-7400  
TELEFAX: (301) 948-9751  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6909 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
US-08-658-340-1

Query Match 78.2%; Score 17.2; DB 2; Length 6909;  
Best Local Similarity 86.4%; Pred. No. 6.8; Indels 3; Gaps 0;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccccttagagatga 22

Db 793 TGACTGTGTACATTAGGGATGA 772

RESULT 9  
US-08-746-111-26/c  
Sequence 26, Application US/08746111  
Patent No. 6066778  
GENERAL INFORMATION:  
APPLICANT: Ginsburg, David  
TITLE OF INVENTION: Compositions And Methods For Screening Compounds For Anticoagulant Activity  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/746.111  
FILING DATE: 06-NOV-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: UM-02536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6909 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-746-111-26

Query Match 78.2%; Score 17.2; DB 3; Length 6909;  
Best Local Similarity 86.4%; Pred. No. 6.8;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22  
||||||| ||||| |||||  
Db 793 TGACTGTGTACATTAGGATGA 772

## RESULT 10

US-08-975-316-61  
Sequence 61, Application US/08975316  
Patent No. 5952486  
GENERAL INFORMATION:  
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka  
APPLICANT: and GRIERSON, Alastair W.  
TITLE OF INVENTION: MATERIALS AND METHODS FOR  
THE MODIFICATION OF PLANT LIGNIN CONTENT  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,316  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/713,000  
FILING DATE: September 11, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: SLEATH, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000/1003C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 913 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-975-316-61

Query Match 73.6%; Score 16.2; DB 2; Length 913;  
Best Local Similarity 85.7%; Pred. No. 17;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaaccttagagatga 22  
||||||| ||||| |||||  
Db 513 GACTGTGAATTTTACAGATGA 533

## RESULT 11

US-08-331-394-1  
Sequence 1, Application US/08331394  
Patent No. 5670319  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Rothe, Mike  
TITLE OF INVENTION: Tumor Necrosis Factor  
RECEPTOR-ASSOCIATED FACTORS  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,394  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/250858  
FILING DATE: 27-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: 897P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3216  
TELEFAX: 415/952-9861  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2088 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-331-394-1

Query Match 71.8%; Score 15.8; DB 1; Length 2088;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ctgtgaaccttagagatga 22  
||||||| ||||| |||||  
Db 336 CTGAGAACTGAGATGA 354

## RESULT 12

US-08-250-858-1  
Sequence 1, Application US/08250858  
Patent No. 5708142  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Rothe, Mike

```

; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,858
; FILING DATE: 27-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-250-858-1

Query Match 71.8%; Score 15.8; DB 1; Length 2088;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatga 22
   ||| ||||| |||||
DB 336 CTGAGAACTGAGAGATGA 354

RESULT 14
US-08-744-139-1
; Sequence 1, Application US/08744139
; Patent No. 5869612
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,139
; FILING DATE: 31-Oct-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 05/27/1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-446-915-1

Query Match 71.8%; Score 15.8; DB 1; Length 2088;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatga 22
   ||| ||||| |||||
DB 336 CTGAGAACTGAGAGATGA 354

RESULT 13
US-08-446-915-1
; Sequence 1, Application US/08446915
; Patent No. 5741667
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,915
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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US-08-744-139-1

Query Match 71.8%; Score 15.8; DB 2; Length 2088;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatga 22  
||| ||||| |||||  
Db 336 CTGAGAACCTGAGAGATGA 354

## RESULT 15

PCT-US95-06639-1  
; Sequence 1, Application PC/TUS9506639  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/06639  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/250858  
; FILING DATE: 27-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/331394  
; FILING DATE: 28-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: 897P2PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-3216  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2088 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; PCT-US95-06639-1

Query Match 71.8%; Score 15.8; DB 5; Length 2088;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatga 22  
||| ||||| |||||  
Db 336 CTGAGAACCTGAGAGATGA 354

Search completed: October 9, 2001, 15:42:12  
Job time: 302 sec